

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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(without alignments)
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ALLEGMENTS

Application US/09616289

NOTES.

3, Ann M.

as, Robert S.

W, Simon W.

TON: NOVEL LOW

TION: NOVEL LOW
TION: PROTEINS

TION: ATHEROSCL

: 10797-004001

ATION NUMBER: U

DATE: 2000-07-11
 ION NUMBER: 115

DATE: 2000-03-02

ION NUMBER: US

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; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
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RESULT 2

US-08-979-608A-7

; Sequence 7, Application US/08979608A

; Patent No. 6355451
GENERAL INFORMATION

GENERAL INFORMATION:
APPLICANT: Lees

Lees, Robert

Law, Simon W.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL TO
BINDING

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Wildlife Service, 2025 Franklin

STREET: 223 FLANK
CITY: Boston

STATE: MA

COUNTRY: USA

11:33:39 2004

us-09-976-740-43.olig.ra1

02110-2804
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TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
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G DATE: 03-JUN-1997
G DATE: 26-NOV-1997
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
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AX: 617/542-8906
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YPE: protein
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ITION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
IT: 225 Franklin Street
Boston
3: MA
TRY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
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APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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TOPOLOGY: linear
MOLECULE TYPE: protein
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Db 181 LTGLSIRLGPALKIYEHKIVLQGHFEDDDPDGFLG 217
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US-09-616-289-7
Sequence 7, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 217

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lication US/09616289
23
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, Ann M.
, Robert S.
, Simon W.
ona, Anibal A.
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ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001
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DATE: 2000-07-14
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TE: 2000-03-02
ON NUMBER: US 08/379,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
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ON NUMBER: US 60/048,547
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lication US/08979608A
151

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-979-608A-3
Query Match 14.1%; Score 76; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.1e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0;
QY 458 DPVWTVMDVVEYFTAGFPEQATAFQOEIDGKSLLMQRTDVLTLGLRGPAL
DB 152 DPVWTVMDVVEYFTAGFPEQATAFQOEIDGKSLLMQRTDVLTLGLRGPAL
QY 518 HHKVLQOQHFEEDDDP 533
DB 212 HHKVLQOQHFEEDDDP 227
RESULT 7
US-09-517-849-3
Sequence 3, Application US/09517849
Patent No. 6605588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

225 Franklin Street
Boston
MA
USA
02110-2804
ADABLE FORM:
4 TYPE: Diskette
TER: IBM Compatible
ING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
ATION NUMBER: US/09/517,849
3 DATE: 02-Mar-2000
ICATION DATA:
ATION NUMBER: 08/979,608
3 DATE: 26-NOV-1997
ENT INFORMATION:
Myers, Louis
RATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-003001
ICATION INFORMATION:
ONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 3:
HARACTERISTICS:
3: 232 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 3:

14.1%; Score 76; DB 4; Length 232;
rity 100.0%; Pred.No. 4.1e-58;
aservative 0; Mismatches 0; Indels 0; Gaps 0;

IVMDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
IVMDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211
LQOQHFEEDDP 533
LQOQHFEEDDP 227

cation US/09616289
3
ON:
Ann M.
Robert S.
Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS
10797-004001
ION NUMBER: US/09/616,289
ATE: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

ORGANISM: Oryctolagus cuniculus
US-09-616-289-3

Query Match 14.1%; Score 76; DB 4; Length 232;
Best Local Similarity 100.0%; Pred.No. 4.1e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK
DB 152 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK
QY 518 HHKVLQOQHFEEDDP 533
DB 212 HHKVLQOQHFEEDDP 227

RESULT 9
US-08-979-608A-4
; Sequence 4, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOS
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-979-608A-4

Query Match 14.1%; Score 76; DB 4; Length 252;
Best Local Similarity 100.0%; Pred.No. 4.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK
DB 172 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALK

VQQGHFEDDDP 533
|||||
VQQGHFEDDDP 247

ication US/09517849

88

ATION:

: Lees, Ann M.

: Lees, Robert S.

: Law, Simon W.

: Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

ESSEE: Fish & Richardson P.C.

ET: 225 Franklin Street

: Boston

E: MA

TRY: USA

02110-2804

READABLE FORM:

UM TYPE: Diskette

UTER: IBM Compatible

ATING SYSTEM: DOS

WARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/517,849

NG DATE: 02-Mar-2000

LICATION DATA:

ICATION NUMBER: 08/979,608

NG DATE: 26-NOV-1997

AGENT INFORMATION:

: Myers, Louis

STRATION NUMBER: 35,965

RENCE/DOCKET NUMBER: 10797-003001

UNICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

R SEQ ID NO: 4:

CHARACTERISTICS:

TH: 252 amino acids

: amino acid

LOGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 4:

14.1%; Score 76; DB 4; Length 252;

arity 100.0%; Pred. No. 4.5e-58;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

WTWMDVVEYFTEAGFPEQATFQEQIDGKSLLMQRTDVLTLGSLRGLPALKIYE 517

WTWMDVVEYFTEAGFPEQATFQEQIDGKSLLMQRTDVLTLGSLRGLPALKIYE 231

VQQGHFEDDDP 533

|||||

VQQGHFEDDDP 247

ication US/09616289

123

ION:

: Ann M.

: Robert S.

: Simon W.

; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/616,289

; CURRENT FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-616-289-4

Query Match 14.1%; Score 76; DB 4; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.5e-58;

Matches 76; Conservative 0; Mismatches 0; Indels 0; C

QY 458 DPVETWMDVVEYFTEAGFPEQATFQEQIDGKSLLMQRTDVLTLGSLRGLPALKI

Db 172 DPVETWMDVVEYFTEAGFPEQATFQEQIDGKSLLMQRTDVLTLGSLRGLPALKI

QY 518 HHKVLQGHFEDDDP 533

|||||

Db 232 HHKVLQGHFEDDDP 247

RESULT 12

US-08-979-608A-2

; Sequence 2, Application US/08979608A

; Patent No. 6355451

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGN

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-No. 6355451-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/596

ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 2:
HARACTERISTICS:
H: 317 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 2:

14.1%; Score 76; DB 4; Length 317;
rity 100.0%; Pred. No. 5.5e-58;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
TVMDVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
TVMDVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 296
LQGHFEDDDP 533
LQGHFEDDDP 312

cation US/09517849
8

TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA

RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
CATION NUMBER: US/09/517,849
G DATE: 02-Mar-2000
ICATION DATA:
CATION NUMBER: 08/979,608
G DATE: 26-NOV-1997
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-003001
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 2:
HARACTERISTICS:
H: 317 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 2:

14.1%; Score 76; DB 4; Length 317;

Best Local Similarity 100.0%; Pred. No. 5.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G:
QY 458 DPVEWTVMVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEWTVMVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
Db 297 HHKVLQGHFEDDDP 312

RESULT 14
US-09-616-289-2
; Sequence 2, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT:
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(317)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-616-289-2

Query Match 14.1%; Score 76; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.5e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G:
QY 458 DPVEWTVMVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEWTVMVVEYFTAGPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
Db 297 HHKVLQGHFEDDDP 312

RESULT 15
US-08-979-608A-20
; Sequence 20, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOE
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-517-849-20

Query Match 4.8%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDEDEEDDVSSEGVPESD 354
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EEEEDDEDEEDDVSSEGVPESD 26

RESULT 17
US-09-616-289-20
; Sequence 20, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-616-289-20

Query Match 4.8%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDEDEEDDVSSEGVPESD 354
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EEEEDDEDEEDDVSSEGVPESD 26

RESULT 18
US-08-979-608A-19
; Sequence 19, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:

```

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
ING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
CATION NUMBER: US/08/979,608A
3 DATE: 26-NOV-1997
ICATION DATA:
CATION NUMBER: US 60/048,547
3 DATE: 03-JUN-1997
CATION NUMBER: US 60/031,930
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 19:
HARACTERISTICS:
H: 15 amino acids
amino acid
YPE: linear
OGY: protein
ESCRPTION: SEQ ID NO: 19:
2.8%; Score 15; DB 4; Length 15;
rity 100.0%; Pred. No. 3.3e-06;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDD 343
| | | | | | | | | |
DDEDEDD 15
ication US/09517849
8
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-517-849-19
Query Match 2.8%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 329 EEEEDDEDEDD 343
| | | | | | | | | |
DB 1 EEEEDDEDEDD 15
RESULT 20
US-09-616-289-19
; Sequence 19, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-616-289-19
Query Match 2.8%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 329 EEEEDDEDEDD 343
| | | | | | | | | |

DDDEDEDD 15

Location US/08979608A

31

ATION:

: Lees, Ann M.

: Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

SSEE: Fish & Richardson P.C.

ET: 225 Franklin Street

: Boston

3: MA

CRY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/08/979,608A

IG DATE: 26-Nov-1997

ICATION DATA:

ICATION NUMBER: US 60/048,547

IG DATE: 03-JUN-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

ISTRATION NUMBER: 35,965

ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

: SEQ ID NO: 21:

CHARACTERISTICS:

H: 11 amino acids

amino acid

OGY: linear

YPE: protein

DESCRIPTION: SEQ ID NO: 21:

2.0%; Score 11; DB 4; Length 11;

urity 100.0%; Pred. No. 0.0074;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354

|||||

EVPSD 11

Location US/09517849

38

ATION:

: Lees, Ann M.

: Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

2.0%; Score 11; DB 4; Length 11;
city 100.0%; Pred. No. 0.0074;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354
|||||
EVPSD 11

ication US/08979608A

ION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
VENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
R: 225 Franklin Street
Boston
MA

RY: USA
2110-2804
ADABLE FORM:
4 TYPE: Diskette
TER: IBM Compatible
ING SYSTEM: DOS
ARE: FastSEQ for Windows Version 2.0
PLICATION DATA:
ATION NUMBER: US/08/979,608A
3 DATE: 26-NOV-1997
ICATION DATA:
ATION NUMBER: US 60/048,547
3 DATE: 03-JUN-1997
ATION NUMBER: US 60/031,930
3 DATE: 27-NOV-1996
ENT INFORMATION:
MYERS, LOUIS

ATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 27;
HARACTERISTICS:
d: 12 amino acids
amino acid
OGY: linear
YPE: protein
SCRIPTION: SEQ ID NO: 27;

2.0%; Score 11; DB 4; Length 12;
city 100.0%; Pred. No. 0.008;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354
|||||
EVPSD 12

ication US/09517849

GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOS
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-517-849-27

Query Match 2.0%; Score 11; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 VSEGSEVPESD 354
|||||
DB 2 VSEGSEVPESD 12

RESULT 26
US-09-616-289-27
Sequence 27, Application US/09616289
Patent No. 6632923
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27

ON NUMBER: US 60/048,547
IE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

2.0%; Score 11; DB 4; Length 12;
arity 100.0%; Pred.No. 0.008;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 12

lication US/08979608A
51

ATION:

: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

ESSEE: Fish & Richardson P.C.
ST: 225 Franklin Street
: Boston

E: MA

TRY: USA

02110-2804

READABLE FORM:

UM TYPE: Diskette

UTER: IBM Compatible

ATING SYSTEM: DOS

WARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/08/979,608A

NG DATE: 26-NO. 6355451-1997

LICATION DATA:

ICATION NUMBER: US 60/048,547

NG DATE: 03-JUN-1997

ICATION NUMBER: US 60/031,930

NG DATE: 27-NOV-1996

AGENT INFORMATION:

: Myers, Louis

STRATION NUMBER: 35,965

RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

R SEQ ID NO: 26:

CHARACTERISTICS:

TH: 28 amino acids

: amino acid

LOGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 26:

2.0%; Score 11; DB 4; Length 28;
arity 100.0%; Pred.No. 0.017;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354

Db 18 VSEGEVPSD 28
|||||||

RESULT 28

US-09-517-849-26

; Sequence 26, Application US/09517849

; Patent No. 6605588

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGN
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/517,849

; FILING DATE: 02-Mar-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608

; FILING DATE: 26-NOV-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-003001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-517-849-26

Query Match 2.0%; Score 11; DB 4; Length 28;
Best Local Similarity 100.0%; Pred.No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

Qy 344 VSEGEVPSD 354

|||||||

Db 18 VSEGEVPSD 28

RESULT 29

US-09-616-289-26

; Sequence 26, Application US/09616289

; Patent No. 6632923

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

ION NUMBER: US/09/616,289
ATE: 2000-07-14
Y NUMBER: US 09/517,849
Z: 2000-03-02
X NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
S: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

olagus cuniculus

2.0%; Score 11; DB 4; Length 28;
rity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
3VPESD 354
|||||
3VPESD 28

ication US/09135994A

3
DN:
et al.
DN: SCA7 GENE AND METHODS OF USE
University of Minnesota
ION NUMBER: US/09/135,994A
ATE: 1998-08-18
ION NUMBER: 60/056,170
ATE: 1997-08-19
NOS: 14
In Ver. 2.0

sapiens

2.0%; Score 11; DB 3; Length 129;
city 100.0%; Pred. No. 0.07; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
2PPQPQ 232
|||||
2PPQPQ 44

.cation US/09684843A

3
DN:
et al.
DN: SCA7 GENE AND METHODS OF USE
regence of the University of Minnesota
ION NUMBER: US/09/684,843A
ATE: 2000-10-06
X NUMBER: 60/056,170
Z: 1997-08-19
Y NUMBER: 09/135,994
S: 1998-08-18
NOS: 14
In Ver. 2.0

LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-09-684-843A-12

Query Match 2.0%; Score 11; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 222 QQQPPPPPPQ 232
|||||
Db 34 QQQPPPPPPQ 44
|||||

RESULT 32

US-08-979-608A-22
; Sequence 22, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOSIS
; TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-Nov-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-979-608A-22

Query Match 1.9%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 529 EDDDPDGFLG 538
|||||
Db 1 EDDDPDGFLG 10
|||||

RESULT 33

lication US/08979608A
31
ATION:
: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
DENCE ADDRESS:
ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street
: Boston
3: MA
TRY: USA
02110-2804
READABLE FORM:
JM TYPE: Diskette
JTER: IBM Compatible
ATING SYSTEM: DOS
WARE: FastSEQ for Windows Version 2.0
PLICATION DATA:
ICATION NUMBER: US/08/979,608A
NG DATE: 26-NOV-1997
ICATION DATA:
ICATION NUMBER: US 60/048,547
NG DATE: 03-JUN-1997
ICATION NUMBER: US 60/031,930
NG DATE: 27-NOV-1996
AGENT INFORMATION:
: Myers, Louis
ISTRATION NUMBER: 35,965
RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
PHONE: 617/542-5070
FAX: 617/542-8906
R SEQ ID NO: 28
CHARACTERISTICS:
TH: 10 amino acids
: amino acid
LOGR: linear
TYPE: protein
DESCRIPTION: SEQ ID NO: 28:

1.9%; Score 10; DB 4; Length 10;
arity 100.0%; Pred. No. 0.05;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441
|||||
PALPGA 10

lication US/09517849
38
ATION:
: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
DENCE ADDRESS:
ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-517-849-22

Query Match 1.9%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 529 EDDPDGFLG 538
Db 1 EDDPDGFLG 10

RESULT 35
US-09-517-849-28
; Sequence 28, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNO
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,849
; FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis

INATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-003001

ICATION INFORMATION:

HONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 28:

HARACTERISTICS:

H: 10 amino acids

amino acid

OGY: linear

YPE: protein

ESCRPTION: SEQ ID NO: 28:

1.9%; Score 10; DB 4; Length 10;

ity 100.0%; Pred. No. 0.05;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

ALPGA 441

|||||

ALPGA 10

ication US/09616289

3

ON:

Ann M.

, Robert S.

, Simon W.

na, Anibal A.

ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ON: ATHEROSCLEROSIS

10797-004001

ION NUMBER: US/09/616,289

ATE: 2000-07-14

N NUMBER: US 09/517,849

E: 2000-03-02

N NUMBER: US 08/979,608

E: 1997-11-26

N NUMBER: US 60/031,930

E: 1996-11-27

N NUMBER: US 60/048,547

E: 1997-06-03

NOS: 53

Q for Windows Version 4.0

sapiens

1.9%; Score 10; DB 4; Length 10;

ity 100.0%; Pred. No. 0.05;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

DGFLG 538

|||||

DGFLG 10

ication US/09616289

3

ON:

Ann M.

, Robert S.

, Simon W.

na, Anibal A.

ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

; FILE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/616,289

; CURRENT FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-616-289-28

Query Match

Best Local Similarity 1.9%; Score 10; DB 4; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 432 PPGKPALPGA 441

|||||

Db 1 PPGKPALPGA 10

RESULT 38

US-09-489-039A-8583

; Sequence 8583, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8583

; LENGTH: 126

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8583

Query Match

Best Local Similarity 1.9%; Score 10; DB 4; Length 126;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 118 APAAAAAAP 127

|||||

Db 92 APAAAAAAP 101

RESULT 39

US-09-328-352-7651

; Sequence 7651, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T

; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 7651

; LENGTH: 254

stobacter baumannii

1.9%; Score 10; DB 4; Length 254;
arity 100.0%; Pred. No. 0.96;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 146
|||||
AAAAA 157

3
36
Application US/09489039A

ION:

/ Breton et. al
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
ION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

2709.2004001

ION NUMBER: US/09/489.039A

DATE: 2000-01-27

ION NUMBER: US 60/117,747

CE: 1999-01-29

) NOS: 14342

siella pneumoniae

1.9%; Score 10; DB 4; Length 324;
arity 100.0%; Pred. No. 1.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127
|||||
AAAAA 266

cation US/09056226B

4

ION:

anti, Joseph J.
resan, Venkatesan
ION: Control of Floral Induction in Plants
ON: and Uses Therefor

CSHL94-04A4

ION NUMBER: US/09/056,226B

ATE: 1998-04-07

ION NUMBER: US 09/000,640

ATE: 1997-12-30

ION NUMBER: US 08/804,104

ATE: 1997-02-20

ION NUMBER: PCT/US96/03466

ATE: 1996-03-15

ION NUMBER: US 08/406,186

ATE: 1995-03-16

) NOS: 20

QX for Windows Version 3.0

ays

1.9%; Score 10; DB 3; Length 436;
arity 100.0%; Pred. No. 1.6;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 PLPPPPPPA 219
Db 45 PLPPPPPPA 54

RESULT 42

US-08-938-291A-9

; Sequence 9, Application US/08938291A

; Patent No. 6117673

; GENERAL INFORMATION:

; APPLICANT: Lev, Sima

; APPLICANT: Plowman, Gregory D.

; APPLICANT: Schlessinger, Joseph

; TITLE OF INVENTION: RDGB PROTEINS AND RELATED

; TITLE OF INVENTION: PRODUCTS AND METHODS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 60/027,337

; FILING DATE: October 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 228/172

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1250 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-938-291A-9

Query Match 1.9%; Score 10; DB 3; Length 1250;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 EEEEDDEDE 338

Db 324 EEEEDDEDE 333

RESULT 43

US-09-589-619-9

; Sequence 9, Application US/09589619

; Patent No. 6576442

; GENERAL INFORMATION:

; APPLICANT: Lev, Sima

; APPLICANT: Plowman, Gregory D.

; APPLICANT: Schlessinger, Joseph

; TITLE OF INVENTION: RDGB PROTEINS AND RELATED

PRODUCTS AND METHODS

SEQUENCES: 11
SOURCE ADDRESS:
SSEE: Lyon & Lyon
: 633 West Fifth Street
Suite 4700
Los Angeles
California
RY: U.S.A.
0071-2066
ADABLE FORM:
1 TYPE: 3.5" Diskette, 1.44 Mb
TER: IBM Compatible
TING SYSTEM: IBM P.C. DOS 5.0
ARE: FastSeq
PLICATION DATA:
ATION NUMBER: US/09/589,619
DATE: 07-Jun-2000
ICATION: <Unknown>
ICATION DATA:
ATION NUMBER: US/08/938,291
DATE: September 26, 1997
ATION NUMBER: 60/027,337
DATE: October 11, 1996
ENT INFORMATION:
Warburg, Richard J.
ATION NUMBER: 32,327
ENCE/DOCKET NUMBER: 228/172
ATION INFORMATION:
ONE: (213) 489-1600
X: (213) 955-0440
: 67-3510
SEQ ID NO: 9:
HARACTERISTICS:
I: 1250 amino acids
amino acid
EDNESS: single
XY: linear
PE: peptide
SCRIPTION: SEQ ID NO: 9:

1.9%; Score 10; DB 4; Length 1250;
ity 100.0%; Pred.No. 4.1;
servative 0; Mismatches 0; Indels 0; Gaps 0;
DEDE 338
|||
DEDE 333

OBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
RON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
A C.; DANFORTH, HARRY D.
ION: GENETICALLY ENGINEERED COCCIDIOSIS
ANTIGEN, AC-6B
NCES: 11
ATION DATA:
NUMBER: US/07/581,693
12-SEP-1990
ON DATA:
NUMBER: 215,162
05-JUL-1988
NUMBER: 746,520
19-JUN-1985
NUMBER: 627,811
05-JUL-1984

5273901-11

Query Match 1.7%; Score 9; DB 6; Length 76;
Best Local Similarity 100.0%; Pred.No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AAAAAAAAAA 126
Db 23 AAAAAAAAAA 31

RESULT 45
5482709-10
; Patent No. 5482709
; APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
; SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
; TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
; ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,432
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 581,693
; FILING DATE: 12-SEP-1990
; APPLICATION NUMBER: 215,162
; FILING DATE: 05-JUL-1989
; APPLICATION NUMBER: 746,520
; FILING DATE: 19-JUN-1985
; APPLICATION NUMBER: 627,811
; FILING DATE: 05-JUL-1984
; SEQ ID NO: 10:
; LENGTH: 76
5482709-10

Query Match 1.7%; Score 9; DB 6; Length 76;
Best Local Similarity 100.0%; Pred.No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AAAAAAAAAA 126
Db 23 AAAAAAAAAA 31

RESULT 46
US-09-314-268-133
; Sequence 133, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAP
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/314,268
; EARLIER FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus type 20
US-09-314-268-133

Query Match 1.7%; Score 9; DB 4; Length 99;
Best Local Similarity 100.0%; Pred.No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 FLPPPPQPP 218
Db 69 FLPPPPQPP 77

43 Application US/09252991A
95
ION:
C J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

monas aeruginosa
43

1.7%; Score 9; DB 4; Length 145;
arity 100.0%; Pred. No. 4.2; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PARAP 149
|||||
PARAP 10

30 Application US/09252991A
95
ION:
C J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

monas aeruginosa
30

1.7%; Score 9; DB 4; Length 180;
arity 100.0%; Pred. No. 5.2; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PARAP 149
|||||
PARAP 116

1
CORSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
ARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
IA C.; DANFORTH, HARRY D.
ATION: GENETICALLY ENGINEERED COCCIDIOSIS
3 ANTIGEN, AC-6B
JENCES: 11

43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/581,693
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO: 7;
LENGTH: 180
5273901-7

Query Match 1.7%; Score 9; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 AAAAAAAAAA 126
Db 73 AAAAAAAAAA 81

RESULT 50
5482709-6
Patent No. 5482709
APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;
AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO: 6;
LENGTH: 180
5482709-6

Query Match 1.7%; Score 9; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 AAAAAAAAAA 126
Db 73 AAAAAAAAAA 81

RESULT 51
US-09-702-705-1816
Sequence 1816, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF LUNG CANCER

210121.478C14
ION NUMBER: US/09/702,705
ATE: 2000-10-30
NOS: 1833
EQ for Windows Version 3.0

sapiens

1.7%; Score 9; DB 4; Length 325;
city 100.0%; Pred. No. 8.9;
iservative 0; Mismatches 0; Indels 0; Gaps 0;

APPP 129
|||||
APPP 72

Application US/09736457

3
DN:
Tongtong
Mr. Chaitanya S.
Mr. Michael A.
Mr. Gary
Mr. Tom
Mr. Darrick
Mr. Marc
Mr. Jane
Mr. Liqun
Mr. Aijun

DN: COMPOSITIONS AND METHODS FOR THE THERAPY AND

DN: DIAGNOSIS OF LUNG CANCER

210121.478C15
ION NUMBER: US/09/736,457
ATE: 2000-12-13
NOS: 1864
EQ for Windows Version 3.0

sapiens

1.7%; Score 9; DB 4; Length 325;
city 100.0%; Pred. No. 8.9;
iservative 0; Mismatches 0; Indels 0; Gaps 0;

APPP 129
|||||
APPP 72

Application US/09671325

DN:
Tongtong
Mr. Chaitanya S.
Mr. Michael A.
Mr. Gary
Mr. Tom
Mr. Darrick
Mr. Marc
Mr. Jane
Mr. Liqun

DN: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DN: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-671-325-1816

Query Match 1.7%; Score 9; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AAAAAAAPP 129
|||||
DB 64 AAAAAAAPP 72

RESULT 54

US-09-252-991A-28443
Sequence 28443, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TO THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28443
LENGTH: 333
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28443

Query Match 1.7%; Score 9; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 PPAGPRRAP 200
|||||
DB 103 PPAGPRRAP 111

RESULT 55

US-08-710-249-4
Sequence 4, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
  NUMBER: US/08/710,249
  : 13-SEP-1996
  ION: 536
  ION DATA:
    NUMBER: US 08/583,808
    : 05-JAN-1996
  ION DATA:
    NUMBER: US 60/003,492
    : 08-SEP-1995
  I INFORMATION:
    ella, John R.
  N NUMBER: 32,944
  CCKET NUMBER: 015389-001220US
  TION INFORMATION:
    (415) 576-0200
    415) 576-0300
  SEQ ID NO: 4:
  ATERISTICS:
    4 amino acids
    c acid
    linear
    : protein

    1.7%; Score 9; DB 2; Length 434;
    arity 100.0%; Pred. No. 12;
    nservative 0; Mismatches 0; Indels 0; Gaps 0;

    AAAAA 126
    |||||
    AAAAA 352

    ication US/09220157A
    10
    illepointeau, Bryant
    eng, Junli
    adrews, William H.
    dams, Robert R.
    NTION: Methods and Reagents for Regulating
    NTION: Telomere Length and Telomerase Activity
    UENCES: 26
    E ADDRESS:
    Townsend and Townsend and Crew LLP
    c Embarcadero Center, Eighth Floor
    Francisco
    ifornia
    SA
    -3834
    ABLE FORM:
    : Floppy disk
    IBM PC compatible
    SYSTEM: PC-DOS/MS-DOS
    PatentIn Release #1.0, Version #1.30
    CATION DATA:
      NUMBER: US/09/220,157A
      :
    ION:
    TION DATA:
      NUMBER: US/08/710,249
      : 13-SEP-1996
      NUMBER: US 08/583,808
      : 05-JAN-1996
    ION DATA:
      NUMBER: US 60/003,492
      : 08-SEP-1995
    I INFORMATION:
      Baum, Peter
      : TITLE OF INVENTION: Molecules Designated B7L1

```

```

NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
  INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 434 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
  US-09-220-157A-4

  Query Match 1.7%; Score 9; DB 4; Length 434;
  Best Local Similarity 100.0%; Pred. No. 12;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; G

  QY 118 AAAAAAAAA 126
  |||||
  Db 344 AAAAAAAAA 352

  RESULT 57
  US-09-866-028-61
  : Sequence 61, Application US/09866028
  : Patent No. 6642360
  : GENERAL INFORMATION:
  : APPLICANT: Baker, Kevin
  : APPLICANT: Botstein, David
  : APPLICANT: Eaton, Dan
  : APPLICANT: Ferrara, Napoleone
  : APPLICANT: Filvaroff, Ellen
  : APPLICANT: Gerritsen, Mary
  : APPLICANT: Goddard, Audrey
  : APPLICANT: Godowski, Paul
  : APPLICANT: Grimaldi, Christopher
  : APPLICANT: Gurney, Austin
  : APPLICANT: Hillan, Kenneth
  : APPLICANT: Kijavlin, Ivar
  : APPLICANT: Napier, Mary
  : APPLICANT: Roy, Margaret
  : APPLICANT: Tumas, Daniel
  : APPLICANT: Wood, William
  : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
  : TITLE OF INVENTION: ACIDS ENCODING THE SAME
  : FILE REFERENCE: P2548P1C1
  : CURRENT APPLICATION NUMBER: US/09/866,028
  : CURRENT FILING DATE: 2001-05-25
  : Prior application data removed - consult PALM or file wrapper
  : NUMBER OF SEQ ID NOS: 120
  : SEQ ID NO 61
  : LENGTH: 440
  : TYPE: PRT
  : ORGANISM: Homo Sapien
  US-09-866-028-61

  Query Match 1.7%; Score 9; DB 4; Length 440;
  Best Local Similarity 100.0%; Pred. No. 12;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; G

  QY 120 AAAAAAAPP 128
  |||||
  Db 14 AAAAAAAPP 22

  RESULT 58
  US-09-778-510-20
  : Sequence 20, Application US/09778510
  : Patent No. 6512095
  : GENERAL INFORMATION:
  : APPLICANT: Baum, Peter
  : TITLE OF INVENTION: Molecules Designated B7L1

```

2844-US
ION NUMBER: US/09/778,510
ATE: 2001-02-07
N NUMBER: PCT/US99/17906
E: 1999-08-05
N NUMBER: 60/095,663
E: 1998-08-07
NOS: 22
tentIn Ver. 2.0

sapien

1.7%; Score 9; DB 4; Length 442;
rity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPP 128
|||||
AAPP 22

cation US/09930803

3

OHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

ES, Roger

INOKI, Muramaki

JHUI770-1

ION NUMBER: US/09/930,803

ATE: 2001-08-15

NOS: 22

In version 3.0

sapiens

1.7%; Score 9; DB 4; Length 442;
rity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPP 128
|||||
AAPP 22

4 Application US/09252991A

5

J. Rubenfield et al.

ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

107196.136

ION NUMBER: US/09/252,991A

ATE: 1999-02-18

N NUMBER: US 60/074,788

E: 1998-02-18

N NUMBER: US 60/094,190

E: 1998-07-27

NOS: 33142

omonas aeruginosa

US-09-252-991A-22614

Query Match 1.7%; Score 9; DB 4; Length 458;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 PLAAPPAP 184

Db 73 PLAAPPAP 81

RESULT 61

US-09-023-905A-10

; Sequence 10, Application US/09023905A

; Patent No. 6475778

; GENERAL INFORMATION:

; APPLICANT: Roberts, Thomas M.

; APPLICANT: King, Frederick J.

; APPLICANT: Harris, David F.

; APPLICANT: Hu, Erding

; APPLICANT: Spiegelman, Bruce

; APPLICANT: Chan, Joanne

; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses

; TITLE OF INVENTION: therefor

; FILE REFERENCE: DFN-021

; CURRENT APPLICATION NUMBER: US/09/023,905A

; CURRENT FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/038,191

; PRIOR FILING DATE: 1997-02-14

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 903

; TYPE: PRT

; ORGANISM: Danio rerio

US-09-023-905A-10

Query Match

Best Local Similarity 1.7%; Score 9; DB 4; Length 903;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 PAPPAPPAP 139

Db 824 PAPPAPPAP 832

RESULT 62

US-09-252-991A-18882

; Sequence 1882, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18882

; LENGTH: 955

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18882

Query Match

Best Local Similarity 1.7%; Score 9; DB 4; Length 955;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAPP 128

|||||
AAPP 70

ication US/08764870

16

ION:

anlan, Thomas S

xter, John D

etterick, Robert J

agner, Richard L

shner, Peter J

xilietti, James W

st, Brian

ATION: Nuclear Receptor Ligands and Ligand

ATION: Binding Domains

JENCES: 16

ADDRESS:

Cooley Godward

re Palo Alto Square, 3000 El Camino Real

Alto

3A

ABLE FORM:

Floppy disk

IBM PC compatible

STEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

ATION DATA:

NUMBER: US/08764,870

ION: 530

ION DATA:

NUMBER: US 60/008,540

ION DATA:

NUMBER: US 60/008,543

ION DATA:

NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

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NUMBER: US 60/008,606

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NUMBER: US 60/008,606

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NUMBER: US 60/008,606

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NUMBER: US 60/008,606

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NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

ION DATA:

NUMBER: US 60/008,606

ION DATA:

APPLICANT: Scanlan, Thomas S.

APPLICANT: Baxter, John D.

APPLICANT: Fletcher, Robert J.

APPLICANT: Wagner, Richard L.

APPLICANT: Kushner, Peter J.

APPLICANT: Apriletti, James W.

APPLICANT: West, Brian L.

APPLICANT: Shiau, Andrew K.

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOM

FILE REFERENCE: UCAL-246/02US

CURRENT APPLICATION NUMBER: US/08/980,115

CURRENT FILING DATE: 1997-11-26

EARLIER APPLICATION NUMBER: 08/764,870

EARLIER FILING DATE: 1996-12-13

EARLIER APPLICATION NUMBER: 60/008,606

EARLIER FILING DATE: 1995-12-14

EARLIER APPLICATION NUMBER: 60/008,543

EARLIER FILING DATE: 1995-12-13

EARLIER APPLICATION NUMBER: 60/008,540

EARLIER FILING DATE: 1995-12-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 984

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (695)...(969)

OTHER INFORMATION: minimal ligand binding domain

US-08-980-115-15

Query Match

Best Local Similarity 1.7%; Score 9; DB 3; Length 984;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 221 PQQQPPPP 229

Db 689 PQQQPPPP 697

RESULT 65

US-09-976-594-127

Sequence 127, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Buchbinder, Jenny

APPLICANT: Furness, Michael

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREA

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SEQ ID NO 127

LENGTH: 984

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 3230770CD1

US-09-976-594-127

Query Match

Best Local Similarity 1.7%; Score 9; DB 4; Length 984;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 221 PQQQPPPP 229

Db 689 PQQQPPPP 697

ication US/08980115

22

ION:

5-1
5-2
5-3
5-4
5-5
5-6
5-7
5-8
5-9

cation US/09412545

5

ott, Stephen M.

Li

, Elie

ON: HUMAN DIACYLGLYCEROL KINASE IOTA

1321.2.25

ION NUMBER: US/09/412,545

ATE: 1999-10-05

ION NUMBER: 60/103,079

ATE: 1998-10-05

NOS: 8

In Ver. 2.0

sapiens

1.7%; Score 9; DB 3; Length 1065;

ity 100.0%; Pred. No. 26;

servative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126

||||

AAAA 30

plication US/09489039A

6

ON:

Breton et. al

ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

ON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

2709.2004001

ION NUMBER: US/09/489,039A

ATE: 2000-01-27

V NUMBER: US 60/117,747

E: 1999-01-29

NOS: 14342

iella pneumoniae

1.7%; Score 9; DB 4; Length 1079;

ity 100.0%; Pred. No. 27;

servative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 146

||||

AAAA 565

ication US/08431080

6

ION:

tschling, Daniel E.

nger, Miriam S.

ION: Telomerase Compositions and Methods

ENCES: 32

ADDRESS:

Arnold, White & Durkee

. Box 4433

CITY: Houston
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-080-28

Query Match 1.7%; Score 9; DB 1; Length 1085;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 329 EEEEDDDDD 337

Db 133 EEEEDDDDD 141

RESULT 69

US-08-938-534-28

; Sequence 28, Application US/08938534

; Patent No. 5916752

; GENERAL INFORMATION:

; APPLICANT: Gottschling, Daniel E.

; TITLE OF INVENTION: Telomerase Compositions and Methods

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TEXAS

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/938,534

; FILING DATE: 26-SEP-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/431,080

; FILING DATE:

; APPLICATION NUMBER: SN 08/326,781

; FILING DATE: October 20, 1994

; ATTORNEY/AGENT INFORMATION:

Dr. David L.
DCKET NUMBER: 32,165
TION INFORMATION:
(512) 418-3000
713) 789-2679
924
SEQ ID NO: 28;
ACTERISTICS:
5 amino acids
acid
single
linear

1.7%; Score 9; DB 2; Length 1085;
arity 100.0%; Pred. No. 27;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDED 337
DEDED 141

ication US/09345294

ATION:
Gottschling, Daniel E.
Singer, Miriam S.
INVENTION: Telomerase Compositions and Methods
SEQUENCES: 32
ENCE ADDRESS:
SSEE: Arnold, White & Durkee
ET: P.O. Box 4433
Houston
TEXAS
RY: UNITED STATES OF AMERICA
77210

READABLE FORM:
M TYPE: Floppy disk
ATING SYSTEM: PC-DOS/MS-DOS/ASCII
ARE: Patentin Release #1.0, Version #1.30
PLICATION DATA:
ICATION NUMBER: US/09/345,294
G DATE: 30-Jun-1999
IFICATION: <Unknown>
ICATION DATA:
ICATION NUMBER: 08/431,080
G DATE: <Unknown>
AGENT INFORMATION:
Parker, David L.
TRATION NUMBER: 32,165
RENCE/DOCKET NUMBER: ARCD:155/PAR
ICATION INFORMATION:
PHONE: (512) 418-3000
FAX: (713) 789-2679
79-0924
SEQ ID NO: 28;
CHARACTERISTICS:
TH: 1085 amino acids
amino acid
NEDNESS: single
LOGY: linear
DESCRIPTION: SEQ ID NO: 28;

1.7%; Score 9; DB 4; Length 1085;
arity 100.0%; Pred. No. 27;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 EEEEDDED 337
Db 133 EEEEDDED 141

RESULT 71

US-09-252-991A-29927
; Sequence 29927, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29927
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29927

Query Match 1.7%; Score 9; DB 4; Length 1129;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATAP 159
Db 1006 AAAAAATAP 1014

RESULT 72

US-09-252-991A-31760
; Sequence 31760, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31760
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760

Query Match 1.7%; Score 9; DB 4; Length 1706;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAAPA 146
Db 465 APVAAAAAPA 473

RESULT 73

US-08-159-339A-163
; Sequence 163, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.

ny, Howard M.
ite, Alessandro
lis, Esteban
TION: HLA Binding peptides and Their
TION: Uses
ENCES: 1254
ADDRESS:
Townsend and Townsend and Crew LLP
Embarcadero Center, Eighth Floor
San Francisco

A
3834
3LE FORM:
Diskette
3M Compatible
STEM: DOS
astSEQ for Windows Version 2.0
ATION DATA:
NUMBER: US/08/159,339A
29-NOV-1993
ON: 424
ION DATA:
NUMBER: US 07/926,666
07-AUG-1992
NUMBER: US 08/027,746
05-MAR-1993
NUMBER: US 08/103,396
06-AUG-1993
INFORMATION:
, Ellen Lauver
NUMBER: 32,762
CKET NUMBER: 018623-005030US
ION INFORMATION:
(415) 576-0200
15) 576-0300

SEQ ID NO: 163:
TERISTICS:
mino acids
acid
: single
linear
peptide
1.5%; Score 8; DB 3; Length 9;
city 100.0%; Pred. No. 3e+05;
servative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125
|||
AAA 8

ication US/08199776
)
ION:
anner, Michael B.
cker, Christina M.
TION: No. 5594120el integrin alpha subunit
ENCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue
A

3LE FORM:
Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-199-776-17

Query Match 1.5%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 LEKEEED 333
|||
Db 2 LEKEEED 9

RESULT 75
US-08-663-731-17
Sequence 17, Application US/08663731
Patent No. 6057423
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 6057423el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,731
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,776
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 17:

CHARACTERISTICS:
amino acids
acid
single
linear
peptide
YES
internal
homo sapiens

1.5%, Score 8; DB 3; Length 10;
arity 100.0%; Pred. No. 2.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

Location US/08879338A

16
[ON: Michael B.
er, Christina M.
[ON: Antibodies to No. 6063906el Integrin Alpha
[ON: Subunit

B0801/7080/ERP
[ION NUMBER: US/08/879,338A
DATE: 1997-06-20
[ION NUMBER: US 08/663,731
DATE: 1996-06-14
[ION NUMBER: US 08/199,776
DATE: 1994-02-18
[ONOS: 31
EQ for Windows Version 3.0

Sapiens

1.5%, Score 8; DB 3; Length 10;
arity 100.0%; Pred. No. 2.7;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

Location US/09293238B

42

ION: Michael B.
ker, Christina M.
ION: A Method of Treating Ulcerative Colitis
ION: or Crohn's Disease by Administering an Antibody to Alpha B
ION: Beta 7 Integrin
L0560/7005/ERP
TION NUMBER: US/09/293,238B
DATE: 1999-04-16
ON NUMBER: US 08/879,338
TE: 1997-06-20
ON NUMBER: US 08/663,731
TE: 1996-06-14
ON NUMBER: US 08/199,776

PRIOR FILING DATE: 1994-02-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapien
US-09-293-238B-17

Query Match 1.5%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 326 LEKEEED 333
Db 2 LEKEEED 9

RESULT 78

PCT-US95-02044-17
Sequence 17, Application PC/TUS9502044
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02044
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,776
FILING DATE: 18 February 1994
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-02044-17

Query Match 1.5%; Score 8; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 326 LEKEEED 333
Db 2 LEKEEED 9

ST
-C
Se
Pa
Q
G

ation US/07814220
:
eci, Thomas
h, Thomas E.
manski, Maria B.W.
ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
on Intl. Center, 11800 Sunrise Valley Dr.,
e 900
1
A

FILE FORM:
Floppy disk
M PC compatible
ITEM: PC-DOS/MS-DOS
tentIn Release #1.0, Version #1.30
TION DATA:
NUMBER: US/07/814,220
23-DEC-1991
N: 435
ION DATA:
NUMBER: US 07/588,437
25-SEP-1990
INFORMATION:
um, Michael E.
NUMBER: 32,635
KET NUMBER: CIT.016
ION INFORMATION:
03-391-2510
-391-9035
SEQ ID NO: 11:
TERISTICS:
amino acids
acid
near
peptide

1.5%; Score 8; DB 2; Length 11;
ity 100.0%; Pred.No.3;
servative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
||
ATA 9

ation US/07812421
:
eci, Thomas
h, Thomas E.
manski, Maria B.W.
ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
on Intl. Center, 11800 Sunrise Valley Dr.,
e 900
1

STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-11

Query Match 1.5%; Score 8; DB 2; Length 11;
Best Local Similarity 100.0%; Pred.No.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AAAAAATA 158
Db 2 AAAAAATA 9
|||||

RESULT 81
US-08-199-776-19
Sequence 19, Application US/08199776
Patent No. 5594120
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 5594120el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 19:

ACTERISTICS:
amino acids
acid
single
linear
peptide
YES
NO internal
CE:
Homo sapiens

1.5%; Score 8; DB 1; Length 14;
arity 100.0%; Pred.No. 3.7;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

EEED 333
|||||
SEED 9

lication US/07814220

ION:
acaci, Thomas
oth, Thomas E.
zumanski, Maria B.W.
TION: SYNTHETIC ANTIPREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
JENCES: 43

E ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
on

SA

ABLE FORM:
Floppy disk.
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
NUMBER: US/07/814,220
: 23-DEC-1991

ION DATA:
NUMBER: US 07/588,437
: 25-SEP-1990
F INFORMATION:
am, Michael E.
X NUMBER: 32,635
CKET NUMBER: CIT.016
TION INFORMATION:
703-391-2510
03-391-9035
SEQ ID NO: 30:

ACTERISTICS:
amino acids
acid
S:
linear
peptide

1.5%; Score 8; DB 2; Length 14;
arity 100.0%; Pred.No. 3.7;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 AAAAAATA 158
|||||
Db 4 AAAAAATA 11

RESULT 83

US-07-812-421-30
; Sequence 30, Application US/07812421
; Patent No. 5932697
; GENERAL INFORMATION:
; APPLICANT: Cacaci, Thomas
; APPLICANT: Toth, Thomas E.
; APPLICANT: Szumanski, Maria B.W.
; TITLE OF INVENTION: SYNTHETIC ANTIPREEZE PEPTIDE AND
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
; STREET: Suite 900
; CITY: Reston
; STATE: VA
; COUNTRY: USA
; ZIP: 20191

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-30

Query Match 1.5%; Score 8; DB 2; Length 14;
Best Local Similarity 100.0%; Pred.No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 151 AAAAAATA 158
|||||
Db 4 AAAAAATA 11

RESULT 84

US-08-663-731-19
; Sequence 19, Application US/08663731
; Patent No. 6057423
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: No. 6057423el integrin alpha subunit
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
; STREET: 600 Atlantic Avenue

FILE FORM:
 Floppy disk
 IBM PC compatible
 ITEM: PC-DOS/MS-DOS
 Attention Release #1.0, Version #1.25
 ACTION DATA:
 NUMBER: US/08/663,731

DN:
 CON DATA:
 NUMBER: 08/199,776

INFORMATION:
 C. Elizabeth R.
 NUMBER: 36,637
 KEY NUMBER: B0801/7020
 CON INFORMATION:
 517-720-3500
 720-2441
 SEQ ID NO: 19:
 CHARACTERISTICS:
 amino acids
 acid
 single
 near
 peptide
 YES
 internal

amo sapiens
 1.5%; Score 8; DB 3; Length 14;
 ity 100.0%; Pred. No. 3.7;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;

ED 333
 ED 9

ication US/08879338A

DN:
 r, Michael B.
 Christina M.
 DN: Antibodies to No. 6063906el Integrin Alpha
 DN: Subunit
 0801/7080/ERP
 CON NUMBER: US/08/879,338A
 TE: 1997-06-20
 CON NUMBER: US 08/663,731
 TE: 1996-06-14
 CON NUMBER: US 08/199,776
 TE: 1994-02-18
 NOS: 31
 for Windows Version 3.0

sapiens

1.5%; Score 8; DB 3; Length 14;
 ity 100.0%; Pred. No. 3.7;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 LEKEEED 333
 Db 2 LEKEEED 9

RESULT 86
 US-09-293-238B-19
 ; Sequence 19, Application US/09293238B
 ; Patent No. 6455042
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenner, Michael B.
 ; APPLICANT: Parker, Christina M.
 ; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis
 ; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody
 ; TITLE OF INVENTION: Beta 7 Integrin
 ; FILE REFERENCE: L0560/7005/ERP
 ; CURRENT APPLICATION NUMBER: US/09/293,238B
 ; CURRENT FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: US 08/879,338
 ; PRIOR FILING DATE: 1997-06-20
 ; PRIOR APPLICATION NUMBER: US 08/663,731
 ; PRIOR FILING DATE: 1996-06-14
 ; PRIOR APPLICATION NUMBER: US 08/199,776
 ; PRIOR FILING DATE: 1994-02-18
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-293-238B-19

Query Match 1.5%; Score 8; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 LEKEEED 333
 Db 2 LEKEEED 9

RESULT 87
 PCT-US95-02044-19
 ; Sequence 19, Application PC/TUS9502044
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Novel integrin alpha subunit
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02044
 ; FILING DATE: herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/199,776
 ; FILING DATE: 18 February 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7020
 ; TELECOMMUNICATION INFORMATION:

617-720-3500

17-720-2441 19:

SEQ ID NO: 19:

ACTERISTICS:

amino acids

o acid

s: single

linear

: peptide

: YES

NO

: internal

DE:

Homo sapiens

1.5%; Score 8; DB 5; Length 14;

arity 100.0%; Pred.No.3.7;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

3EED 333

|||||

3EED 9

Application US/08602999A

15

TION:

SPARKS, Andrew B.

AY, Brian K.

JORN, Judith M.

JILLIAM, Lawrence A.

ER, Channing J.

JWLKES, Dana M.

IDER, James E.

TION: SH3 BINDING PEPTIDES AND METHODS OF

ATION: ISOLATING AND USING SAME

ENCES: 467

3 ADDRESS:

Pennie & Edmonds

15 Avenue of the Americas

York

S.A.

-2711

ABLE FORM:

: Floppy disk

IBM PC compatible

STEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

ATION DATA:

NUMBER: US/08/602,999A

: 16-FEB-1996

ION: 435

TION INFORMATION:

ck, S. Leslie

Y NUMBER: 18,872

CKET NUMBER: 1101-202

TION INFORMATION:

(212) 790-9090

212) 869-9741/8864

11 PENNIE

SEQ ID NO: 439:

ACTERISTICS:

amino acids

o acid

unknown

: peptide

1.5%; Score 8; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 212 PPPQPQA 219

Db 6 PPPQPQA 13

RESULT 89

US-09-500-124-439

; Sequence 439, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 439:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-09-500-124-439

Query Match

Best Local Similarity 1.5%; Score 8; DB 4; Length 15;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 212 PPPQPQA 219

Db 6 PPPQPQA 13

RESULT 90

US-08-630-916A-99

; Sequence 99, Application US/08630916A

; Patent No. 601137

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

Y, Brian K.
wikes, Dana M.
TION: IDENTIFICATION AND ISOLATION OF NOVEL
TION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
ENCES: 124
ADDRESS:
Pennie & Edmonds
5 Avenue of the Americas
York
ited States
2711
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/08/630,916A
03-APR-1996
ON: 435
INFORMATION:
CK, S. LESLIE
NUMBER: 18,872
CKET NUMBER: 1101-203
ION INFORMATION:
(212) 790-9090
12) 896-8864/9741
SEQ ID NO: 99:
CTERISTICS:
amino acids
acid
:
nknown
peptide
1.5%; Score 8; DB 3; Length 16;
rity 100.0%; Pred. No. 4.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PPA 138
|||
PPA 12
lication US/08630915A
ION:
ARKS, Andrew B.
FFMAN, No. 6309820h
Y, Brian K.
ALKES, Dana M.
CONNELL, Stephen J.
TION: POLYPEPTIDES HAVING A FUNCTIONAL
TION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
ION: USING SAME
ENCES: 227
ADDRESS:
Pennie & Edmonds LLP
5 Avenue of the Americas
ork
York
A
2711
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
atentIn Release #1.0, Version #1.30
ATION DATA:

APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Miskock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLESCULE TYPE: peptide
US-08-630-915A-155
Query Match 1.5%; Score 8; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 PAPPPPPA 138
|||
Db 5 PAPPPPPA 12
|||
RESULT 92
US-08-199-776-21
Sequence 21, Application US/08199776
Patent No. 5594120
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 5594120el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,776
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLESCULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

11:33:39 2004

us-09-976-740-43.olig.ra1

1.5%; Score 8; DB 1; Length 20;
arity 100.0%; Pred.No. 5.1;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
SEED 333
|||||
SEED 9

lication US/07814220
40
TION:
aceci, Thomas E.
oth, Thomas E.
zumanski, Maria B.W.
TION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
JENCES: 43
E ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
on

3A
ABLE FORM:
: Floppy disk
IBM PC compatible
STEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
TION DATA:
NUMBER: US/07/814,220
: 23-DEC-1991
ION: 435
TION DATA:
NUMBER: US 07/588,437
: 25-SEP-1990
TION INFORMATION:
am, Michael E.
V NUMBER: 32,635
CKET NUMBER: CIT.016
TION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 27:
ACTERISTICS:
amino acids
o acid
3:
linear
: Peptide

1.5%; Score 8; DB 2; Length 20;
arity 100.0%; Pred.No. 5.1;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 9

lication US/07814241
97
TION:
aceci, Thomas

APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-27

Query Match 1.5%; Score 8; DB 2; Length 20;
Best Local Similarity 100.0%; Pred.No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
|||||
Db 2 AAAAAATA 9

RESULT 95
US-08-663-731-21
Sequence 21, Application US/08663731
Patent No. 6057423
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Parker, Christina M.
TITLE OF INVENTION: No. 6057423el integrin alpha subunit
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,731

CN:
 ION DATA:
 NUMBER: 08/199,776
 INFORMATION:
 r, Elizabeth R.
 NUMBER: 36,637
 CKET NUMBER: B0801/7020
 ION INFORMATION:
 617-720-3500
 7-720-2441
 SEQ ID NO: 21:
 CTERISTICS:
 amino acids
 acid
 : single
 inear
 peptide
 YES
 O internal
 E:
 omo sapiens

1.5%; Score 8; DB 3; Length 20;
 rity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
 ||||
 EED 9

ication US/08879338A

CN:
 r, Michael B.
 r, Christina M.
 CN: Antibodies to No. 6063906el Integrin Alpha
 CN: Subunit
 B0801/7080/ERP
 ION NUMBER: US/08/879,338A
 ATE: 1997-06-20
 ION NUMBER: US 08/663,731
 ATE: 1996-06-14
 ION NUMBER: US 08/199,776
 ATE: 1994-02-18
 NOS: 31
 Q for Windows Version 3.0

Sapiens

1.5%; Score 8; DB 3; Length 20;
 rity 100.0%; Pred. No. 5.1;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

EED 333
 ||||
 EED 9

ication US/09293238B
 2
 CN:

; APPLICANT: Brenner, Michael B.
 ; APPLICANT: Parker, Christina M.
 ; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis
 ; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibody
 ; TITLE OF INVENTION: Beta 7 Integrin
 ; FILE REFERENCE: L0560/7005/ERP
 ; CURRENT APPLICATION NUMBER: US/09/293,238B
 ; CURRENT FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: US 08/879,338
 ; PRIOR FILING DATE: 1997-06-20
 ; PRIOR APPLICATION NUMBER: US 08/663,731
 ; PRIOR FILING DATE: 1996-06-14
 ; PRIOR APPLICATION NUMBER: US 08/199,776
 ; PRIOR FILING DATE: 1994-02-18
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-293-238B-21

Query Match 1.5%; Score 8; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

QV 326 LEKEEED 333
 |||||
 Db 2 LEKEEED 9

RESULT 98

PCT-US95-02044-21
 ; Sequence 21, Application PC/TUS9502044
 ; GENERAL INFORMATION:

; APPLICANT:
 ; TITLE OF INVENTION: Novel integrin alpha subunit

; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02044
 ; FILING DATE: herewith
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/199,776
 ; FILING DATE: 18 February 1994

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637

; REFERENCE/DOCKET NUMBER: B0801/7020
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441

; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO

11:33:39 2004

us-09-976-740-43.olig.ra1

1

```

: internal
CE:
Homo sapiens

1.5%; Score 8; DB 5; Length 20;
arity 100.0%; Pred.No.5.4; Indels 0; Gaps 0;
conservative 0; Mismatches 0;

SEED 333
|||||
SEED 9

ication US/08199776
20
TION:
renner, Michael B.
arker, Christina M.
ATION: No. 5594120e1 integrin alpha subunit
ENCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue
on

3A
ABLE FORM:
: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
ATION DATA:
NUMBER: US/08/199,776

ION: 514
T INFORMATION:
ar, Elizabeth R.
NUMBER: 35,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
SEQ ID NO: 5:
ACTERISTICS:
amino acids
acid
3: single
linear
: peptide
YES
NO
: internal
E:
Homo sapiens

1.5%; Score 8; DB 1; Length 21;
arity 100.0%; Pred.No.5.4; Indels 0; Gaps 0;
conservative 0; Mismatches 0;

SEED 333
|||||
SEED 9

lication US/07814220
40

: GENERAL INFORMATION:
: APPLICANT: Caceci, Thomas
: APPLICANT: Toth, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/814,220
: FILING DATE: 23-DEC-1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/588,437
: FILING DATE: 25-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Whitham, Michael E.
: REGISTRATION NUMBER: 32,635
: REFERENCE/DOCKET NUMBER: CIT.016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-391-2510
: TELEFAX: 703-391-9035
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07-814-220-24

Query Match 1.5%; Score 8; DB 2; Length 21;
Best Local Similarity 100.0%; Pred.No.5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
Db 1 AAAAAATA 8

RESULT 101
US-07-812-421-24
: Sequence 24, Application US/07812421
: Patent No. 5932697
: GENERAL INFORMATION:
: APPLICANT: Caceci, Thomas
: APPLICANT: Toth, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
```

IBM PC compatible
 ITEM: PC-DOS/MS-DOS
 Patent In Release #1.0, Version #1.30
 ACTION DATA:
 NUMBER: US/07/812,421
 23-DEC-1991

IN: 435
 ON DATA:
 NUMBER: US 07/598,437
 25-SEP-1990

INFORMATION:
 INVENTOR:
 NAME: Michael E.

NUMBER: 32,635
 PCT NUMBER: CIT.016
 ON INFORMATION:
 703-391-2510
 391-9035

SEQ ID NO: 24:

TERISTICS:
 amino acids
 acid

linear
 peptide

1.5%; Score 8; DB 2; Length 21;
 city 100.0%; Pred. No. 5.4;
 conservative 0; Mismatches 0; Indels 0;

ATA 158
 ||||
 ATA 8

ation US/08663731

ON:
 anner, Michael B.

cker, Christina M.

CTION: No. 6057423el integrin alpha subunit

ENCES: 25

ADDRESS:
 Wolf, Greenfield and Sacks, P.C.
 Atlantic Avenue

1

1

1

1

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ficial Sequence

ION: Synthetic Peptide

1.5%; Score 8; DB 3; Length 21;
arity 100.0%; Pred.No. 5.4;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

ication US/09293238B

42

ION:

ner, Michael B.

ker, Christina M.

ION: A Method of Treating Ulcerative Colitis

ION: or Crohn's Disease by Administering an Antibody to Alpha E

ION: Beta 7 Integrin

L0560/7005/ERP

TION NUMBER: US/09/293,238B

DATE: 1999-04-16

ON NUMBER: US 08/879,338

TE: 1997-06-20

TE: 1996-06-14

ON NUMBER: US 08/663,731

ON NUMBER: US 08/199,776

TE: 1994-02-18

D NOS: 31

EQ for Windows Version 3.0

sapien

1.5%; Score 8; DB 4; Length 21;
arity 100.0%; Pred.No. 5.4;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEED 333
|||||
SEED 9

lication US/09293238B

42

ION:

ner, Michael B.

ker, Christina M.

ION: A Method of Treating Ulcerative Colitis

ION: or Crohn's Disease by Administering an Antibody to Alpha E

ION: Beta 7 Integrin

L0560/7005/ERP

TION NUMBER: US/09/293,238B

DATE: 1999-04-16

ON NUMBER: US 08/879,338

TE: 1997-06-20

ON NUMBER: US 08/663,731

TE: 1996-06-14

ON NUMBER: US 08/199,776

TE: 1994-02-18

D NOS: 31

EQ for Windows Version 3.0

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Peptide

US-09-293-238B-26

Query Match 1.5%; Score 8; DB 4; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Oy 326 LEKEEED 333
|||||
Db 2 LEKEEED 9

RESULT 107

PCT-US95-02044-5

; Sequence 5, Application PC/TUS9502044

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Novel integrin alpha subunit

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/02044

; FILING DATE: herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/199,776

; FILING DATE: 18 February 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Plumer, Elizabeth R.

; REGISTRATION NUMBER: 36,637

; REFERENCE/DOCKET NUMBER: B0801/7020

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-720-3500

; TELEFAX: 617-720-2441

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

PCT-US95-02044-5

Query Match 1.5%; Score 8; DB 5; Length 21;
Best Local Similarity 100.0%; Pred.No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Oy 326 LEKEEED 333
|||||
Db 2 LEKEEED 9

RESULT 108

ication US/07814220
 ION:
 cec, Thomas
 th, Thomas E.
 amanski, Maria B.W.
 ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 ENCES: 43

ADDRESS:
 WHITHAM, CURTIS & WHITHAM
 ton Intl. Center, 11800 Sunrise Valley Dr.,
 te 900
 n

A
 BLE FORM:
 Floppy disk
 BM PC compatible
 STEM: PC-DOS/MS-DOS
 atentIn Release #1.0, Version #1.30
 ATION DATA:
 NUMBER: US/07/814,220
 23-DEC-1991

ON: 435
 ION DATA:
 NUMBER: US 07/588,437

25-SEP-1990
 INFORMATION:
 am, Michael E.
 NUMBER: 32,635
 CKET NUMBER: CIT.016
 ION INFORMATION:
 703-391-2510
 3-391-9035

SEQ ID NO: 33:
 amino acids

TERISTICS:
 amino acids

acid

inear

peptide

city 1.5%; Score 8; DB 2; Length 25;
 100.0%; Pred. No. 6.3;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

ATA 19

ication US/07814241

ION:

ceci, Thomas

th, Thomas E.

amanski, Maria B.W.

ION: SYNTHETIC ANTIFREEZE PEPTIDE AND
 ION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
 ENCES: 43

ADDRESS:

WHITHAM, CURTIS & WHITHAM

ton Intl. Center, 11800 Sunrise Valley Dr.,

te 900

1

1

ZIP: 20191
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/812,421
 FILING DATE: 23-DEC-1991
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/588,437

FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Whitham, Michael E.

REGISTRATION NUMBER: 32,635

REFERENCE/DOCKET NUMBER: CIT.016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-391-2510

TELEFAX: 703-391-9035

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-812-421-33

Query Match 1.5%; Score 8; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 AAAAAATA 158

Db 12 AAAAAATA 19

RESULT 110

US-07-814-220-36

Sequence 36, Application US/07814220

Patent No. 5925540

GENERAL INFORMATION:

APPLICANT: Caceci, Thomas

APPLICANT: Toth, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,

STREET: Suite 900

CITY: Reston

STATE: VA

COUNTRY: USA

ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/814,220

FILING DATE: 23-DEC-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/588,437

FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Whitham, Michael E.

REGISTRATION NUMBER: 32,635

REFERENCE/DOCKET NUMBER: CIT.016

TION INFORMATION:

703-391-2510

03-391-9035

SEQ ID NO: 36:

ACTERISTICS:

amino acids

acid

linear

peptide

1.5%, Score 8; DB 2; Length 28;

arity 100.0%; Pred.No. 7;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

|||||

ATA 19

Location US/07812421

77

TION:

aceci, Thomas

th, Thomas E.

umanski, Maria B.W.

TION: SYNTHETIC ANTIFREEZE PEPTIDE AND

TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

ENCES: 43

ADDRESS:

WHITHAM, CURTIS & WHITHAM

ston Intl. Center, 11800 Sunrise Valley Dr.,

ite 900

on

IA

ABLE FORM:

Floppy disk

IBM PC compatible

STEM: PC-DOS/MS-DOS

Patent In Release #1.0, Version #1.30

TION DATA:

NUMBER: US/07/812,421

23-DEC-1991

ION: 435

TION DATA:

NUMBER: US 07/588,437

25-SEP-1990

INFORMATION:

am, Michael E.

NUMBER: 32,635

CKET NUMBER: CIT.016

TION INFORMATION:

703-391-2510

03-391-9035

SEQ ID NO: 36:

ACTERISTICS:

amino acids

acid

linear

peptide

1.5%, Score 8; DB 2; Length 28;

arity 100.0%; Pred.No. 7;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

Db

|||||

12 AAAAAATA 19

RESULT 112

US-08-180-524-1

Sequence 1, Application US/08180524

Patent No. 5849537

GENERAL INFORMATION:

APPLICANT: Tripp, Matthew

APPLICANT: Lusk, Lance

APPLICANT: Rhodes, Thomas

APPLICANT: Huige, Nick

APPLICANT: Kot, Edward

APPLICANT: Chicove, Etzer

APPLICANT: Barney, Michael C.

APPLICANT: Bower, Patricia A.

APPLICANT: Cronan, Charles L.

TITLE OF INVENTION: METHOD OF

EXPRESSING ANTIFREEZE PROTEINS

IN YEAST

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thad Kryshak, Quarles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MSWORD Version 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/180,524

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/917,216

FILING DATE:

APPLICATION NUMBER: US 07/486,333

FILING DATE: 28-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/409,217

FILING DATE: 19-SEP-1989

ATTORNEY/AGENT INFORMATION:

NAME: Kryshak, Thad

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 66-005-9234-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5707

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Pseudopleuronectus americanus

US-08-180-524-1

Query Match

Best Local Similarity 1.5%; Score 8; DB 2; Length 37;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

151 AAAAAATA 158

|||||

Db

29 AAAAAATA 36

US-08-180524
7
ION: Matthew
sk, Lance
odes, Thomas
ige, Nick
t, Edward
icoye, Etzer
rney, Michael C.
onan, Charles L.
TION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
TION: IN YEAST
ENCES: 10
ADDRESS:
Thad Kryshak, Quarles & Brady
East Wisconsin Avenue
ukee
onsin
A
BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
SWORD Version 5.0
TION DATA:
NUMBER: US/08/180,524
ON: 435
ION DATA:
NUMBER: US/07/917,216
NUMBER: US 07/486,333
ION DATA:
NUMBER: US 07/409,217
19-SEP-1989
INFORMATION:
ak, Thad
NUMBER: 35,433
CKET NUMBER: 66-005-9234-1
ION INFORMATION:
(414) 277-5707
14) 277-5591
SEQ ID NO: 8:
TERISTICS:
amino acids
acid
: single
inear
protein
NO
)
1.5%; Score 8; DB 2; Length 37;
city 100.0%; Pred. No. 9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||
ATA 36
ication US/08180524
7
GENERAL INFORMATION:
APPLICANT: Tripp, Matthew
APPLICANT: Lusk, Lance
APPLICANT: Rhodes, Thomas
APPLICANT: Huige, Nick
APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.
APPLICANT: Cronan, Charles L.
TITLE OF INVENTION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
NUMBER OF INVENTIONS: IN YEAST
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Thad Kryshak, Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,524
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/917,216
FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/409,217
FILING DATE: 19-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kryshak, Thad
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-180-524-10
Query Match 1.5%; Score 8; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 AAAAAATA 158
DB 29 AAAAAATA 36
RESULT 115
US-08-975-166-1
; Sequence 1, Application US/08975166
; Patent No. 5928877
; GENERAL INFORMATION:
; APPLICANT: Tripp, Matthew
; APPLICANT: Lusk, Lance
; APPLICANT: Rhodes, Thomas
; APPLICANT: Huige, Nick

APPLICANT: Chicoye, Etzer
 APPLICANT: Barney, Michael C.
 APPLICANT: Bower, Patricia A.
 APPLICANT: Cronan, Charles L.
 TITLE OF INVENTION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
 TITLE OF INVENTION: IN YEAST
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Thad Kryshak, Quarles & Brady
 STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MSWORD Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,166
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,524
FILING DATE:
APPLICATION NUMBER: US/07/917,216
FILING DATE:
APPLICATION NUMBER: US 07/486,333
FILING DATE: 28-FEB-1990
PROB. APPLICATION DATA:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/409,217
 FILING DATE: 19-SEP-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Krushak Thad

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 66-005-9234-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5707
TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 37 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

Query Match 1.5%; Score 8; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G:

Qy 151 AAAAAATA 158
|||
Db 29 AAAAAATA 36

RESULT 117
US-08-975-166-10
; Sequence 10, Application US/08975166
; Patent No. 5928877

APPLICANT: Tripp, Matthew
APPLICANT: Lusk, Lance
APPLICANT: Rhodes, Thomas
APPLICANT: Huige, Nick
APPLICANT: Kot, Edward
APPLICANT: Chicoye, Etzer
APPLICANT: Barney, Michael C.
APPLICANT: Bower, Patricia A.

onan, Charles L.
TION: METHOD OF EXPRESSING ANTIFREEZE PROTEINS
TION: IN YEAST
ENCES: 10

ADDRESS:
Thad Kryshak, Quarles & Brady
East Wisconsin Avenue
ukee
onsin
A

BLE FORM:
Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
SWORD Version 5.0
TION DATA:
NUMBER: US/08/975,166

DN: 435
ION DATA:
NUMBER: US/08/180,524

NUMBER: US/07/917,216

NUMBER: US 07/486,333
28-FEB-1990

ION DATA:
NUMBER: US 07/409,217
19-SEP-1989
INFORMATION:

ak, Thad
NUMBER: 35,433
CKET NUMBER: 66-005-9234-1
ION INFORMATION:
(414) 277-5707

(4) 277-5591

SEQ ID NO: 10:

TERISTICS:
amino acids
acid

: single

linear

protein

NO

)

ity 1.5%; Score 8; DB 2; Length 37;
servative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158

||

ATA 36

cation US/09117121

ION:

g, Choy

ION: Intracellular Antifreeze Polypeptides

ION: and Nucleic Acids

ENCES: 46

ADDRESS:

ownsend and Townsend and Crew LLP

Embarcadero Center, Eighth Floor

ancisco

ornia

A

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062

FILING DATE: 30-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 016252-001610US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: -

LOCATION: 1..37

OTHER INFORMATION: /note= "HPLC-6"

US-09-117-121-39

Query Match 1.5%; Score 8; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 AAAAAATA 158

|||||

Db 29 AAAAAATA 36

RESULT 119

US-09-117-121-42

; Sequence 42; Application US/09117121

; Patent No. 6307020

; GENERAL INFORMATION:

; APPLICANT: Hew, Choy

; APPLICANT: Gong, Zhiyuan

; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

; TITLE OF INVENTION: and Nucleic Acids

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/117,121

; FILING DATE: 20-NOV-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/CA97/00062

; FILING DATE: 30-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Kenneth A.

Q NUMBER: 31,677
DOCKET NUMBER: 016252-001610US
FION INFORMATION:
(415) 576-0200
415) 576-0300
SEQ ID NO: 42:
ACTERISTICS:
o acid
linear
: protein
1.5%; Score 8; DB 4; Length 37;
arity 100.0%; Pred. No. 9;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 36
ication US/09344529
93
ION:
Choy L.
Research and Development Limited Partnership
ION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
016252-002620US
TION NUMBER: US/09/344,529
DATE: 1999-06-24
TION NUMBER: US 60/090,794
DATE: 1998-06-26
TION NUMBER: US 60/095,713
DATE: 1998-08-07
NOS: 19
in Ver. 2.0
conectes americanus
ION: Winter flounder liver-type antifreeze polypeptide
ION: (wflAFP-6)
1.5%; Score 8; DB 4; Length 37;
arity 100.0%; Pred. No. 9;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 36
ication US/07814220
to
TION:
aceci, Thomas
oth, Thomas E.
zumanaki, Maria B.W.
ATION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43
3 ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
on

STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-1
Query Match 1.5%; Score 8; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 151 AAAAAATA 158
Db 29 AAAAAATA 36
RESULT 122
US-07-812-421-1
Sequence 1, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.

NUMBER: 22,635
 CKET NUMBER: CIT.016
 ION INFORMATION:
 703-391-2510
 13-391-9035
 SEQ ID NO: 1:
 CHARACTERISTICS:
 amino acids
 ; acid
 ; linear
 ; peptide

1.5%; Score 8; DB 2; Length 38;
 rity 100.0%; Pred. No. 9.2;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATA 158
 ||||
 ATA 36

ication US/09117121
 0

ION:
 w, Choy
 ng, Zhiyuan
 TION: Intracellular Antifreeze Polypeptides
 TION: and Nucleic Acids
 ENCS: 46

ADDRESS:
 Townsend and Townsend and Crew LLP
 Embarcadero Center, Eighth Floor
 rancisco
 rancia
 A

3834
 BLE FORM:
 Floppy disk
 BM PC compatible
 STEM: PC-DOS/MS-DOS
 atentin Release #1.0, Version #1.30
 ATION DATA:
 NUMBER: US/09/117,121
 20-NOV-1998
 ON: 435

ION DATA:
 NUMBER: WO PCT/CA97/00062
 30-JAN-1997
 INFORMATION:
 , Kenneth A.

CKET NUMBER: 016252-001610US
 ION INFORMATION:
 (415) 576-0200
 15) 576-0300
 SEQ ID NO: 28:
 CHARACTERISTICS:
 amino acids
 ; acid
 ; linear
 ; protein

1.5%; Score 8; DB 4; Length 39;
 rity 100.0%; Pred. No. 9.5;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125
 ||||

Db 3 APAAAAAA 10

RESULT 124

US-09-117-121-30
 ; Sequence 30, Application US/09117121
 ; Patent No. 6307020
 ; GENERAL INFORMATION:
 ; APPLICANT: Hew, Choy
 ; APPLICANT: Gong, Zhiyuan
 ; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
 ; TITLE OF INVENTION: and Nucleic Acids
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/117,121
 ; FILING DATE: 20-NOV-1998
 ; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/CA97/00062
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Kenneth A.
 ; REGISTRATION NUMBER: 31,677
 ; REFERENCE/DOCKET NUMBER: 016252-001610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 54 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-117-121-30

Query Match 1.5%; Score 8; DB 4; Length 54;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 APAAAAAA 125

|||||
 Db 3 APAAAAAA 10

RESULT 125

US-08-199-776-4
 ; Sequence 4, Application US/08199776
 ; Patent No. 5594120
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenner, Michael B.

; APPLICANT: Parker, Christina M.
 ; TITLE OF INVENTION: No. 5594120el integrin alpha subunit
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield and Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210

; COMPUTER READABLE FORM:
 ;

```
; Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
CAUTION DATA:
NUMBER: US/08/199,776
;
ION: 514
T INFORMATION:
er, Elizabeth R.
N NUMBER: 36,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
SEQ ID NO: 4:
ACTERISTICS:
amino acids
o acid
S: single
linear
: peptide
YES
NO
: internal
CE:
Homo sapiens
1.5%; Score 8; DB 1; Length 55;
arity 100.0%; Pred. No. 13;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
EED 333
|||||
EED 43
ication US/08663731
23
TION:
renner, Michael B.
arker, Christina M.
NTION: No. 6057423el integrin alpha subunit
ENCES: 25
E ADDRESS:
Wolf, Greenfield and Sacks, P.C.
0 Atlantic Avenue
on
SA
ABLE FORM:
; Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
CAUTION DATA:
NUMBER: US/08/663,731
;
ION:
TION DATA:
NUMBER: 08/199,776
;
T INFORMATION:
er, Elizabeth R.
N NUMBER: 36,637
CKET NUMBER: B0801/7020
TION INFORMATION:
617-720-3500
17-720-2441
```

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-663-731-4
Query Match 1.5%; Score 8; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 326 LEKEEED 333
|||||
Db 36 LEKEEED 43
RESULT 127
US-08-879-338-4
; Sequence 4, Application US/08879338A
; Patent No. 6063906
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: Antibodies to No. 6063906el Integrin Alpha
; TITLE OF INVENTION: Subunit
; FILE REFERENCE: B0801/7080/ERP
; CURRENT APPLICATION NUMBER: US/08/879,338A
; CURRENT FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: US 08/663,731
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: US 08/199,776
; EARLIER FILING DATE: 1994-02-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-879-338-4
Query Match 1.5%; Score 8; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 326 LEKEEED 333
|||||
Db 36 LEKEEED 43
RESULT 128
US-09-293-238B-4
; Sequence 4, Application US/09293238B
; Patent No. 6455042
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Parker, Christina M.
; TITLE OF INVENTION: A Method of Treating Ulcerative Colitis
; TITLE OF INVENTION: or Crohn's Disease by Administering an Antibod
; TITLE OF INVENTION: Beta 7 Integrin
; FILE REFERENCE: L0560/7005/ERP
; CURRENT APPLICATION NUMBER: US/09/293,238B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 08/879,338
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: US 08/663,731
; PRIOR FILING DATE: 1996-06-14
```

NUMBER: US 08/199,776
3: 1994-02-18
NOS: 31
Q for Windows Version 3.0

sapien

1.5%; Score 8; DB 4; Length 55;
city 100.0%; Pred. No. 13;
servative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
|||
SED 43

ation PC/TUS9502044
ION:

ION: Novel integrin alpha subunit
ENCES: 25
ADDRESS:
Wolf, Greenfield and Sacks, P.C.
Atlantic Avenue

3LE FORM:

Floppy disk
3M PC compatible
ITEM: PC-DOS/MS-DOS
ation in Release #1.0, Version #1.25
TION DATA:
NUMBER: PCT/US95/02044
herewith

ION DATA:
NUMBER: 08/199,776
18 February 1994
INFORMATION:
Elizabeth R.
NUMBER: 36,637
XET NUMBER: B0801/7020
ION INFORMATION:
17-720-3500
7-720-2441
SEQ ID NO: 4:
TERISTICS:
mino acids
acid
: single
inear
peptide
YES
internal
3:
omo sapiens

1.5%; Score 8; DB 5; Length 55;
city 100.0%; Pred. No. 13;
servative 0; Mismatches 0; Indels 0; Gaps 0;

SED 333
|||
SED 43

RESULT 130
5496550-8
; Patent No. 5496550
; APPLICANT: WALLACH, MICHAEL; PUGATSCH, THEA; MENCHER, DAVID
; TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
; OOCYSTS FROM A NEWBORN CHICK
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/108,763
; FILING DATE: 17-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 642,219
; FILING DATE: 16-JAN-1991
; APPLICATION NUMBER: 310,603
; FILING DATE: 14-FEB-1989
; APPLICATION NUMBER: 155,245
; FILING DATE: 12-FEB-1988
; APPLICATION NUMBER: 896,611
; FILING DATE: 14-AUG-1986
; SEQ ID NO: 8:
; LENGTH: 62
5496550-8

Query Match 1.5%; Score 8; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
|||
Db 37 AAAAAAAP 44

RESULT 131
US-09-621-976-3951
; Sequence 3951, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3951
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -70...-1
US-09-621-976-3951

Query Match 1.5%; Score 8; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
|||
Db 30 AAAAAAAP 37

RESULT 132
US-09-540-236-2315
; Sequence 2315, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ION: FOR DIAGNOSTICS AND THERAPEUTICS
2709.2005-001
ION NUMBER: US/09/540,236
DATE: 2000-04-04
NOS: 3840

arrhalis

1.5%; Score 8; DB 4; Length 96;
arity 100.0%; Pred. No. 22; 0; Indels 0;
nservative 0; Mismatches 0; Gaps 0;

AASS 24
|||||
AASS 79

ication US/07814220
40
TION:
ceci, Thomas
th, Thomas E.
umanski, Maria B.W.
TION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
ENCES: 43
ADDRESS:
WHITHAM, CURTIS & WHITHAM
ston Intl. Center, 11800 Sunrise Valley Dr.,
ite 900
on

3A

ABLE FORM:
: Floppy disk
IBM PC compatible
(STEM: PC-DOS/MS-DOS
patentin Release #1.0, Version #1.30
ATION DATA:
NUMBER: US/07/814,220
: 23-DEC-1991
ION: 435
TION DATA:
NUMBER: US 07/588,437
: 25-SEP-1990
T INFORMATION:
am, Michael E.
NUMBER: 32,635
CKET NUMBER: CIT.016
TION INFORMATION:
703-391-2510
3-391-9035
SEQ ID NO: 2:
ACTERISTICS:
amino acids
o acid
linear
: protein

1.5%; Score 8; DB 2; Length 98;
arity 100.0%; Pred. No. 22;
nservative 0; Mismatches 0; Indels 0;
AATA 158
|||||
AATA 15

RESULT 134
US-07-812-421-2
: Sequence 2, Application US/07812421
: Patent No. 5932697
: GENERAL INFORMATION:
: APPLICANT: Caceci, Thomas
: APPLICANT: Toth, Thomas E.
: APPLICANT: Szumanski, Maria B.W.
: TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
: TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WHITHAM, CURTIS & WHITHAM
: STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
: STREET: Suite 900
: CITY: Reston
: STATE: VA
: COUNTRY: USA
: ZIP: 20191
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/812,421
: FILING DATE: 23-DEC-1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/588,437
: FILING DATE: 25-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Whitham, Michael E.
: REGISTRATION NUMBER: 32,635
: REFERENCE/DOCKET NUMBER: CIT.016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-391-2510
: TELEFAX: 703-391-9035
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 98 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-812-421-2

Query Match 1.5%; Score 8; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 151 AAAAAATA 158
|||||
Db 8 AAAAAATA 15

RESULT 135
US-08-702-344-16
: Sequence 16, Application US/08702344
: Patent No. 572315
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: LaVallie, Edward
: APPLICANT: Racie, Lisa
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Spaulding, Vikki
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
: TITLE OF INVENTION: ENCODING THEM
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:

Genetics Institute, Inc.
CambridgePark Drive
Irvine
California
S.A.

FILE FORM:
FLOPPY disk
BM PC compatible
STEM: PC-DOS/MS-DOS
attentIn Release #1.0, Version #1.30
ATTION DATA:
NUMBER: US/08/702,344

ON: 536

INFORMATION:

Scott A.

NUMBER: 32,724

TON INFORMATION:

(617) 498-8224

SEQ ID NO: 16:

CHARACTERISTICS:

amino acids

acid

linear

protein

1.5%; Score 8; DB 1; Length 116;

identity 100.0%; Pred. No. 26;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

PAL 438

||||

PAL 68

publication US/09621976

3

ON:

Malne Edwards, J.B.

rt, S.

dano, J.Y.

ON: ESTs and Encoded Human Proteins.

GENSET.054PR2

TON NUMBER: US/09/621,976

DATE: 2000-07-21

NOS: 19335

.pm

sapiens

EE

ON: Xaa = *,Trp

EE

ON: Xaa = Ala,Pro

EE

ON: Xaa = Asp,His

1.5%; Score 8; DB 4; Length 117;

identity 100.0%; Pred. No. 26;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 AAAAAAAP 127
Db |||||
2 AAAAAAAP 9

RESULT 137

US-09-072-596-243

; Sequence 243, Application US/09072596

; Patent No. 6458366

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Twardzik, Daniel R.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Hendrickson, Ronald C.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

; NUMBER OF SEQUENCES: 350

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/072,596

; FILING DATE: 05-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.417C9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 243:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 123 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-072-596-243

Query Match 1.5%; Score 8; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 GGGGGAGG 266
Db |||||
107 GGGGGAGG 114

RESULT 138

US-09-072-967-248

; Sequence 248, Application US/09072967

; Patent No. 6592877

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Campos-Neto, Antonio

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

wardzik, Daniel R.
odes, Michael J.
endrickson, Ronald C.
NTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TION: AND DIAGNOSIS OF TUBERCULOSIS
UENCES: 355
E ADDRESS:
SEED and BERRY LLP
00 Columbia Center, 701 Fifth Avenue
tle
hington
SA
-7092
ABLE FORM:
: Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
CATION DATA:
NUMBER: US/09/072,967
: 05-MAY-1998
ION:
T INFORMATION:
David J.
N NUMBER: 31,392
CKET NUMBER: 210121.411C9
TION INFORMATION:
(206) 622-4900
206) 682-6031
SEQ ID NO: 248:
ACTERISTICS:
3 amino acids
o acid
S: single
linear
: protein

1.5%; Score 8; DB 4; Length 123;
arity 100.0%; Pred. No. 27;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
GAGG 266
|||
GAGG 114
plication US/09198452A
94
ION:
fais, R.
ION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
ION: thereof and uses thereof, in particular for the diagnosis, preve
ION: and treatment of infection
9710-003-999
TION NUMBER: US/09/198,452A
DATE: 1998-11-24
D NOS: 6849

mydia pneumoniae

1.5%; Score 8; DB 4; Length 125;
arity 100.0%; Pred. No. 27;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
ATAP 159
|||
ATAP 96

RESULT 140
US-09-252-991A-30453
; Sequence 30453, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30453
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30453

Query Match 1.5%; Score 8; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 135 PPPAPVAA 142
|||
Db 43 PPPAPVAA 50

RESULT 141
US-09-489-039A-8788
; Sequence 8788, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8788
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8788

Query Match 1.5%; Score 8; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 15 AATTAAAA 22
|||
Db 18 AATTAAAA 25

RESULT 142
US-09-252-991A-21247
; Sequence 21247, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

N NUMBER: US 60/074,788
E: 1998-02-18
N NUMBER: US 60/094,190
E: 1998-07-27
NOS: 33142

omonas aeruginosa
7

1.5%; Score 8; DB 4; Length 137;
rity 100.0%; Pred. No. 30;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PSR 316
|||
PSR 134

7
6
pplication US/09489039A

ON:

Bretton et. al
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
ON: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
2709.2004001
ION NUMBER: US/09/489,039A
ATE: 2000-01-27
N NUMBER: US 60/117,747
E: 1999-01-29
NOS: 14342

iella pneumoniae
7

1.5%; Score 8; DB 4; Length 146;
rity 100.0%; Pred. No. 32;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 155
|||
AAA 75

2
5
pplication US/09252991A

ON:

J. Rubenfield et al.
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
ION NUMBER: US/09/252,991A
ATE: 1999-02-18
N NUMBER: US 60/074,788
E: 1998-02-18
N NUMBER: US 60/094,190
E: 1998-07-27
NOS: 33142

omonas aeruginosa
2

1.5%; Score 8; DB 4; Length 148;
rity 100.0%; Pred. No. 32;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 148 APRAAAAA 155
|||
Db 117 APRAAAAA 124

RESULT 145

US-09-489-039A-10001
; Sequence 10001, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TO PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10001
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10001

Query Match 1.5%; Score 8; DB 4; Length 149;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 GSGGGAGG 266
|||
Db 94 GSGGGAGG 101

RESULT 146

US-09-433-241A-4
; Sequence 4, Application US/09433241A
; Patent No. 6525244
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Ralfalski, Antoni
; TITLE OF INVENTION: Plant Histidinol-Phosphate Aminotransferase Homoc
; FILE REFERENCE: BB1256 US NA
; CURRENT APPLICATION NUMBER: US/09/433,241A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,273
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Oryza sp.
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (88)
; OTHER INFORMATION: Xaa = ANY AMINO ACID
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa = ANY AMINO ACID
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (137)
; OTHER INFORMATION: Xaa = ANY AMINO ACID
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (138)
; OTHER INFORMATION: Xaa = ANY AMINO ACID
US-09-433-241A-4

1.5%; Score 8; DB 4; Length 162;
arity 100.0%; Pred. No. 35;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
|||||
AAAA 63

location US/09140749
95
ION:
k, Peter
house, Mark A.
er, Samar
; Alfred W.K.
; Alan, Sean V.
ION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
2318-205
TION NUMBER: US/09/140,749
DATE: 1998-08-26
TION NUMBER: U.S. 08/791,115
DATE: 1997-01-30
TION NUMBER: U.S. 60/057,750
DATE: 1997-08-26
TION NUMBER: U.S. 60/083,563
DATE: 1998-04-30
D NOS: 64
tin ver. 2.0

musculus

1.5%; Score 8; DB 4; Length 194;
arity 100.0%; Pred. No. 41;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127
|||||
AAAP 39

26
Application US/09252991A
95
ION:
c J. Rubenfield et al.
ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
TION NUMBER: US/09/252,991A
DATE: 1999-02-18
ON NUMBER: US 60/074,788
TE: 1998-02-18
ON NUMBER: US 60/094,190
TE: 1998-07-27
D NOS: 33142

domonas aeruginosa
26

1.5%; Score 8; DB 4; Length 202;
arity 100.0%; Pred. No. 42;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 AAAAAAP 127
Db 92 AAAAAAP 99
|||||

RESULT 149
US-08-463-115-92
; Sequence 92, Application US/08463115
; Patent No. 5703221
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,115
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: Four
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5703221ember 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-115-92

Query Match 1.5%; Score 8; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 133 PPPPPAPV 140
Db 197 PPPPPAPV 204
|||||

RESULT 150
US-08-465-388-92
; Sequence 92, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:

1:33:39 2004

us-09-976-740-43.olig.ra

P

LIAM JOHN MARTIN
ION: ISOLATED STEALTH VIRUSES
ION: AND RELATED VACCINES

ENCES: 104
ADDRESS:

Lyon & Lyon
West Fifth Street
te 4700
geles
ornia
S.A.
2066

BLE FORM:
3.5" Diskette, 1.44 Mb
Storage

BM Compatible
STEM: IBM P.C. DOS 5.0
astSeq Version 1.5
ATION DATA:

NUMBER: US/08/465,388
June 5, 1995

DN: 435

ION DATA: including application

ION DATA: described below:

Four

NUMBER: 08/157,811

No. 575348ember 23, 1993

NUMBER: 07/887,502

May 22, 1992

NUMBER: 07/704,814

May 23, 1991

NUMBER: 07/763,039

September 20, 1991

INFORMATION:

g, Richard J.

NUMBER: 32,327

ION NUMBER: 213/300

ION INFORMATION:

(213) 489-1600

(3) 955-0440

310

SEQ ID NO: 92:

TERISTICS:

amino acids

acid

single

near

1.5%; Score 8; DB 1; Length 218;

ity 100.0%; Pred.No.46;

servative 0; Mismatches 0; Indels 0; Gaps 0;

PV 140

||

PV 204

rch 30, 2004, 15:04:24

GenCore version 5.1.6
copyright (c) 1993 - 2004 Compugen Ltd.

n search, using sw model

ch 30, 2004, 14:54:16 ; Search time 60 Seconds
(without alignments)
2533.509 Million cell updates/sec

09-976-740-43

AGPPALPPPTAAATAA.....HKVLQGHFDDDDPFGFLG 538

30

cp 60.0 , Gapext 60.0

6107 seqs, 282547505 residues

s satisfying chosen parameters: 1586107

th: 0

ch: 2000000000

sting first 150 summaries

Genesep29Jan04.*

genesep1980s.*

genesep1990s.*

genesep2000s.*

genesep2001s.*

genesep2002s.*

genesep2003as.*

genesep2003bs.*

genesep2004s.*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
i by analysis of the total score distribution.

SUMMARIES

cy	Length	DB	ID	Description
0	538	4	AAB82806	Aab82806 Human low
3	217	2	AAW49041	Aaw49041 Human low
3	217	4	AAB82803	Aab82803 Human low
5	132	7	ADe59158	Ad59158 Human Pro
8	241	3	AAB58957	Aab58957 Breast an
4	550	4	AAB82807	Aab82807 Rabbit lo
1	232	4	AAB82799	Aab82799 Rabbit lo
1	252	4	AAB82800	Aab82800 Rabbit lo
1	317	4	AAB82798	Aab82798 Rabbit lo
3	61	3	AAB34365	Aab34365 Human sec
0	317	2	AAW49038	Aaw49038 Rabbit lo
4	316	4	AAU31793	Aau31793 Novel hum
8	26	4	AAB82810	Aab82810 Human low
8	15	4	AAB82809	Aab82809 Human pol
8	102	4	AAAM39592	Aam39592 Human pol
8	102	4	ABP50215	Abp50215 Human tra
8	108	5	ABP58930	Abp58930 Human cel
8	114	4	AAW41378	Aaw41378 Human pol
8	116	6	ADA55289	Ada55289 Human pro
2	104	4	ABE67522	Ab67522 Drosophil
2	2280	4	ABE61650	Ab61650 Drosophil
0	11	4	AAAB2811	Aab2811 Human low
0	12	4	AAAB2817	Aab2817 Rabbit lo
0	28	4	AAAB2816	Aab2816 Rabbit lo
0	129	3	AAAY51200	Aay51200 Human sca

Aar22382 Ant
Abg76914 Ric
Abg17272 Nov
Add18910 Hun
Adc59312 Hun
Aae37017 Hun
Aab28212 Hun
Aab28218 Rak
Aau97858 Prc
Abb64202 Drc
Abb69039 Drc
Abr43149 Rye
Aag34163 Zee
Aab17208 Prc
Ada36364 Ac1
Aay25630 Phl
Adc34880 Tin
Aay25633 Phl
Adc34883 Tin
Aag34499 Ara
Aab42629 Hum
Aag34498 Ara
Abp54691 Met
Aay32114 Mai
Abp51652 Mai
Aag34497 Ara
Aag34497 Prc
Aba47065 Prc
Abu22735 Prc
Abu15059 Prc
Aab18192 Pla
Aab62471 Drc
Aba47568 Prc
Abu47065 Prc
Abu22735 Prc
Abg17677 Nov
Abp60866 Drc
Abb607036 Mou
Aaw59361 Dro
Abb65508 Dro
Abd65470 Dro
Aab76536 Cor
Abb65129 Dro
Aba65152 Hum
Abp73792 Can
Abd08801 Yea
Abb08807 Yea
Abb08803 Yea
Abb08805 Yea
Abb08802 Yea
Abb08806 Yea
Abb08804 Yea
Abr52621 Pro
Aba8253 Nov
Aba90132 Nov
Aba96434 Nov
Aba99043 Nov
Aba98258 Nov
Aba91964 Nov
Aba95204 Nov
Aba85268 Nov
Aba00407 Nov
Aba88958 Nov
Aba06454 Nov
Aba95514 Nov
Aba95204 Nov
Aba90752 Nov
Aba93914 Nov
Aba86188 Nov
Aba82043 Nov
Aba07904 Nov
Aba94224 Nov
Aba00097 Nov
Aba87108 Nov

L-9 1894 6 ABU91349 Novel hum
 L-9 1894 6 ABU90442 Novel hum
 L-9 1894 6 ABU97033 Novel hum
 L-9 1894 6 ABO05229 Novel hum
 L-9 2012 4 AAB76534 Coryneb
 L-9 2993 4 AAG92485 Coryneb
 L-7 43 3 AAG34648 C glucam
 L-7 49 3 AAG52678 Arabidops
 L-7 51 3 AAG52700 Arabidops
 L-7 52 4 ABUS2912 Human ute
 L-7 66 3 AAG01387 Human sec
 L-7 68 3 AAG34705 Arabidops
 L-7 68 3 AAG28554 Arabidops
 L-7 68 3 AAG52668 Arabidops
 L-7 68 3 AAG52680 Arabidops
 L-7 68 3 AAG21112 Arabidops
 L-7 69 3 AAG41928 Arabidops
 L-7 70 3 AAG34561 Arabidops
 L-7 74 3 AAG34647 Arabidops
 L-7 76 2 AAR22394 Antigen t
 L-7 79 3 AAG34372 Arabidops
 L-7 80 3 AAG52677 Arabidops
 L-7 81 3 AAG52679 Arabidops
 L-7 82 3 AAG52699 Arabidops
 L-7 84 3 AAG34371 Arabidops
 L-7 84 6 ABR69624 Human CGD
 L-7 87 3 AAG34646 Arabidops
 L-7 93 3 AAG52676 Arabidops
 L-7 95 3 AAG52698 Arabidops
 L-7 96 3 AAG13034 Arabidops
 L-7 99 3 AAG21111 Arabidops
 L-7 99 3 AAG28553 Arabidops
 L-7 99 3 AAG34704 Arabidops
 L-7 99 3 AAG52667 Arabidops
 L-7 99 3 AAG52671 Arabidops
 L-7 100 3 AAG52671 Arabidops
 L-7 101 3 AAG34560 Arabidops
 L-7 105 4 ABG25320 Novel hum
 L-7 109 3 AAG34350 Zea may
 L-7 111 4 AAM19703 Peptide #
 L-7 111 4 ABB71018 Drosophil
 L-7 111 4 ABB39430 Peptide #
 L-7 111 4 ABB32953 Peptide #
 L-7 111 4 ABB24202 Protein #
 L-7 111 4 AAM72722 Human bon
 L-7 111 4 AAM60110 Human bra
 L-7 111 4 ABG54420 Human liv
 L-7 111 5 ABG42546 Human pep
 L-7 112 2 AAY18127 Clone 1 o
 L-7 112 3 AAG34703 Arabidops
 L-7 112 3 AAG52670 Arabidops
 L-7 112 3 AAG21110 Arabidops

ALIGNMENTS

lard; protein; 538 AA.

(first entry)

ity lipoprotein binding protein 2 (LBP-2).

poprotein binding protein 2; LBP-2; LDL; human;
 s; antiarteriosclerotic; therapy; diagnosis; vaccine.

XX 07-SEP-2001.
 PD
 XX 28-FEB-2001; 2001WO-US006356.
 PF
 XX 02-MAR-2000; 2000US-00517849.
 PR 14-JUL-2000; 2000US-00616289.
 XX (BOST-) BOSTON HEART FOUND INC.
 XX
 PI Lees AM, Lees RS, Law SW, Arjona AA;
 XX WPI; 2001-565505/63.
 DR N-PSDB; AAB26499.
 DR
 XX New isolated low density lipoprotein binding polypeptide for trea
 PT diagnosing and/or identifying therapeutic agents for atherosclero
 XX Claim 13(j); Fig 7A; 143pp; English.

The present sequence is that of novel human low density lipoprote
 binding protein 2 (LBP-2). The amino acid sequence was deduced fr
 coding region of isolated genomic DNA (see AAB26499). It differs
 sequence predicted from an LBP-2 cDNA clone (see AAB82803) by the
 presence of an additional 321 amino acids at the N-terminus (the
 clone is 5' truncated). Human LBP-2 is an example of claimed LBP
 polypeptides of the invention that are capable of binding to nati
 methylated low density lipoproteins. Also claimed are biological
 fragments and analogues of LBPs, polynucleotides encoding LBPs, a
 as expression vectors, cells and methods of producing the LBPs.
 CC Polypeptides having amino acid residues 329-343, 329-354, 344-354
 CC -538 (see AAB82809-12) of the present sequence are claimed. Method
 CC determining if an animal is at risk for atherosclerosis, methods
 CC evaluating an agent for use in treating atherosclerosis, and meth
 CC treating a cell having an abnormality in structure or metabolism;
 CC are claimed. Pharmaceutical compositions comprising an LBP polypep
 CC nucleic acid, and vaccine compositions, are also claimed

XX Sequence 538 AA;

Query Match 100.0%; Score 538; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; G;

QY 1 MAGPPALPPETAAATTAATAAASSAASHYQWILDTIDSLRSRKARPDLEIRICI
 DB 1 MAGPPALPPETAAATTAATAAASSAASHYQWILDTIDSLRSRKARPDLEIRICI
 QY 61 RHGPEPTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRRGATPPAPPRAPR
 DB 61 RHGPEPTRAELEKLIQORAVLRVSYKGSISYRNAARVQPPRRGATPPAPPRAPR
 QY 121 AAAAAAPPTTAPPPPPAPVAAAAPARAAPAAAAATAPSPGAPQAPRAOAAAP
 DB 121 AAAAAAPPTTAPPPPPAPVAAAAPARAAPAAAAATAPSPGAPQAPRAOAAAP
 QY 181 PPAPAPPAVAPAGERRAPPAPPAAREPLPPPPPPQPPAPPQQQPPPPQPPPPPK
 DB 181 PPAPAPPAVAPAGERRAPPAPPAAREPLPPPPPPQPPAPPQQQPPPPQPPPPPK
 QY 241 RAGGAARPVSLREVRYLGGSGGAGRLTRGRVQGLLEEEAAARGRLERLALAI
 DB 241 RAGGAARPVSLREVRYLGGSGGAGRLTRGRVQGLLEEEAAARGRLERLALAI
 QY 301 DRPGRAPPAASARPSRSGEERVLEKEEEDDEDEDEDEDDVSGSVPSDRP
 DB 301 DRPGRAPPAASARPSRSGEERVLEKEEEDDEDEDEDEDDVSGSVPSDRP
 QY 361 HHQLNGERGQSAKERVKEWTFQPHQGDGGRGAPGSGTGRQVFSMAAMNKEGGT
 DB 361 HHQLNGERGQSAKERVKEWTFQPHQGDGGRGAPGSGTGRQVFSMAAMNKEGGT
 QY 421 TQPDSPSPVPLPGKALPGADTFFGCPGGRKEKPSDPVETVMDVVEYFTEAGFI

|||||
 ?SVPLPPGKPAFGADGTFPGCGPKPKSPDVEWTVMDVVEYFTEAGFPPEQA 480
 DEIDGKSLMLMQRDVLTLGLSIRLGPALKIYEHKIKVLQOQHFEDEDDPDGFLG 538
 DEIDGKSLMLMQRDVLTLGLSIRLGPALKIYEHKIKVLQOQHFEDEDDPDGFLG 538

ard; protein; 217 AA.

first entry)

ity lipoprotein binding protein LBP-2.

oprotein binding protein; LDL binding protein 2; LBP-2;
 1; atherosclerosis; diagnosis; therapy; vaccine.

Location/Qualifiers

8..33 "Claim 2"
 /note= "Claim 2"
 8..22
 /note= "Claim 2"
 23..33
 /note= "Claim 2"
 208..217
 /note= "Claim 2"

97WO-US021857.

96US-0031930P.
 97US-0048547P.

HEART FOUND INC.

RS, Law SW, Arjona AA;

5/28.
 8.

coding low density lipoprotein binding proteins and
 - transformed cells, proteins, and modulators of binding,
 tment and diagnosis of atherosclerosis and for identifying
 ik.

47pp; English.

le comprises novel human low density lipoprotein (LDL)
 LBP-2 that is capable of binding both native and methyl
 acid sequence was deduced from an isolated cDNA clone (see
 clones (see AAV32834-39) and encoded rabbit and human
 037-42) are claimed. An abnormality in an aspect of LBP
 structure is diagnostic of a risk for atherosclerosis. The
 des: methods for determining if an animal is at risk for
 (e.g. for prenatal screening); methods for treating
 (including gene therapy) using e.g. LBP polypeptides to
 hereby prevent formation of atherosclerotic plaque; and
 ating a cell having an abnormality in LBP structure or
 pharmaceutical and vaccine compositions are also provided, as
 nant vectors and host cells used to produce recombinant

Query Match 40.3%; Score 217; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 2.8e-182;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gs
 QY 322 EERVLEKEHEDEDEDEDDVSEGVPSDRPAGAHQHLNGERGPQSAKERVK
 DB 1 EERVLEKEHEDEDEDEDDVSEGVPSDRPAGAHQHLNGERGPQSAKERVK
 QY 382 PCGPHQODEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVLPKPKFAL
 DB 61 PCGPHQODEGRGAPGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVLPKPKFAL
 QY 442 DGTFFGCGPPGKPKSPDVEWTVMDVVEYFTEAGFPPEQATAFQEQEI DGKSLMLMQR
 DB 121 DGTFFGCGPPGKPKSPDVEWTVMDVVEYFTEAGFPPEQATAFQEQEI DGKSLMLMQR
 QY 502 LTGLSIRLGPALKIYEHKIKVLQOQHFEDEDDPDGFLG 538
 DB 181 LTGLSIRLGPALKIYEHKIKVLQOQHFEDEDDPDGFLG 217

RESULT 3

AAB82803
 ID AAB82803 standard; protein; 217 AA.

XX AC AAB82803;

XX DT 12-NOV-2001 (first entry)

XX DE Human low density lipoprotein binding protein 2 (LBP-2).

XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;
 XX KW atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine
 XX OS Homo sapiens.

XX EN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SW, Arjona AA;

XX DR WPI; 2001-565505/63.

XX DR N-PSDB; AAB26494.

XX FT New isolated low density lipoprotein binding polypeptide for treat:
 XX FT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Claim 13(g); Fig 7B; 143pp; English.

XX CC The present sequence is that of the N-terminal portion of novel hu
 CC density lipoprotein binding protein 2 (LBP-2). The amino acid sequ
 CC deduced from an isolated partial cDNA clone (see AAB26494). A full-
 CC sequence is given in AAB82806. Human LBP-2 is an example of claimed
 CC polypeptides of the invention that are capable of binding to native
 CC methylated low density lipoproteins. Also claimed are biologically
 CC fragments and analogues of LBPs, polynucleotides encoding LBPs, as
 CC as expression vectors, cells and methods of producing the LBPs. Met
 CC of determining if an animal is at risk for atherosclerosis, methods
 CC evaluating an agent for use in treating atherosclerosis, and method
 CC treating a cell having an abnormality in structure or metabolism of
 CC are claimed. Pharmaceutical compositions comprising an LBP polypept
 CC nucleic acid, and vaccine compositions, are also claimed

XX SQ Sequence 217 AA;

40.3%; Score 217; DB 4; Length 217;
 rity 100.0%; Pred. No. 2.8e-182;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EKEREDDDDEDEDDVSEGEVPSDRPAGAHQHLNGRGPSAKERVKEWT 381
 EKEREDDDDEDEDDVSEGEVPSDRPAGAHQHLNGRGPSAKERVKEWT 60
 IQQDEGRGPAGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVLPKPGALPGA 441
 IQQDEGRGPAGSGTRQVFSMAAMNKEGGTASVATGPDSPSPVLPKPGALPGA 120
 GCPGRKXKPSDPVWTWMDVVVEYFTEAGFPEQATFQOEIDGKSLLMQRTDV 501
 GCPGRKXKPSDPVWTWMDVVVEYFTEAGFPEQATFQOEIDGKSLLMQRTDV 180
 IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 538
 IRLGPALKIYEHKIKVLOQGHFEDDDPDGFLG 217

ard; protein; 132 AA.

(first entry)

XP_031299, SEQ ID NO 5049.

neural tissue; gene therapy;
 al nerve injury; chronic constriction injury; CCI;
 njury; SNI; Chung.

2.

002WO-US025765.

001US-0312147P.

001US-0346382P.

001US-0333347P.

OSPITAL CORP.

AG.

so D, Befort K, Costigan M;

12/26.

1299.

on comprising two or more isolated polypeptides, useful for
 dicament for treating pain in an animal.

1017pp; English.

discloses a composition comprising two or more isolated rat
 nucleotides or a polynucleotide which represents a fragment,
 allelic variation of the nucleic acid sequence. Also
 vector comprising the novel polynucleotide, a host cell
 a vector, a method for identifying a nucleotide sequence
 essentially regulated in an animal subjected to pain and a
 the method, an array, a method for identifying an agent
 or decreases the expression of the polynucleotide sequence
 essentially expressed in neuronal tissue of a first animal
 pain, a method for identifying a compound which regulates
 of a polynucleotide sequence which is differentially
 an animal subjected to pain, a method for identifying a
 regulates the activity of one or more of the

polynucleotides, a method for producing a pharmaceutical composi
 method for identifying a compound or small molecule that regulate
 activity in an animal of one or more of the polypeptides given in
 specification, a method for identifying a compound useful in trea
 pain and a pharmaceutical composition comprising the one or more
 polypeptides or their antibodies. The polynucleotide or the compo
 modulates its activity is useful for preparing a medicament for t
 pain (e.g. spinal segmental nerve injury (Chung), chronic constr
 injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. ge
 therapy). The sequence presented is a human protein (shown in Tab
 the specification) which is differentially expressed during pain.
 the sequence data for this patent did not form part of the printer
 specification, but was obtained in electronic form directly from
 ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 132 AA;

Query Match 24.5%; Score 132; DB 7; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; G

QY 407 MAAMNKEGGTASVATGPDSPSPVLPKPGALPGADTFFGCPGKKEKPSDPVW
 Db 1 MAAMNKEGGTASVATGPDSPSPVLPKPGALPGADTFFGCPGKKEKPSDPVW

QY 467 VVEYFTEAGFPEQATFQOEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHKIKV
 Db 61 VVEYFTEAGFPEQATFQOEIDGKSLLMQRTDVLTLGLSIRLGPALKIYEHKIKV

QY 527 HFEDDDPDGFLG 538

Db 121 HFEDDDPDGFLG 132

RESULT 5

AAB58957

ID AAB58957 standard; protein; 241 AA.

XX AAB58957;

DT 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated antigen protein sequence SEQ

XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressi
 KW nootropic; neuroprotective; antiviral; antiallergic; hepatotropic
 KW antidiabetic; antiinflammatory; antitumor; vulnerrary; anticonvuls
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disord
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.

OS Homo sapiens.

XX WO200055173-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005881.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

DR N-PSDB; AAF21860.

XX New human breast and ovarian cancer associated gene sequences and
 PT polypeptides encoded by these genes, useful in the prevention, tre
 and diagnosis of cancer, immune disorders, cardiovascular disorder

seases.

1112; 1299pp; English.

614 - AAF22031 represent DNA sequences encoding human breast and ovarian cancer. Included in the invention are AAF22040 and AAF59129 which are used in the characterisation of the DNA and protein sequences of the breast and ovarian cancer associated DNA, protein, agonist sequences exhibit cytostatic; immunosuppressive; nontropic; antiviral; antiallergic; hepatotropic; antidiabetic; antitumor; antineoplastic; anticonvulsant; antibacterial; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly human cancer. The nucleic acid sequences, proteins, agonists and also be used in the diagnosis, prevention and treatment of cancer. e.g. Addison's disease, allergies, autoimmune disease, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, rheumatoid arthritis and ulcerative colitis; disorders such as myocardial ischaemia; wound healing; diseases such as cerebral anoxia and epilepsy; and diseases

;

20.8%; Score 112; DB 3; Length 241;

city 100.0%; Pred. No. 7e-90;

servative 0; Mismatches 0; Indels 0; Gaps 0;

APRSKRGGEERVLKEKEDEDEDEDEDDVSEGEVPESDRPAQHQLNG 366

APRSKRGGEERVLKEKEDEDEDEDEDDVSEGEVPESDRPAQHQLNG 69

AKERYKWTGCGPHQDGEGRGAPGSGTRQVFSMAAMNKEGGTAS 418

AKERYKWTGCGPHQDGEGRGAPGSGTRQVFSMAAMNKEGGTAS 121

urd; protein; 550 AA.

first entry)

ity lipoprotein binding protein 2 (LBP-2).

oprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine.

iculus.

01WO-US006356.

00US-00517849.

00US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

15/63.

10.

ow density lipoprotein binding polypeptide for treating, or identifying therapeutic agents for atherosclerosis.

PS Claim 13(k); Fig 2a; 143pp; English.
XX The present sequence is that of a full-length sequence of novel ra
CC low density lipoprotein binding protein 2 (LBP-2). The amino acid
CC sequence is deduced from an isolated cDNA clone (see AAF26500). Ra
CC LBP-2 is an example of claimed polypeptides of the invention, term
CC LBP, that are capable of binding to native and methylated low den
CC lipoproteins. Also claimed are biologically active fragments and
CC analogues of LBPs, polynucleotides encoding LBPs, as well as expe
CC vectors, cells and methods of producing the LBPs. Polypeptides hav
CC amino acid residues 338-353, 338-365, 354-365 or 444-453 (see AAB8
CC 18) of the present sequence are claimed. Methods for evaluating an a
CC animal is at risk for atherosclerosis, methods for evaluating a ce
CC for use in treating atherosclerosis, and methods for treating a ce
CC having an abnormality in structure or metabolism of LBP are also c
CC as are pharmaceutical compositions comprising an LBP polypeptide o
CC nucleic acid, and vaccine compositions
XX
SQ Sequence 550 AA;

Query Match 18.4%; Score 99; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Ga

QY 19 AAAASSAASPHYQEWILDTIDSLRSKARPDLEICRMVRRRHGPEPTRAELEK
Db 20 AAAASSAASPHYQEWILDTIDSLRSKARPDLEICRMVRRRHGPEPTRAELEK

QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPAPRPRG 117

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPRPRG 118

RESULT 7

AAB82799

ID AAB82799 standard; protein; 232 AA.

AC AAB82799;

DT 12-NOV-2001 (first entry)

DE Rabbit low density lipoprotein binding protein 2 (LBP-2).

KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
KW atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine
OS Oryctolagus cuniculus.

PN WO200164874-A2.

XX 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006356.

XX 02-MAR-2000; 2000US-00517849.

PR 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

XX Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.

DR N-PSDB; AAF26489.

PT New isolated low density lipoprotein binding polypeptide for treat;
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

PS Claim 13(c); Fig 3; 143pp; English.

XX The present sequence is that of a partial sequence of novel rabbit
CC density lipoprotein binding protein 2 (LBP-2). The amino acid sequ
CC deduced from an isolated cDNA clone (see AAF26489). Full-length ra
CC LBP-2 is given in AAB82807. Rabbit LBP-2 is an example of claimed

of the invention, termed LBP-3, that are capable of binding methylated low density lipoproteins. Also claimed are active fragments and analogues of LBP-3, polynucleotides, as well as expression vectors, cells and methods of LBP-3. Methods of determining if an animal is at risk for is, methods for evaluating an agent for use in treating is, and methods for treating a cell having an abnormality in metabolism of LBP are also claimed, as are pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine

AA;
arity 14.1%; Score 76; DB 4; Length 232;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
ATVMDVVEYTEAGPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALYIE 517
ATVMDVVEYTEAGPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPALYIE 211
VLOQGHFEDDDP 533
VLOQGHFEDDDP 227

iard; protein; 252 AA.

(first entry)

isity lipoprotein binding protein 3 (LBP-3).

ipoprotein binding protein 3; LBP-3; LDL; rabbit;
is; antiarteriosclerotic; therapy; diagnosis; vaccine.

miculus.

2.

2001WO-US006356.

2000US-00517849.

2000US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

505/63.

190.

low density lipoprotein binding polypeptide for treating,
i/or identifying therapeutic agents for atherosclerosis.

Fig 4; 143pp; English.

sequence is that of a partial sequence of novel rabbit low
protein binding protein 3 (LBP-3). The amino acid sequence is
in isolated cDNA clone (see AAH26490). A full-length
rabbit LBP-3 is given in AAH2801. Rabbit LBP-3 is an
aimed polypeptides of the invention, termed LBP-3, that are
adding to native and methylated low density lipoproteins.
are biologically active fragments and analogues of LBP-3,
as encoding LBP-3, as well as expression vectors, cells and
producing the LBP-3. Methods of determining if an animal is at
therosclerosis, and methods for evaluating an agent for use in
therosclerosis, and methods for treating a cell having an

CC abnormality in structure or metabolism of LBP are also claimed, a
CC pharmaceutical compositions comprising an LBP polypeptide or nucl
CC acid, and vaccine compositions
XX
SQ Sequence 252 AA;

Query Match 14.1%; Score 76; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.4e-58;
Matches 76; Conservative 0; Mismatches 0; Indels 0; G

QY 458 DPVEWTVMVVEYTEAGPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 172 DPVEWTVMVVEYTEAGPEQATFOEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQOQHFEEDDP 533
Db 232 HHKVLQOQHFEEDDP 247

RESULT 9

AAH82798

ID AAB82798 standard; protein; 317 AA.

XX AC AAB82798;

XX DT 12-NOV-2001 (first entry)

XX DE Rabbit low density lipoprotein binding protein 2 (LBP-2).

XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;

XX XW atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccin

XX OS Oryctolagus cuniculus.

XX PH Key Location/Qualifiers

FT Misc-difference 10

FT /note= "encoded by TAG"

XX PN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SW, Arjona AA;

XX DR WPI; 2001-565505/63.

XX DR N-PSDB; AAH26488.

XX PT New isolated low density lipoprotein binding polypeptide for treati

XX PT diagnosing and/or identifying therapeutic agents for atherosclero

XX PS Claim 13 (b); Fig 2b; 143pp; English.

XX CC The present sequence is that of a partial sequence of novel rabbit

XX CC density lipoprotein binding protein 2 (LBP-2). The amino acid sequ

XX CC deduced from an isolated cDNA clone (see AAH26488). Full-length r

XX CC LBP-2 is given in AAH2807. Rabbit LBP-2 is an example of claimed

XX CC polypeptides of the invention, termed LBP-2, that are capable of b

XX CC to native and methylated low density lipoproteins. Also claimed a

XX CC biologically active fragments and analogues of LBP-2, polynucleot

XX CC encoding LBP-2, as well as expression vectors, cells and methods of

XX CC producing the LBP-2. Methods of determining if an animal is at ris

XX CC atherosclerosis, methods for evaluating an agent for use in treati

XX CC atherosclerosis, and methods for treating a cell having an abnorma

XX CC structure or metabolism of LBP are also claimed, as are pharmaceut

XX CC compositions comprising an LBP polypeptide or nucleic acid, and v

XX CC compositions

ide comprises novel rabbit low density lipoprotein (LDL) in LBP-2 that is capable of binding both native and methylated apoB-100. The LBP-2 cDNA sequence was deduced from rabbit abdominal aorta cDNA clones (see AAV32834-39) and encoded rabbit and human apoB-100 are claimed. An abnormality in an aspect of the LBP-2 gene is claimed. The LBP-2 gene abnormality provides a method for determining if an animal is at risk for atherosclerosis (e.g. for prenatal screening); methods for treating atherosclerosis (including gene therapy) using e.g. LBP polypeptides to thereby prevent formation of atherosclerotic plaque; and creating a cell having an abnormality in LBP structure or function. Pharmaceutical and vaccine compositions are also provided, as are LBP-2 gene constructs and vectors and cells used to produce recombinant LBP-2 proteins. The LBP-2 gene is also claimed.

1A: 11.0%; Score 59; DB 2; Length 317;
arity 100.0%; Pred. No. 3.7e-43;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
JATAFQEIEIGKSLLMQRTDVLVTGLSIRLGPAKIEYHHIKVLOQGHFEDDDP 533
JATAFQEIEIGKSLLMQRTDVLVTGLSIRLGPAKIEYHHIKVLOQGHFEDDDP 312

iard; protein; 316 AA.

(first entry)

secreted protein #2284.

- ation; gene therapy; nutritional supplement;
- liferation; haematopoiesis; nerve tissue regeneration;
- ession; immune stimulation; anti-inflammatory; leukaemia.

3

001WO-US008656.

:000US-00552929.

001US-00770160.

INC.

C, Drmanac RT;

'25/70.

encoding a range of human polypeptides, useful in genetic testing and therapy.

p. 509; 765pp; English.

relates to novel human secreted polypeptides. The use of antibodies to the polypeptides are useful for the presence of or predisposition to a disease associated with a particular polypeptide. The polypeptides are also useful for the treatment of a pathology related to aberrant expression or interactions of the polypeptide. Vectors comprising the encoding the polypeptides and cells genetically engineered to express the polypeptides are also useful for producing the proteins. The proteins are also useful for identifying a therapeutic agent or antagonist that binds to the protein.

4.8%; Score 26; DB 4; Length 26;
rity 100.0%; Pred.No. 5e-15;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEEDDDVSEGSEVPESD 354
|||||
DDEDEEDDDVSEGSEVPESD 26

ard; peptide; 15 AA.

first entry)

ity lipoprotein binding protein 2 (LBP-2) peptide.

poprotein binding protein 2; LBP-2; LDL; human;
s; antiarteriosclerotic; therapy; diagnosis; vaccine.

001WO-US006356.

000US-00517849.

000US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

05/63.

ow density lipoprotein binding polypeptide for treating,
/or identifying therapeutic agents for atherosclerosis.

age; 143pp; English.

quence is that of a peptide comprising amino acid residues
al human low density lipoprotein binding protein 2 (LBP-2,
Human LBP-2 is an example of claimed LBP polypeptides of
that are capable of binding to native and methylated low
proteins (LDLs). Also claimed are biologically active
analogues of LBPs, polynucleotides encoding LBPs, as well
ectors, cells and methods of producing the LBPs.
iving the present amino acid sequence are among those
is of determining if an animal is at risk for
; methods for evaluating an agent for use in treating
; metabolism of LBP are also claimed, as are pharmaceutical
mprising an LBP polypeptide or nucleic acid, and vaccine
note: the present sequence is not shown in the
ut is derived from the human LBP-2 sequence given in
AAB82806)

2.8%; Score 15; DB 4; Length 15;
city 100.0%; Pred.No. 1.5e-05;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DDEDEEDD 343

|||||

DDEDEEDD 15

AAM39592
ID AAM39592 standard; protein; 102 AA.

XX AAM39592;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2737.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; car
peripheral nervous system; neuropathy; central nervous system; CNS
Alzheimer's; Parkinson's disease; Huntington's disease; haemostati
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammatory
leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wan

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Z

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-FSDB; AAI58748.

XX Novel nucleic acids and polypeptides, useful for treating disorder
as central nervous system injuries.

XX Example 4; SEQ ID NO 2737; 10078pp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) a
encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are
in gene therapy. A composition containing a polypeptide or polynuc
of the invention may be used to treat diseases of the peripheral n
system, such as peripheral nervous injuries, peripheral neuropathy
localised neuropathies and central nervous system diseases, such a
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophi
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemo
and thrombolytic activity, cancer diagnosis and therapy, drug scre
assays for receptor activity, arthritis and inflammation, leukaemi
C.N.S disorders. Note: The sequence data for this patent did not fi
part of the printed specification

XX Sequence 102 AA;

Query Match 2.8%; Score 15; DB 4; Length 102;
Best Local Similarity 100.0%; Pred.No. 7.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 482 AFQEQEIDGKSLIM 496

|||||

Db 51 AFQEQEIDGKSLIM 65

lard; protein; 102 AA.
 (first entry)
 .ption factor TRFX-66.
 .ption factor; TRFX; cell proliferative disease;
 sease; inflammation; neurological disease;
 disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
 re; antiinflammatory; gene therapy.
 .
 :001WO-US008117.
 :000US-0188986P.
 : GENOMICS INC.
 laughn MR, Yue H, Lal P, Lu DAM, Patterson C;
 andman O, Tang YT, Mathur P, Shah P, Au-Young J;
 96/64.
 39.
 tion factor polypeptides, used to treat diseases
 h altered activity and expression of TRFX, and to screen
 able of modulating its activity.
 210; 327pp; English.
 quence is the protein sequence for a human transcription
 anscription factor and its coding sequence are useful in
 treatment and prevention of diseases associated with
 sion of the transcription factor e.g. cell proliferative,
 llamatory, neurological and developmental disorders. A
 ific disorders/diseases are given in the specification,
 eriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
 emia, asthma, autoimmune thyroiditis, bronchitis, atopic
 abetes mellitus, emphysema, Goodpasture's syndrome, gout,
 e, multiple sclerosis, osteoarthritis, pancreatitis,
 umatoid arthritis, systemic lupus erythematosus, ulcerative
 is, Alzheimer's disease, Huntington's disease, Parkinson's
 e, and viral, bacterial, fungal and protozoal infections
 A;
 2.8%; Score 15; DB 4; Length 102;
 rity 100.0%; Pred. No. 7.3e-05;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EIDGKSLLLM 496
 |||||
 EIDGKSLLLM 65
 ard; protein; 108 AA.
 14-APR-2003 (first entry)
 Human cell factor signal inhibitor 11.88.
 Human; cell factor signal inhibitor 11.88; recombinant production
 gene therapy; malignant tumour; cancer; blood disease; HIV infect
 human immunodeficiency virus; immune disorder; inflammatory condi
 cytostatic; antiinflammatory; immunomodulator.
 XX
 OS Homo sapiens.
 XX
 PN CN1361159-A.
 XX
 PD 31-JUL-2002.
 XX
 PF 26-DEC-2000; 2000CN-00136316.
 XX
 PR 26-DEC-2000; 2000CN-00136316.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-751578/82.
 DR N-PSDB; ABZ57768.
 XX
 PT New polypeptide human cell factor signal inhibitor 11.88 and
 polynucleotides encoding this polypeptide.
 PS Claim 1; Page 28 (Disclosure); 34pp; Chinese.
 XX
 CC The invention relates to human cell factor signal inhibitor 11.88
 CC (ABP58930) and nucleic acids encoding it (ABZ57768). The protein
 CC molecular weight of 11.88 kD. The invention also relates to a met
 CC the recombinant production of the protein, an antagonist of the p
 CC and the use of the protein, gene and antagonist in therapeutic
 CC applications. Cell factor signal inhibitor 11.88 can be used in t
 CC treatment of a variety of diseases such as malignant tumours, blo
 CC diseases, HIV (human immunodeficiency virus) infection, immune di
 CC and inflammatory conditions. The present sequence represents huma
 CC factor signal inhibitor 11.88
 XX
 SQ Sequence 108 AA;
 Query Match 2.8%; Score 15; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; G
 QY 482 AFQEQEIDGKSLLLM 496
 Db 57 AFQEQEIDGKSLLLM 71
 RESULT 18
 AAM41378
 ID AAM41378 standard; protein; 114 AA.
 XX
 AC AAM41378;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 6309.
 XX
 XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; can
 KW peripheral nervous system; neuropathy; central nervous system; CNS
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostati
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammatory
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.

00WO-US034263.
 99US-00471275.
 00US-00488725.
 00US-00552317.
 00US-00598042.
 00US-00620312.
 00US-00653450.
 00US-00662191.
 00US-00693036.
 00US-00727344.
 INC.
 2, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 3, Mehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 4, R, Drmanac RT;
 53/47.
 54.
 acids and polypeptides, useful for treating disorders such
 ous system injuries.
 ID NO 6309; 10078pp; English.
 relates to human nucleic acids (AAI57798-AAI61369) and the
 ridies (AAM38643-AAM42213) with nootropic,
 unt and cytostatic activity. The polynucleotides are useful
 n. A composition containing a polypeptide or polynucleotide
 n may be used to treat diseases of the peripheral nervous
 ; peripheral nervous injuries, peripheral neuropathy and
 pathies and central nervous system diseases, such as
 rkinson's disease, Huntington's disease, amyotrophic
 lis, and Shy-Drager Syndrome. Other uses include the
 the activities such as: Immune system suppression,
 c activity, chemotactic/chemokinetic activity, haemostatic
 c activity, cancer diagnosis and therapy, drug screening,
 ptor activity, arthritis and inflammation, leukaemias and
 n. Note: The sequence data for this patent did not form
 nted specification
 2. 2.8%; Score 15; DB 4; Length 114;
 ity 100.0%; Pred. No. 8e-05;
 ervative 0; Mismatches 0; Indels 0; Gaps 0;
 IDGKSLLLM 496
 IDGKSLLLM 77
 ard; protein; 116 AA.
 (first entry)
 SEQ ID 2857.
 i-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 uman; secretory protein; membrane proteins; cancer;
 sease; osteoporosis; neurological disease.

XX 19-MAR-2003.
 XX 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakanatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamec
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53650.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secret
 PT and/or membrane proteins, useful for developing medicines for dise
 PT which the gene is involved, or as target molecules for gene therap
 XX
 PS Claim 14; SEQ ID NO 2857; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 116 AA;
 Query Match 2.8%; Score 15; DB 6; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Ga
 Qy 482 AFQEQEIDGKSLLLM 496
 Db 65 AFQEQEIDGKSLLLM 79
 |||||
 |||||
 RESULT 20
 ABB67522
 ID ABB67522 standard; protein; 104 AA.
 XX
 AC ABB67522;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 29358.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 FN WC200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL11625.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or

relates to an isolated nucleic acid detection reagent acting 1000 or more genes from Drosophila. The invention is encompassed by the following claims.

The present invention relates to a method for determining developmental biology and in elucidating cell signalling and interactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention relates to a method for identifying and characterizing specific nucleic acid sequences (ABL16176-ABL30511), expressed DNA (AB1840-ABL16175) and the encoded proteins (ABB57737-ABL16175). The sequence data for this patent did not form part of the prior art. Sequence data was obtained in electronic format directly from Genbank.

VPESD 11

urd; peptide; 12 AA.

first entry)

ity lipoprotein binding protein 2 (LBP-2) peptide.

oprotein binding protein 2; LBP-2; LDL; rabbit;
; antiarteriosclerotic; therapy; diagnosis; vaccine.
iculus.

101WO-US006356.

:00US-00517849.

:00US-00616289.

HEART FOUND INC.

RS, Law SW, Arjona AA;

5/63.

w density lipoprotein binding polypeptide for treating,
or identifying therapeutic agents for atherosclerosis.

ge; 143pp; English.

quence is that of a peptide comprising amino acid residues
il rabbit low density lipoprotein binding protein 2 (LBP-2,
Rabbit LBP-2 is an example of claimed LBP polypeptides of
hat are capable of binding to native and methylated low
teins (LDLs). Also claimed are biologically active
nalogues of LBPs, polynucleotides encoding LBPs, as well
ectors, cells and methods of producing the LBPs.
ving the present amino acid sequence are among those
s of determining if an animal is at risk for
, methods for evaluating an agent for use in treating
, and methods for treating a cell having an abnormality in
abolism of LBP are also claimed, as are pharmaceutical
mprising an LBP polypeptide or nucleic acid, and vaccine
ote: the present sequence is not shown in the
ut is derived from the rabbit LBP-2 sequence given in
AAB82807)

2.0%; Score 11; DB 4; Length 12;

ity 100.0%; Pred. No. 0.041;

servative 0; Mismatches 0; Indels 0; Gaps 0;

VPESD 354

|||||

VPESD 12

rd; peptide; 28 AA.

first entry)

XX

DE

XX

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PR

XX

XX

PA

XX

XX

PI

XX

XX

XX

DR

XX

XX

FT

XX

PT

XX

XX

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Rabbit low density lipoprotein binding protein 2 (LBP-2) peptide.

Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;

atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine

Oryctolagus cuniculus.

WO200164874-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US006356.

02-MAR-2000; 2000US-00517849.

14-JUL-2000; 2000US-00616289.

(BOST-) BOSTON HEART FOUND INC.

Lees AM, Lees RS, Law SW, Arjona AA;

WPI; 2001-565505/63.

New isolated low density lipoprotein binding polypeptide for treat

diagnosing and/or identifying therapeutic agents for atherosclerosis

Claim 14(c); Page; 143pp; English.

The present sequence is that of a peptide comprising amino acid re

338-365 of novel rabbit low density lipoprotein binding protein 2

see AAB82807). Rabbit LBP-2 is an example of claimed LBP polypepti

the invention that are capable of binding to native and methylated

density lipoproteins (LDLs). Also claimed are biologically active

fragments and analogues of LBPs, polynucleotides encoding LBPs, as

as expression vectors, cells and methods of producing the LBPs.

Polypeptides having the present amino acid sequence are among thos

claimed. Methods of determining if an animal is at risk for

atherosclerosis, and methods for evaluating an agent for use in treati

atherosclerosis, and methods for treating a cell having an abnormal

structure or metabolism of LBP are also claimed, as are pharmaceut

compositions comprising an LBP polypeptide or nucleic acid, and va

cinations. Note: the present sequence is not shown in the

specification but is derived from the rabbit LBP-2 sequence given

figure 2A (see AAB82807)

XX

SQ

Sequence 28 AA;

Query Match 2.0%; Score 11; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.083;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 344 VSEGSSEVPESD 354

|||||

Db 18 VSEGSSEVPESD 28

RESULT 25

AAY51200

ID AAY51200 standard; protein; 129 AA.

XX

AC AAY51200;

XX

XX

DT 04-APR-2000 (first entry)

XX

DE Human SCA7 protein fragment 2.

XX

KW SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;

repeat expansion detection; RED analysis; detection.

XX

OS Homo sapiens.

XX

PN CA2245310-A.

XX

98CA-02245310.
97US-0056170P.
MINNESOTA.
um LP;
[81/09.
individuals at risk of developing spinocerebellar ataxia type
; trinucleotide repeat regions of spinocerebellar ataxia
age 46-47; 66pp; English.
describes a novel method for identifying individuals at
oping spinocerebellar ataxia type 7 (SCA7). The method
yzing the CAG repeat region of a SCA7 gene to detect CAG
; individuals at risk have at least 30 CAG repeats and those
ive less than 19 CAG repeats. The method is useful for
individuals at risk of developing SCA7 and also those at risk
SCA1, 2, 3 or 6. The use of genomic DNA in the repeat
action (RED) analysis allows isolation of any potential
repeat expansion regardless of the expression pattern.
; different oligonucleotides in the RED assay allows any of
trinucleotide repeats to be detected, and the cyclized nature
n makes it extremely sensitive. This sequence represents a
e human SCA7 protein which is described in the method of
A;
2.0%; Score 11; DB 3; Length 129;
arity 100.0%; Pred. No. 0.29;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PPPPQ 232
|||||
PPPPQ 44
lard; protein; 139 AA.
revised)
first entry)
e bile; mucosal immune response; chicken; parasite.
a.
91WO-US006431.
90US-00581694.
CORP.
T AG.
Strausberg RL, Wilson SD, Pope SH, Strausberg SH;

DR WPI; 1992-114366/14.
XX N-PSDB; AAQ23082.
PT Vaccine against avian coccidiosis - comprising recombinant eimeri;
PT antigen mc-4C, mc-5C or mc-30C gene, etc., or microorganisms expr
PT them.
XX Claim 12; Page 65 + Fig 12; 94pp; English.
XX To identify antigens of E. tenella that elicit a mucosal immune r
CC during parasitic infection of chickens, E. tenella cDNA and genom
CC expression libraries in lambda phage were screened with chicken i
CC ble. Phage that produce antigens cross-reactive with the immune l
CC were identified. The DNA inserts from the positive phage were clon
CC bacteriophage M13 and subjected to sequence analysis. E. tenella
CC tc-11e (13.9 kD) was identified. (Updated on 25-MAR-2003 to corre
CC field.)
XX Sequence 139 AA;
SQ Query Match 2.0%; Score 11; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G
QY 118 APAAAAAAPP 128
Db 12 APAAAAAAPP 22
|||||
RESULT 27
ABG76914
ID ABG76914 standard; protein; 189 AA.
XX AC
XX ABG76914;
XX 05-NOV-2002 (first entry)
XX DT
XX Rice WRKY polypeptide #2.
DE WRKY; plant; zinc-finger-type factor; WRKY; SAR; sunflower;
KW SA-dependent structure-activity analysis response; pathogen resist
KW maize; wheat; rice; soybean.
XX
OS Oryza sativa.
XX
XX US2002076775-A1.
XX PD
XX 20-JUN-2002.
XX PF 16-MAR-2001; 2001US-00810264.
XX PR 17-MAR-2000; 2000US-0190467P.
XX (CRAN/) CRANE V C.
PA (FAMO/) FAMODU O.
PA (HUX/) HU X.
PA (LUGG/) LU G.
PA (ZHAN/) ZHANG L.
XX
PI Crane VC, Famodu O, Hu X, Lu G, Zhang L;
XX
XX WPI; 2002-582922/62.
DR N-PSDB; ABS59410.
XX
PT New isolated plant-specific zinc-finger-type factor polynucleotide
PT useful for e.g. regulating the SA-dependent structure-activity ana
PT response in a plant.
XX
PS Claim 9; Page 45-46; 66pp; English.
XX The invention relates to an isolated polynucleotide encoding a pla
CC specific zinc-finger-type factor (WRKY) protein. The DNA and prote
CC used to modulate the level of a WRKY protein in a plant and to reg

at structure-activity analysis (SAR) response in a plant. can be used to engineer plants to resist pathogens such as bacteria, insects and fungi, and to survive stresses. They may be a molecular probe to track inheritance of corresponding genes and facilitate the plant breeding process, to identify and genetically map WRKY and other closely related genes and to find genes and their promoters that are in the WRKY domain. This sequence represents a WRKY polypeptide of

Query Match 2.0%; Score 11; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APVAAA 143
|||||
APVAAA 114

ard; protein; 270 AA.

first entry)

agnostic protein #17263.

ome mapping; gene mapping; gene therapy; forensic;
; medical imaging; diagnostic; genetic disorder.

01WO-US008631.

000US-00540217.

000US-00649167.

INC.

u C, Tang YT;

12/73.

9.

polynucleotide and encoded polypeptides, useful in
diagnostics, gene mapping, identification of mutations
; genetic disorders or other traits and to assess

ID NO 47631; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II)
is useful as hybridisation probes, polymerase chain
primers, oligomers, and for chromosome and gene mapping,
ant production of (II). The polynucleotides are also used
as expressed sequence tags for identifying expressed
useful in gene therapy techniques to restore normal
) or to treat disease states involving (II). (II) is
erating antibodies against it, detecting or quantitating a
tissue, as molecular weight markers and as a food
) and its binding partners are useful in medical imaging
sing (II). (I) and (II) are useful for treating disorders
ant protein expression or biological activity. The
l polynucleotide sequences have applications in
diagnostics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiv
CC and to produce other types of data and products dependent on DNA a
CC amino acid sequences. ABG00010-ABG30377 represent novel human diag
CC amino acid sequences of the invention. Note: The sequence data for
CC patent did not appear in the printed specification, but was obtain
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 270 AA;

Query Match 2.0%; Score 11; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 179 APPAPAPAPPA 189

Db 124 APPAPAPAPPA 134

RESULT 29

ADD18910

ID ADD18910 standard; protein; 892 AA.

XX ADD18910;

DT 15-JAN-2004 (first entry)

XX Human disease related protein SeqID399.

human; disease state; cytostatic; antiinflammatory; ophthalmologic
antiarteriosclerotic; vulnery; gene therapy;
hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptos
inflammation; erythropoiesis; glycolysis; gluconeogenesis;
glucose transportation; catecholamine synthesis; iron transport;
nitric oxide synthesis; cancer; ischaemic condition; reperfusion i
retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
inflammatory condition; wound healing.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD18911.

XX New substantially purified polypeptide, useful for diagnosing or t
a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation,
wound healing.

XX Claim 25; SEQ ID NO 399; 424pp; English.

This invention relates to novel human genes and gene product which
implicated in certain disease states. Compounds which modulate the
proteins of the invention may have cytostatic, antiinflammatory,
ophthalmological, antiarteriosclerotic or vulnerary activities. The
sequences of the invention may be useful for gene therapy. The inv
may be useful for diagnosing or treating a hypoxia-regulated condi
such as tumorigenesis, angiogenesis, apoptosis, inflammation,
erythropoiesis, or the biological response to hypoxia conditions
including processes such as glycolysis, gluconeogenesis, glucose
transportation, catecholamine synthesis, iron transport or nitric

The disease includes cancer, ischaemic conditions, reperfusionopathy, neonatal stress, pre-eclampsia, atherosclerosis, conditions or wound healing. The present sequence is that of a protein of the invention.

 $\Delta A;$

2.0%; Score 11; DB 7; Length 892;

arity 2.0%; score 11, DS 7, length 892;
arity 100.0%; Pred. No. 1.4;

conservative 0: Mismatches 0: Indels 0: Gaps 0: Identity 100.0%; Freq. NO. 1.4;

232 000000

☒ _____
☒ _____
☒ _____
☒ _____
☒ _____
☒ _____

46

lard; protein; 1109 AA.

(first entry)

Side #2.

utamine disease; gene; genealogical polyglutamine disease;
:iconvulsant.

•

2001JP-00236788.

2000JP-00236839.

0001-00230033.
001JP-00108723.

USA DNA KENKYUSHO.

USA DNA KENKIOS.
II PHARM CO LTD.

.53/49.

111.

...line diagnostic marker for polyglutamine disease, useful for diagnosis, prevention and/or treatment, comprises a polyglutamine and its encoded polypeptide.

D NO 4; 72pp: Japanese.

discloses polyglutamine disease related genes and their peptides. Also claimed is a recombinant vector, preparation of the polynucleotides and resultant diagnostic methods and a kit. The genes and encoded proteins are useful in the diagnosis, prevention and treatment of polyglutamine disease. The sequence presented is a part of the invention.

AA:

2.0%; Score 11; DB 7; Length 1109;

urity 2:0%, score 11; DB 7
100.0%; Pred. No 1.7:

```
conservative      0: Mismatches      0: Indels      0: Gaps      0:
accuracy 100.0%, freq: NO: 1: 7;
```

532 ddd0d0

[illegible]

||||| 501

Query Match 2.0%: Score 11: DB 6: Length 1340:

Query Match

Best Local Similarity 100.0%; Pred. No. 2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Ov 225 O P P P P O P P P P 235

db 729 O P P P P O P P P P 739

DE Rabbit low density lipoprotein binding protein 2 (LBP-2) peptide.
 XX
 KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
 XX atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine
 XX
 OS Oryctolagus cuniculus.
 XX
 FN WO200164874-A2.
 XX
 PD 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006356.
 PF
 XX 02-MAR-2000; 2000US-00517849.
 XX
 PR 14-JUL-2000; 2000US-00616289.
 XX
 XX (BOST-) BOSTON HEART FOUND INC.
 PA
 XX
 PI Lees AM, Lees RS, Law SW, Arjona AA;
 XX
 DR WPI; 2001-565505/63.
 XX
 XX New isolated low density lipoprotein binding polypeptide for treat
 PT diagnosing and/or identifying therapeutic agents for atherosclerosis
 XX
 PS Claim 14(c); Page; 143pp; English.
 XX
 CC The present sequence is that of a peptide comprising amino acid re
 CC 444-453 of novel rabbit low density lipoprotein binding protein 2
 CC see AAB82807). Rabbit LBP-2 is an example of claimed LBP polypepti
 CC the invention that are capable of binding to native and methylated
 CC density lipoproteins (LDLs). Also claimed are biologically active
 CC fragments and analogues of LBPs, polynucleotides encoding LBPs, as
 CC as expression vectors, cells and methods of producing the LBPs.
 CC Polypeptides having the present amino acid sequence are among those
 CC claimed. Methods of determining if an animal is at risk for
 CC atherosclerosis, methods for evaluating an agent for use in treati
 CC atherosclerosis, and methods for treating a cell having an abnorma
 CC structure or metabolism of LBP are also claimed, as are pharmaceut
 CC compositions comprising an LBP polypeptide or nucleic acid, and va
 CC compositions. Note: the present sequence is not shown in the
 CC specification but is derived from the rabbit LBP-2 sequence given
 CC figure 2A (see AAB82807)
 XX
 SQ Sequence 10 AA;
 Query Match 1.9%; Score 10; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Ga
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga
 QY 432 PPGKPALEGA 441
 Db 1 PPGKPALEGA 10
 RESULT 34
 AAU97858
 ID AAU97858 standard; protein; 22 AA.
 XX
 AC AAU97858;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Protein inhibitor of activated STAT, piasey, acidic domain.
 KW K+ channel associated protein; KchAP; chaperone protein; agonist;
 KW antagonist; cardiac arrhythmia; hypertension; angina; asthma; diab
 KW renal insufficiency; urinary incontinence; irritable colon; epilep
 KW cerebrovascular ischaemia; autoimmune disease; acidic domain;
 KW protein inhibitor of activated STAT; PIASy.
 XX
 OS Unidentified.
 XX

ard; peptide; 10 AA.
 first entry)
 ity lipoprotein binding protein 2 (LBP-2) peptide.
 poprotein binding protein 2; LBP-2; LDL; human;
 S; antiarteriosclerotic; therapy; diagnosis; vaccine.
 .
 001WO-US006356.
 000US-00517849.
 000US-00616289.
 HEART FOUND INC.
 RS, Law SW, Arjona AA;
 05/63.
 ow density lipoprotein binding polypeptide for treating,
 /or identifying therapeutic agents for atherosclerosis.
 age; 143pp; English.
 quence is that of a peptide comprising amino acid residues
 el human low density lipoprotein binding protein 2 (LBP-2,
 Human LBP-2 is an example of claimed LBP polypeptides of
 that are capable of binding to native and methylated
 oteins (LDLs). Also claimed are biologically active
 analogues of LBPs, polynucleotides encoding LBPs, as well
 vectors, cells and methods of producing the LBPs.
 aving the present amino acid sequence are among those
 is of determining if an animal is at risk for
 s, methods for evaluating an agent for use in treating
 etabolism of LBP are also claimed, as are pharmaceutical
 comprising an LBP polypeptide or nucleic acid, and vaccine
 Note: the present sequence is not shown in the
 but is derived from the human LBP-2 sequence given in
 AAB82806)
 ;
 1.9%; Score 10; DB 4; Length 10;
 city 100.0%; Pred. No. 0.27;
 iservative 0; Mismatches 0; Indels 0; Gaps 0;
 DGFLG 538
 |||||
 DGFLG 10
 ard; peptide; 10 AA.
 first entry)

XX	Venter JC, Adams M, Li PWD, Myers EW;
PI	WPI; 2001-656860/75.
XX	N-PSDB; ABL08105.
DR	
DR	
XX	
XX	New isolated nucleic acid detection reagent for detecting 1000 or
PT	genes from Drosophila and for elucidating cell signaling and cell
PT	interactions.
PT	
XX	
XX	Disclosure; SEQ ID NO 19398; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The inven
CC	useful in developmental biology and in elucidating cell signaling c
CC	cell-cell interactions in higher eukaryotes for the development c
CC	insecticides, therapeutics and pharmaceutical drugs. The inventi
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DN
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC	ABBY2072). The sequence data for this patent did not form part of
CC	printed specification, but was obtained in electronic format dire
CC	cc from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 75 AA;
XX	
XX	Query Match 1.9%; Score 10; DB 4; Length 75;
XX	Best Local Similarity 100.0%; Pred. No. 1.4;
XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY	118 APAAAAAAAAAA 127
DB	40 APAAAAAAAAAA 49
XX	
XX	RESULT 36
ABBS69039	ID ABB69039 standard; protein; 96 AA.
XX	
XX	ABBS69039;
XX	
DT	26-MAR-2002 (first entry)
XX	
XX	Drosophila melanogaster polypeptide SEQ ID NO 33909.
DE	
XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
KW	
XX	Drosophila melanogaster.
OS	
XX	WO200171042-A2.
PN	
XX	27-SEP-2001.
PD	
XX	23-MAR-2001; 2001WO-US009231.
PF	
XX	23-MAR-2000; 2000US-0191637P.
XX	11-JUL-2000; 2000US-00614150.
PR	
XX	(PEKE) PE CORP NY.
PA	
XX	Venter JC, Adams M, Li PWD, Myers EW;
PI	
XX	WPI; 2001-656860/75.
DR	N-PSDB; ABL13142.
DR	
XX	
XX	New isolated nucleic acid detection reagent for detecting 1000 or
PT	genes from Drosophila and for elucidating cell signaling and cell
PT	interactions.
PT	
XX	
XX	Disclosure; SEQ ID NO 33909; 21pp + Sequence Listing; English.
XX	
PS	
XX	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The inven
CC	useful in developmental biology and in elucidating cell signaling c
CC	cell-cell interactions in higher eukaryotes for the development c
CC	insecticides, therapeutics and pharmaceutical drugs. The inventi
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DN
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC	ABBY2072). The sequence data for this patent did not form part of
CC	printed specification, but was obtained in electronic format dire
CC	cc from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 75 AA;
XX	
XX	Query Match 1.9%; Score 10; DB 4; Length 75;
XX	Best Local Similarity 100.0%; Pred. No. 1.4;
XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY	118 APAAAAAAAAAA 127
DB	40 APAAAAAAAAAA 49
XX	
XX	RESULT 36
ABBS69039	ID ABB69039 standard; protein; 96 AA.
XX	
XX	ABBS69039;
XX	
DT	26-MAR-2002 (first entry)
XX	
XX	Drosophila melanogaster polypeptide SEQ ID NO 33909.
DE	
XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
KW	
XX	Drosophila melanogaster.
OS	
XX	WO200171042-A2.
PN	
XX	27-SEP-2001.
PD	
XX	23-MAR-2001; 2001WO-US009231.
PF	
XX	23-MAR-2000; 2000US-0191637P.
XX	11-JUL-2000; 2000US-00614150.
PR	
XX	(PEKE) PE CORP NY.
PA	
XX	Venter JC, Adams M, Li PWD, Myers EW;
PI	
XX	WPI; 2001-656860/75.
DR	N-PSDB; ABL13142.
DR	
XX	
XX	New isolated nucleic acid detection reagent for detecting 1000 or
PT	genes from Drosophila and for elucidating cell signaling and cell
PT	interactions.
PT	
XX	
XX	Disclosure; SEQ ID NO 33909; 21pp + Sequence Listing; English.
XX	
PS	
XX	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The inven
CC	useful in developmental biology and in elucidating cell signaling c
CC	cell-cell interactions in higher eukaryotes for the development c
CC	insecticides, therapeutics and pharmaceutical drugs. The inventi
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DN
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC	ABBY2072). The sequence data for this patent did not form part of
CC	printed specification, but was obtained in electronic format dire
CC	cc from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 75 AA;
XX	
XX	Query Match 1.9%; Score 10; DB 4; Length 75;
XX	Best Local Similarity 100.0%; Pred. No. 1.4;
XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY	118 APAAAAAAAAAA 127
DB	40 APAAAAAAAAAA 49
XX	
XX	RESULT 36
ABBS69039	ID ABB69039 standard; protein; 96 AA.
XX	
XX	ABBS69039;
XX	
DT	26-MAR-2002 (first entry)
XX	
XX	Drosophila melanogaster polypeptide SEQ ID NO 33909.
DE	
XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
KW	
XX	Drosophila melanogaster.
OS	
XX	WO200171042-A2.
PN	

developmental biology and in elucidating cell signalling and reactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention of mic DNA sequences (ABL16176-ABL30511), expressed DNA (1840-ABL16175) and the encoded proteins (ABB57737, sequence data for this patent did not form part of the invention, but was obtained in electronic format directly from the public domain).

1.9%; Score 10; DB 4; Length 96;
 rity 100.0%; Pred. No. 1.7;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAPPP 129
 |||||
 AAPPP 32

ard; protein; 112 AA.

First entry)

5 isoform A protein SEQ ID NO:3.

im perenne; Lol p 5; Phl p 5; Poa p 5; allergen;
 immunotherapy; immunophylactic treatment; hayfever;
 se; ryegrass pollen; immunological; pollen; allergy.

1.

002WO-AU001261.

001AU-00007792.

ELBOURNE.

ugh MB, Bhalla PL, Swoboda I;

16/34.

combinant allergen which lacks or comprises reduced epitopes and/or exhibits reduced binding capacity for IgE, having type I allergic disease, particularly sensitivity to an.

1; 66pp; English.

vention describes a modified recombinant allergen in a form and which is associated with allergic disease sensitive subjects. The modified recombinant allergen amino acid sequence modified from the naturally occurring sequence such that the allergen lacks or comprises reduced epitopes and/or exhibits reduced binding capacity for IgE, reduced IgE production stimulatory activity while having antigenicity. Also described: (1) a composition of modified allergen which lacks or comprises reduced numbers and/or exhibits reduced binding capacity for IgE and/or reduced IgE production stimulatory activity while retaining T-cell activity, and one or more pharmaceutical carriers and/or (2) prophylaxis or treatment of an allergic disease subject, by administering a modified allergen defined as a recombinant allergen is useful in the immunotherapy of allergic diseases such as type I

allergic disease, particularly sensitivity to ryegrass pollen, and treating sensitivity to ryegrass pollen or pollen from an immunologic relative of ryegrass in a mammal sensitive to such pollen. The peptide may also be used to modify IgE response to the grass pollen allergen. study the mechanism of immunotherapy of Lolium perenne allergy, to modified derivatives or analogues useful in immunotherapy, and in manufacture of a medicament for the treatment or prophylaxis of allergic sensitive individuals. The present sequence represents a ryegrass isoform A protein, which is given in the exemplification of the present invention

SQ Sequence 112 AA;

Query Match 1.9%; Score 10; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 PPLPPPPQPP 218
 |||||
 Db 96 PPLPPPPQPP 105

RESULT 38

AAG34164

ID AAG34164 standard; protein; 132 AA.

XX AC AAG34164;

XX DT 18-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 41527.

XX KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; protein termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0130891P.

XX PR 30-APR-1999; 99US-0131449P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 18-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

XX PR 19-MAY-1999; 99US-0134941P.

99US-0135124P.
99US-0135353P.
99US-0135629P.
99US-0136021P.
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99US-0137502P.
99US-0137724P.
99US-0138094P.
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99US-0139817P.
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99US-0145919P.
99US-0145951P.

PR 02-AUG-1999;
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PR 11-AUG-1999;
PR 12-AUG-1999;
PR 13-AUG-1999;
PR 13-AUG-1999;
PR 16-AUG-1999;
PR 17-AUG-1999;
PR 18-AUG-1999;
PR 20-AUG-1999;
PR 20-AUG-1999;
PR 23-AUG-1999;
PR 23-AUG-1999;
PR 25-AUG-1999;
PR 26-AUG-1999;
PR 27-AUG-1999;
PR 27-AUG-1999;
PR 30-AUG-1999;
PR 31-AUG-1999;
PR 01-SEP-1999;
PR 07-SEP-1999;
PR 10-SEP-1999;
PR 13-SEP-1999;
PR 15-SEP-1999;
PR 16-SEP-1999;
PR 20-SEP-1999;
PR 22-SEP-1999;
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PR 24-SEP-1999;
PR 28-SEP-1999;
PR 29-SEP-1999;
PR 04-OCT-1999;
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PR 22-OCT-1999;
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PR 26-OCT-1999;
PR 26-OCT-1999;

99US-0146386P.
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99US-0147302P.
99US-0147192P.
99US-0147260P.
99US-0147303P.
99US-0147416P.
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99US-0149426P.
99US-0149722P.
99US-0149723P.
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99US-0149902P.
99US-0149930P.
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99US-0156596P.
99US-0157117P.
99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
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99US-0160767P.
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99US-0160815P.
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99US-0160989P.
99US-0161404P.
99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161360P.

99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
1.9%; Score 10; DB 3; Length 132;
city 100.0%; Pred.No. 2.3;
iservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 127
AAAA 130
ard; protein; 171 AA.
First entry)
in fragment SEQ ID NO: 41526.
ication; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
ence; corn.
. may.
000EP-00301439.
99US-0121823P.
99US-0123180P.
99US-0123548P.
99US-0125789P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
99US-0131449P.
99US-0132048P.
99US-0132407P.
99US-0132484P.
99US-0132485P.
99US-0132486P.
99US-0132487P.
99US-0132863P.
99US-0134256P.
99US-0134218P.
99US-0134219P.
99US-0134221P.
99US-0134370P.
99US-0134941P.
99US-0135124P.
99US-0135353P.
99US-0135629P.
99US-0136021P.
99US-0136392P.
99US-0136782P.
99US-0137222P.
99US-0137528P.
99US-0137502P.
99US-0137724P.
99US-0138094P.
99US-0138540P.
99US-0138847P.
99US-0139119P.
99US-0139452P.
99US-0139453P.
99US-0139492P.
99US-0139454P.
99US-0139455P.
99US-0139456P.
99US-0139457P.
99US-0139458P.
99US-0139459P.
99US-0139460P.
99US-0139461P.
99US-0139462P.
99US-0139463P.
99US-0139750P.
99US-0139763P.
99US-0139817P.
99US-0139899P.
99US-0140353P.
99US-0140354P.
99US-0140695P.
99US-0140823P.
99US-0140911P.
99US-0141287P.
99US-0141842P.
99US-0142154P.
99US-0142055P.
99US-0142390P.
99US-0142803P.
99US-0142920P.
99US-0142977P.
99US-0143542P.
99US-0143624P.
99US-0144005P.
99US-0144085P.
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99US-0144325P.
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99US-0144335P.
99US-0144352P.
99US-0144632P.
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99US-0145918P.
99US-0145919P.
99US-0145951P.
99US-0146386P.
99US-0146388P.
99US-0146389P.
99US-0147038P.
99US-0147204P.
99US-0147302P.
99US-0147192P.

99US-0147260P.
99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
99US-0148171P.
99US-0148319P.
99US-0148341P.
99US-0148565P.
99US-0148684P.
99US-0149368P.
99US-0149175P.
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99US-0149723P.
99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
99US-0150884P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-0156458P.
99US-0156596P.
99US-0157117P.
99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159233P.
99US-0159294P.
99US-0159295P.
99US-0159329P.
99US-0159330P.
99US-0159331P.
99US-0159637P.
99US-0159638P.
99US-0159584P.
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160770P.
99US-0160814P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0160989P.
99US-0161404P.
99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161922P.
99US-0161993P.
99US-0162142P.

1.9%; Score 10; DB 3; Length 171;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G:
QY 118 AAAAAAAAAAP 127
|||||
Db 160 AAAAAAAAAAP 169
RESULT 40
ABU17208
ID ABU17208 standard; protein; 238 AA.
XX
AC ABU17208;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #2735.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug d
XX
OS Acinetobacter baumannii.
XX
PN WC200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WC-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
N-PSDB; ACA21078.
XX
PT New antisense nucleic acids, useful for identifying proteins or s
PT for homologous nucleic acids required for cellular proliferation;
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 45132; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any
CC the 6213 antisense sequences given in the specification where exp
CC of the nucleic acid inhibits proliferation of a cell. Also includ
CC (1) a vector comprising a promoter operably linked to the nucleic
CC encoding a polypeptide whose expression is inhibited by the antis
CC nucleic acid; (2) a host cell containing the vector; (3) an isolat
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically b
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cel
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the act
CC the gene product or that has an activity against a biological pat
CC required for proliferation, or that inhibits cellular proliferati
CC identifying a gene required for cellular proliferation or the bio
CC pathway in which a proliferation-required gene or its gene product
CC or a gene on which the test compound that inhibits proliferation
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which th
CC product is overexpressed or underexpressed; (12) determining the
CC to which each of the strains is present in a culture or collection
CC strains; or (13) identifying the target of a compound that inhibit
CC proliferation of an organism. The antisense nucleic acids are usef
CC identifying proteins or screening for homologous nucleic acids rec
CC for cellular proliferation to isolate candidate molecules for rati
CC drug discovery programs, or for screening homologous nucleic acid

oliferation in cells other than *S. aureus*, *S. typhimurium*, or *P. aeruginosa*. The present sequence is encoded by one of a set of three genes. Note: The sequence data for this form part of the printed specification, but was obtained from a direct sequencing of the cDNA from WIPO at the following address: WIPO, 300, rue de la Bourse, 1000 Brussels, Belgium.

1.9%; Score 10; DB 6; Length 238;
Identity 100.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 141

Protein; 254 AA.

First entry

baumannii protein #3525.

baumannii; bacterial disease; antibacterial; vaccine;
agent.

baumannii.

99US-00328352.

98US-0088701P.

THERAPEUTICS CORP.

1 D;

22/54.

38.

er baumannii proteins and nucleic acids, useful as reagents for a bacterial disease, as components of antibacterial agents for antibacterial drugs, or as biocontrol agents for

NO 7651; 328pp; English.

relates to isolated *Acinetobacter baumannii* nucleic acids. The present sequence is encoded by one of a set of three genes. Note: The sequence data for this form part of the printed specification, but was obtained from a direct sequencing of the cDNA from WIPO at the following address: WIPO, 300, rue de la Bourse, 1000 Brussels, Belgium.

1.9%; Score 10; DB 6; Length 254;

Identity 100.0%; Pred. No. 3.9;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||

Db 148 PAPVAAAAA 157
RESULT 42
AAY25630
ID AAY25630 standard; protein; 257 AA.
XX
AC AAY25630;
XX
DT 30-SEP-1999 (first entry)
XX
DE Phleum sp. allergen Phl p 5 protein fragment #11.
XX

Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; s chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; hon screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

Phleum sp.

WO9934826-A1.

15-JUL-1999.

11-JAN-1999; 99WO-GB0000080.

09-JAN-1998; 98GB-00000445.

21-SEP-1998; 98GB-00020474.

(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Larche M, Kay AB;

WPI; 1999-458255/38.

Desensitizing patients to polypeptide allergens.

Example 6; Page 64; 117pp; English.

This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a polypeptide derived from the allergen where restriction to a MHC Class II molecule is demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honey bee, non-biting midge larvae, bee moth larvae, mealworm, cockroach, larva, Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5 allergen

Sequence 257 AA;

Query Match 1.9%; Score 10; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 PPLPPPPPP 218
|||||

DB 231 PPLPPPPPP 240
|||||

RESULT 43
ADC34880
ID ADC34880 standard; protein; 257 AA.
XX

(first entry)

allergen Phl p 5.

igen; hyporesponsive; desensitisation; immunomodulator;
timothy grass.

32.

2002WO-GB005548.

2001US-0338385P.

SSIA LTD.

lger PW;

267/49.

an individual to a selected polypeptide antigen comprises a composition containing polypeptide antigens in an amount as a state of hyporesponsiveness to the antigen to allow on.

age 33-34; 57pp; English.

relates to a novel method for desensitising an individual polypeptide antigen. The method comprises administering a at contains polypeptide antigens in an amount that the individual a state of hyporesponsiveness to the antigen sensitisation to one or more polypeptide antigens. The method on has immunomodulator activity, and may have a use in gene composition and method are useful in manufacturing a desensitising an individual to a selected polypeptide generating in the individual a state of hyporesponsiveness to allow desensitisation to one or more polypeptide present sequence is used in the exemplification of the

A;

1.9%; Score 10; DB 7; Length 257;

urity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0; unservative 0; Mismatches 0; Indels 0; Gaps 0;

PPQPP 218

PPQPP 240

ard; protein; 285 AA.

first entry)

ergen Phl p 5a protein fragment #3.

patibility complex; class II; desensitising; human; s; tree; weed; pollen; fungi; mould; food; insect; sting; ider; mite; housefly; fruit fly; sheep blow fly; honeybee; ; grain weevil; silkworm; bee moth; larvae; mealworm; cat; tle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig; vaccine; treatment; prevention; hypersensitivity.

OS Phleum sp.
XX W09934826-A1.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX PF 09-JAN-1998; 98GB-00000445.
XX PR 21-SEP-1998; 98GB-00020474.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Larche M, Kay AB;
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens.
XX
XX Example 6; Page 64-65; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient polypeptide allergen and comprises administering to the patient a derived from the allergen where restriction to a MHC Class II mol. possessed by the patient can be demonstrated for the peptide and peptide is able to induce a late phase response in an individual possesses the MHC Class II molecule. The methods can be used for desensitising patients to allergens present in e.g. grass, tree a (including ragweed) pollens, fungi and moulds, foods, stinging in the chironomidae (non-biting midges), spiders and mites, housefly, fly, sheep blow fly, screw worm fly, grain weevil, silkworm, hone; non-biting midge larvae, bee moth larvae, mealworm, cockroach, la; Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pi; sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be produce immunological vaccines which may be used to prevent and/o conditions involving hypersensitivity to allergens. This sequence represents a Phleum sp. (Timothy grass) Phl p 5a allergen
XX
XX Sequence 285 AA;
SQ
Query Match 1.9%; Score 10; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 209 PPLPPPPQPP 218
Db 259 PPLPPPPQPP 268
RESULT 45
ADC34883
ID ADC34883 standard; protein; 285 AA.
XX
XX ADC34883;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Timothy grass allergen Phl p 5a.
DE
XX
XX allergen; antigen; hyporesponsive; desensitisation; immunomodulator; gene therapy; timothy grass.
KW
XX
XX Phleum sp.
OS
XX
XX W02003047618-A2.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 05-DEC-2002; 2002WO-GB005548.
PF
XX
XX 05-DEC-2001; 2001US-0338385P.
PR
XX
XX (CIRC-) CIRCASSIA LTD.
PA

ger PW;
67/49.
an individual to a selected polypeptide antigen comprises
a composition containing polypeptide antigens in an amount
a state of hyporesponsiveness to the antigen to allow
m.
ge 34; 57pp; English.
relates to a novel method for desensitising an individual
polypeptide antigen. The method comprises administering a
at contains polypeptide antigens in an amount that
he individual a state of hyporesponsiveness to the antigen
situation to one or more polypeptide antigens. The method
on has immunomodulator activity, and may have a use in gene
composition and method are useful in manufacturing a
desensitising an individual to a selected polypeptide
generating in the individual a state of hyporesponsiveness
to allow desensitisation to one or more polypeptide
present sequence is used in the exemplification of the
A;
rity 1.9%; Score 10; DB 7; Length 285;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PQQP 218
|||||
PQQP 268
ard; protein; 320 AA.
first entry)
aliana protein fragment SEQ ID NO: 41987.
fication; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
quence.
aliana.
000EP-00301439.
99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
99US-0131449P.
30-APR-1999; 99US-0132048P.
30-APR-1999; 99US-0132407P.
04-MAY-1999; 99US-0132484P.
05-MAY-1999; 99US-0132485P.
06-MAY-1999; 99US-0132486P.
06-MAY-1999; 99US-0132487P.
07-MAY-1999; 99US-0132863P.
11-MAY-1999; 99US-0134256P.
14-MAY-1999; 99US-0134218P.
14-MAY-1999; 99US-0134219P.
14-MAY-1999; 99US-0134221P.
14-MAY-1999; 99US-0134370P.
18-MAY-1999; 99US-0134768P.
19-MAY-1999; 99US-0134941P.
20-MAY-1999; 99US-0135124P.
21-MAY-1999; 99US-0135353P.
24-MAY-1999; 99US-0135629P.
25-MAY-1999; 99US-0136021P.
27-MAY-1999; 99US-0136392P.
28-MAY-1999; 99US-0136782P.
01-JUN-1999; 99US-0137222P.
03-JUN-1999; 99US-0137528P.
04-JUN-1999; 99US-0137502P.
07-JUN-1999; 99US-0137724P.
08-JUN-1999; 99US-0138094P.
10-JUN-1999; 99US-0138540P.
10-JUN-1999; 99US-0138847P.
14-JUN-1999; 99US-0139119P.
16-JUN-1999; 99US-0139452P.
16-JUN-1999; 99US-0139453P.
17-JUN-1999; 99US-0139492P.
18-JUN-1999; 99US-0139454P.
18-JUN-1999; 99US-0139455P.
18-JUN-1999; 99US-0139456P.
18-JUN-1999; 99US-0139457P.
18-JUN-1999; 99US-0139458P.
18-JUN-1999; 99US-0139459P.
18-JUN-1999; 99US-0139460P.
18-JUN-1999; 99US-0139461P.
18-JUN-1999; 99US-0139462P.
18-JUN-1999; 99US-0139463P.
18-JUN-1999; 99US-0139750P.
18-JUN-1999; 99US-0139763P.
21-JUN-1999; 99US-0139817P.
22-JUN-1999; 99US-0139899P.
23-JUN-1999; 99US-0140353P.
23-JUN-1999; 99US-0140354P.
24-JUN-1999; 99US-0140695P.
28-JUN-1999; 99US-0140823P.
29-JUN-1999; 99US-0140991P.
30-JUN-1999; 99US-0141287P.
01-JUL-1999; 99US-0141842P.
01-JUL-1999; 99US-0142154P.
02-JUL-1999; 99US-0142055P.
06-JUL-1999; 99US-0142390P.
08-JUL-1999; 99US-0142803P.
09-JUL-1999; 99US-0142920P.
12-JUL-1999; 99US-0142977P.
13-JUL-1999; 99US-0143542P.
14-JUL-1999; 99US-0143624P.
15-JUL-1999; 99US-0144005P.
16-JUL-1999; 99US-0144085P.
16-JUL-1999; 99US-0144086P.
19-JUL-1999; 99US-0144325P.
19-JUL-1999; 99US-0144331P.
19-JUL-1999; 99US-0144332P.
19-JUL-1999; 99US-0144333P.
19-JUL-1999; 99US-0144334P.
19-JUL-1999; 99US-0144335P.
20-JUL-1999; 99US-0144352P.
20-JUL-1999; 99US-0144632P.
20-JUL-1999; 99US-0144884P.
21-JUL-1999; 99US-0144814P.

PR 99US-0145086P.
PR 99US-0145088P.
PR 99US-0145089P.
PR 99US-0145087P.
PR 99US-0145089P.
PR 99US-0145192P.
PR 99US-0145145P.
PR 99US-0145218P.
PR 99US-0145224P.
PR 99US-0145276P.
PR 99US-0145913P.
PR 99US-0145918P.
PR 99US-0145919P.
PR 99US-0145951P.
PR 99US-0146388P.
PR 99US-0146389P.
PR 99US-0146389P.
PR 99US-0147038P.
PR 99US-0147204P.
PR 99US-0147302P.
PR 99US-0147192P.
PR 99US-0147260P.
PR 99US-0147303P.
PR 99US-0147416P.
PR 99US-0147493P.
PR 99US-0147935P.
PR 99US-0148171P.
PR 99US-0148319P.
PR 99US-0148341P.
PR 99US-0148565P.
PR 99US-0148684P.
PR 99US-0149368P.
PR 99US-0149175P.
PR 99US-0149426P.
PR 99US-0149722P.
PR 99US-0149723P.
PR 99US-0149929P.
PR 99US-0149902P.
PR 99US-0149930P.
PR 99US-0150566P.
PR 99US-0150884P.
PR 99US-0151065P.
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PR 99US-0151080P.
PR 99US-0151303P.
PR 99US-0151438P.
PR 99US-0151930P.
PR 99US-0152363P.
PR 99US-0153070P.
PR 99US-0153758P.
PR 99US-0154018P.
PR 99US-0154039P.
PR 99US-0154779P.
PR 99US-0155139P.
PR 99US-0155486P.
PR 99US-0155659P.
PR 99US-0156458P.
PR 99US-0156596P.
PR 99US-0157117P.
PR 99US-0157753P.
PR 99US-0157865P.
PR 99US-0158029P.
PR 99US-0158232P.
PR 99US-0158369P.
PR 99US-0159233P.
PR 99US-0159294P.
PR 99US-0159295P.
PR 99US-0159329P.
PR 99US-0159330P.
PR 99US-0159331P.
PR 99US-0159637P.
PR 99US-0159638P.
PR 99US-0159584P.

PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 21-OCT-1999; 99US-0160880P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.9%; Score 10; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 222 QQQPPPPQP 231
Db 288 QQQPPPPQP 297

RESULT 47

AAB42629
ID AAB42629 standard; protein; 322 AA.

XX AAB42629;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF2393 polypeptide sequence SEQ ID NO:4786.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatoto
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprote
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; ca
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypert
KW neurodegenerative disorder; osteoarthritis; graft vs host disease
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID;
KW cholesterol ester storage; systemic lupus erythematosus; infectio
KW severe combined immunodeficiency; malaria; autoimmune disorder; a
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound
KW bone damage; cartilage damage; antinflammatory disease; coagulat
KW thrombosis; contraceptive.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008621.

XX 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC76838.

acids and peptides derived from open reading frame X,
 including e.g. cancers, proliferative disorders,
 and disorders and cardiovascular disease.

3968-3969; 5507pp; English.

77606 encode the proteins given in AAB40237 to AAB43397,
 the human ORFX open reading frames 1 to 3161. The ORFX
 activities such as: cytostatic; hepatotropic; vulnery;
 antiparkinsonian; nootropic; neuroprotective; osteopathic;
 antiarthritic; immunosuppressant; immunostimulant;
 hydrolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 immunosuppressive; antiinflammatory; antibacterial;
 fungicidal; antirheumatic; antithyroid; and antianaemic. The
 are used for determining the presence of or predisposition
 to or treating pathological conditions associated with an
 disorder. The nucleic acids can be used to express ORFX
 in therapy vectors. The proteins and nucleic acids may be
 used in the treatment of cancers, proliferative disorders, neurodegenerative
 diseases, arthritis, graft vs host disease, cardiovascular disease,
 lupus, hypertension, hypothyroidism, cholesterol ester
 deficiency, lupus erythematosus, severe combined immunodeficiency
 virus, bacterial or fungal infection, malaria, autoimmune
 disease, allergies, aplastic anaemia, burns, wounds, bone and
 joint, nocturnal haemoglobinuria, antiinflammatory disease; to
 inhibit thrombosis; and as a contraceptive

17

1.9%; Score 10; DB 3; Length 322;

Identity 100.0%; Pred. No. 4.7;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127

|||||

AAAAA 300

ard; protein; 401 AA.

first entry

liana protein fragment SEQ ID NO: 41986.

ication; signal transduction pathway; metabolic pathway;
 assay; genetic mapping; gene expression control; promoter;
 vidence.

liana.

00EP-00301439.

99US-0121825P.

99US-0123180P.

99US-0123548P.

99US-0125788P.

99US-0126264P.

99US-0126785P.

99US-0127462P.

99US-0128234P.

99US-0128714P.

99US-0129845P.

99US-0130077P.

99US-0130449P.

23-APR-1999; 99US-0130510P.
 23-APR-1999; 99US-0130891P.
 28-APR-1999; 99US-0131449P.
 30-APR-1999; 99US-0132048P.
 30-APR-1999; 99US-0132407P.
 04-MAY-1999; 99US-0132484P.
 05-MAY-1999; 99US-0132485P.
 06-MAY-1999; 99US-0132486P.
 07-MAY-1999; 99US-0132487P.
 11-MAY-1999; 99US-0132863P.
 14-MAY-1999; 99US-0134218P.
 14-MAY-1999; 99US-0134219P.
 14-MAY-1999; 99US-0134221P.
 18-MAY-1999; 99US-0134370P.
 18-MAY-1999; 99US-0134768P.
 19-MAY-1999; 99US-0134941P.
 20-MAY-1999; 99US-0135124P.
 21-MAY-1999; 99US-0135353P.
 24-MAY-1999; 99US-0135629P.
 25-MAY-1999; 99US-0136021P.
 27-MAY-1999; 99US-0136392P.
 28-MAY-1999; 99US-0136782P.
 01-JUN-1999; 99US-0137222P.
 03-JUN-1999; 99US-0137528P.
 04-JUN-1999; 99US-0137502P.
 07-JUN-1999; 99US-0137724P.
 08-JUN-1999; 99US-0138094P.
 10-JUN-1999; 99US-0138540P.
 10-JUN-1999; 99US-0138847P.
 14-JUN-1999; 99US-0139119P.
 16-JUN-1999; 99US-0139452P.
 16-JUN-1999; 99US-0139453P.
 17-JUN-1999; 99US-0139492P.
 18-JUN-1999; 99US-0139454P.
 18-JUN-1999; 99US-0139455P.
 18-JUN-1999; 99US-0139456P.
 18-JUN-1999; 99US-0139457P.
 18-JUN-1999; 99US-0139458P.
 18-JUN-1999; 99US-0139459P.
 18-JUN-1999; 99US-0139460P.
 18-JUN-1999; 99US-0139461P.
 18-JUN-1999; 99US-0139462P.
 18-JUN-1999; 99US-0139463P.
 18-JUN-1999; 99US-0139750P.
 18-JUN-1999; 99US-0139763P.
 21-JUN-1999; 99US-0139817P.
 22-JUN-1999; 99US-0139899P.
 23-JUN-1999; 99US-0140353P.
 23-JUN-1999; 99US-0140354P.
 24-JUN-1999; 99US-0140695P.
 28-JUN-1999; 99US-0140823P.
 29-JUN-1999; 99US-0140891P.
 30-JUN-1999; 99US-0141267P.
 01-JUL-1999; 99US-0141842P.
 01-JUL-1999; 99US-0142154P.
 02-JUL-1999; 99US-0142055P.
 06-JUL-1999; 99US-0142390P.
 08-JUL-1999; 99US-0142803P.
 09-JUL-1999; 99US-0142920P.
 12-JUL-1999; 99US-0142977P.
 13-JUL-1999; 99US-0143542P.
 14-JUL-1999; 99US-0143624P.
 15-JUL-1999; 99US-0144005P.
 16-JUL-1999; 99US-0144085P.
 16-JUL-1999; 99US-0144086P.
 19-JUL-1999; 99US-0144325P.
 19-JUL-1999; 99US-0144331P.
 19-JUL-1999; 99US-0144332P.
 19-JUL-1999; 99US-0144333P.
 19-JUL-1999; 99US-0144334P.
 19-JUL-1999; 99US-0144335P.
 20-JUL-1999; 99US-0144352P.

99US-0144632P.
99US-0144844P.
99US-0144814P.
99US-0145086P.
99US-0145088P.
99US-0145085P.
99US-0145087P.
99US-0145089P.
99US-0145192P.
99US-0145145P.
99US-0145218P.
99US-0145224P.
99US-0145276P.
99US-0145913P.
99US-0145918P.
99US-0145919P.
99US-0145951P.
99US-0146386P.
99US-0146388P.
99US-0146389P.
99US-0147038P.
99US-0147204P.
99US-0147302P.
99US-0147192P.
99US-0147260P.
99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
99US-0148171P.
99US-0148319P.
99US-0148341P.
99US-0148565P.
99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149426P.
99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
99US-0150884P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-0156458P.
99US-0156596P.
99US-0157117P.
99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159293P.
99US-0159294P.
99US-0159295P.
99US-0159329P.
99US-0159330P.
99US-0159331P.

PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.9%; Score 10; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G;

QY 222 QQQQPPPPQ 231
|||||
Db 369 QQQQPPPPQ 378

RESULT 49

ABP54691
ID ABP54691 standard; protein; 402 AA.

XX AC ABP54691;

XX DT 30-DEC-2002 (first entry)

XX DE Metastatic colorectal cancer-associated polypeptide.

XX KW Colorectal cancer; metastasis; differential expression; cytostatic
XX diagnosis; gene therapy; vaccine.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 387 /note= "encoded by CGN"

XX PN WO200268677-A2.

XX PD 06-SEP-2002.

XX PF 27-FEB-2002; 2002WO-US006001.

XX PR 27-FEB-2001; 2001US-0272206P.

XX PR 02-APR-2001; 2001US-0281149P.

XX PR 17-APR-2001; 2001US-0284555P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX PI Mack DH, Markowitz SD;

XX DR WPI; 2002-698677/75.

XX DR N-PSDB; ABP81557.

XX PT New genes that are up- or down-regulated in colorectal cancer, use
PT diagnosing colorectal cancer in a subject, or for identifying modu
PT of colorectal cancer-associated proteins and genes for treating
PT colorectal cancer.

252; 260pp; English.

ence is the protein sequence of a human polypeptide
ne that exhibits increased expression in colon cancer-
ies compared to normal colon tissue. It is an example of
ides that are encoded by genes which are differentially
tastic colorectal cancer cells. Such polypeptides are
ostic and prognostic assays, for raising antibodies useful
herapy, and in screening for modulator compounds of
lue

1;

1.9%; Score 10; DB 5; Length 402;

city 100.0%; Pred.No. 5.6;
servative 0; Mismatches 0; Indels 0; Gaps 0;

APAAP 187

|||||
APAAP 245

ird; protein; 436 AA.

irst entry)

n.

rotein; Id protein; maize; corn; flower induction;
n; transgenic plant.

Location/Qualifiers

98. .118

/note= "zinc finger 1"

199. .219

/note= "zinc finger 2"

99WO-US007157.

98US-00056226.

PRING HARBOR LAB.

Sundaresan V;

17/54.

9.

oral induction gene, used for producing plants with
of transition from the vegetative to the flowering stage.

80pp; English.

represents the maize chromosome 1 indeterminate (Id)
a zinc finger regulatory protein that plays a crucial role
from vegetative to reproductive development, controlling
of other genes required for floral development. Loss of Id
; prolonged vegetative development. Understanding the
is regulation provides a basis for producing specialized
i to flower and produce seed independent of native internal
ronmental effects. Methods are provided for producing
ected times of transition from the vegetative to the

CC flowering stage. They can result in either earlier cessation of
CC vegetative growth and initiation of flowering, or in later floweri
CC the absence of floral induction. The plants can be induced to flow
CC set seed prior to adverse weather. Similarly, flower induction can
CC prolonged for short-season plants grown in areas with long periods
CC warm weather. As a result of the extra vegetative mass and carbohy
CC these plants can produce more and/or larger flowers and, consequen
CC more seed. Plants can even be prevented from flowering, thus provi
CC nutritious silage biomass. They can also be used to eliminate the
CC for detasseling in the production of hybrids

XX Sequence 436 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 2; Length 436;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 210 PLPPPPQPPA 219

|||||

Db 45 PLPPPPQPPA 54

RESULT 51

ABP51652
ID ABP51652 standard; protein; 436 AA.

XX AC ABP51652;

XX 30-SEP-2002 (first entry)

DE Maize indeterminate 1 (Id1) protein SEQ ID NO:10.

XX Lolium perenne; perennial ryegrass; indeterminate protein; plant;
KW life cycle; growth phase; flower.

XX Zea mays.

XX WO200238768-A1.

XX 16-MAY-2002.

XX 07-NOV-2001; 2001WO-AU001432.

XX 08-NOV-2000; 2000AU-00001313.

XX (MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.

XX Spangenberg G, Liu B, Truman D;

XX WPI; 2002-575206/61.

XX Novel polypeptide referred to as indeterminate 1 from ryegrass or
PT species, useful for modifying plant life cycles and growth phases
PT flowering processes, plant architecture, inflorescence, flower
PT development.

XX Example 2; Fig 7; 80pp; English.

XX The present invention describes a substantially purified or isolat
CC polypeptide (I) from a ryegrass (Lolium) or fescue (Festuca) spec
CC from indeterminate 1 (Id1) and Id1-like proteins, its functionall
CC fragments and variants. Polynucleotide sequences (II) encoding (I)
CC used for modifying plant life cycles and/or growth phases such as
CC flowering processes, flowering and plant architecture, inflorescen
CC flower development. (II) can also be used as a genetic marker. (I)
CC (II) can be used for facilitating immunological screening of cDNA
CC expression libraries. (II) is useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species,
CC hybridisation probes to screen libraries from the desired plant. (I
CC useful in amplification protocols to amplify longer nucleic acid o
CC nucleic acid fragments encoding homologous genes for DNA or RNA. (I
CC also useful as a molecular genetic marker for quantitative trait lo
CC (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assist

particularly in ryegrasses and fescues. (II) is also used as
 atic markers in forage and turf grass improvement e.g.,
 for herbage quality traits, flowering intensity, flowering
 of tillers, leafiness, bushiness, seasonal growth pattern,
 flower architecture, plant stature. The present sequence
 maize indeterminate 1 (ID1) which is given in comparison
 inate proteins isolated from Lolium perenne (perennial
 the exemplification of the present invention

1A;
 1.9%; Score 10; DB 5; Length 436;
 arity 100.0%; Pred.No. 6;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

PPQPPA 219

|||||

PPQPPA 54

dard; protein; 448 AA.

(first entry)

haliana protein fragment SEQ ID NO: 41985.

ification; signal transduction pathway; metabolic pathway;
 assay; genetic mapping; gene expression control; promoter;
 equence.

haliana.

2000EP-00301439.

99US-0121825P.

99US-0123180P.

99US-0123548P.

99US-0125789P.

99US-0126264P.

99US-0126785P.

99US-0127462P.

99US-0128234P.

99US-0128714P.

99US-0129845P.

99US-0130077P.

99US-013049P.

99US-0130510P.

99US-0130891P.

99US-0131449P.

99US-0132048P.

99US-0132407P.

99US-0132484P.

99US-0132485P.

99US-0132486P.

99US-0132487P.

99US-0132863P.

99US-0134256P.

99US-0134218P.

99US-0134219P.

99US-0134221P.

99US-0134370P.

99US-0134768P.

99US-0134941P.

99US-0135124P.

99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
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 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.

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99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
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99US-0151438P.
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99US-0153070P.
99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-0156458P.
99US-0156596P.
99US-0157117P.
99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159233P.
99US-0159294P.
99US-0159295P.
99US-0159329P.
99US-0159330P.
99US-0159331P.
99US-0159637P.
99US-0159638P.
99US-0159584P.
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160770P.
99US-0160814P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0161040P.
99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.9%; Score 10; DB 3; Length 448;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
QY 222 QQQQPPPPPP 231
Db 416 QQQQPPPPPP 425

RESULT 53
ABG66745
ID ABG66745 standard; protein; 581 AA.
XX
AC ABG66745;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #80.
XX
KW Human; inflammatory condition; shock; sepsis; immune response; can wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; myeloid cell disorder; lymphoid cell disorder; platelet disorder; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; fungal infection.
XX
OS Homo sapiens.
XX
PN W0200244340-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US047004.
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSBQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang I
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX
DR WPI; 2002-508509/54.
XX
PS N-PSDB; ABK94969.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 655-656; 672pp; English.
XX
CC The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn disease, ischaemia-reperfusion injury, shock, sepsis, immune response and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, tissue regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and pericard disease. The sequences of the invention are also useful for gut

regeneration and treatment of lung or liver fibrosis, injury in various tissues, immune deficiencies and disorders are combined immunodeficiency (SCID), bacterial or fungal autoimmune disorders e.g. multiple sclerosis and myasthenia gravis conditions such as asthma, thrombolytic or thrombotic disorders. Sequences ABG66666-ABG666758 represent human sides of the invention

AA;

arity 1.9%; Score 10; DB 5; Length 581;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPQP 234

|||||

PQPQP 97

hard; protein; 588 AA.

(first entry)

ed by Prokaryotic essential gene #8262.

okaryotic essential gene; cell proliferation; drug design.

allele.

2.

2002WO-US009107.

2001US-00815242.

2001US-00948993.

2001US-0342923P.

2002US-00072851.

2002US-0362699P.

PHARM INC.

lio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

ck JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

26/02.

05.

nucleic acids, useful for identifying proteins or screening nucleic acids required for cellular proliferation to late molecules for rational drug discovery programs.

ID NO 50659; 1766pp; English.

relates to an isolated nucleic acid comprising any one of sense sequences given in the specification where expression acid inhibits proliferation of a cell. Also included are: comprising a promoter operably linked to the nucleic acid typeptide whose expression is inhibited by the antisense (2) a host cell containing the vector; (3) an isolated its fragment whose expression is inhibited by the eic acid; (4) an antibody capable of specifically binding ie.(5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for

(7) identifying a compound that influences the activity of act or that has an activity against a biological pathway proliferation, or that inhibits cellular proliferation; (8) gene required for cellular proliferation or the biological

pathway in which a proliferation-required gene or its gene product or a gene on which the test compound that inhibits proliferation organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which t product is overexpressed or underexpressed; (12) determining the to which each of the strains is present in a culture or collecti strains; or (13) identifying the target of a compound that inhibi proliferation of an organism. The antisense nucleic acids are use for cellular proliferation to isolate candidate molecules for rat drug discovery programs, or for screening homologous nucleic acid required for proliferation in cells other than S. aureus, S. typh K. pneumoniae or P. aeruginosa. The present sequence is encoded b the target prokaryotic essential genes. Note: The sequence data f patent did not form part of the printed specification, but was ob in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 588 AA;

Query Match 1.9%; Score 10; DB 6; Length 588;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 118 APAAAAAAP 127

Db 476 APAAAAAAP 485

RESULT 55

ABU15059

ID ABU15059 standard; protein; 613 AA.

XX AC ABU15059;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #596.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug d

XX OS Escherichia coli.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX DR N-PSDB; ACA18929.

XX PT New antisense nucleic acids, useful for identifying proteins or s

XX PT for homologous nucleic acids required for cellular proliferation t

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 42983; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any

XX CC the 6213 antisense sequences given in the specification where exp

XX CC of the nucleic acid inhibits proliferation of a cell. Also include

XX CC (1) a vector comprising a promoter operably linked to the nucleic

ypeptide whose expression is inhibited by the antisense
(2) a host cell containing the vector; (3) an isolated
its fragment whose expression is inhibited by the
eic acid; (4) an antibody capable of specifically binding
e;(5) producing the polypeptide; (6) inhibiting cellular
or the activity of a gene in an operon required for
(7) identifying a compound that influences the activity of
ct or that has an activity against a biological pathway
roliferation, or that inhibits cellular proliferation; (8)
gene required for cellular proliferation or the biological
ch a proliferation-required gene or its gene product lies
hich the test compound that inhibits proliferation of an
(9) manufacturing an antibiotic; (10) profiling a
ivity; (11) a culture comprising strains in which the gene
repressed or underexpressed; (12) determining the extent
of the strains is present in a culture or collection of
3) identifying the target of a compound that inhibits the
of an organism. The antisense nucleic acids are useful for
oteins or screening for homologous nucleic acids required
roliferation to isolate candidate molecules for rational
programs, or for screening homologous nucleic acids
roliferation in cells other than *S. aureus*, *S. typhimurium*,
or *P. aeruginosa*. The present sequence is encoded by one of
karyotic essential genes. Note: The sequence data for this
form part of the printed specification, but was obtained
format directly from WIFO at
ub/published_pct_sequences

A;

1.9%; Score 10; DB 6; Length 613;

ity 100.0%; Pred. No. 8;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EDED 342

|||||

ard; protein; 635 AA.

first entry)

ciparum chromosome 2 related protein SEQ ID NO:49.

ciparum; chromosome 2; human malaria parasite; vaccine;
malaria; protozoacide; infection; insecticide.

ciparum.

99WO-US026796.

98US-0107131P.

Y S.
I D.
R M.
J C.

rucci D, Gardner M, Venter JC;

47/31.

ad by chromosome 2 of the human malaria parasite.
ciparum, useful as antimalarial vaccines and in the

diagnosis of *P. falciparum* infection.

Disclosure; Page 115-116; 577pp; English.

The present invention describes proteins and their fragments (I) &
by chromosome 2 of the human malaria parasite, *Plasmodium falciparum*.
Also described are: (i) nucleotide sequences (II) encoding (I); or
vaccines against *P. falciparum* infection comprising (I) or (II).
(II) are useful for the development of vaccines against *P. falciparum*.
infection. (I) and polyclonal antisera or a monoclonal antibody &
immunogens comprising the sequences of (I), are useful in the detection
of infection with *P. falciparum*. Furthermore, (I) (especially when
are refined or secreted or membrane proteins) can aid the identification
of drugs to treat or prevent *P. falciparum* infection, or they can
to identify drug resistance in *P. falciparum*. Sequencing of the
Plasmodium chromosome 2 and the subsequent identification of proteins
encoded by it will help to expand our understanding of parasite biology
a process hampered by the complexity of the parasitic life cycle, &
provide new targets for vaccine and drug development. Parasite resistance
to drugs and mosquito resistance to insecticides have led to a resurgence
of malaria in many parts of the world, and there is a pressing need
for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18144
represent nucleotide and protein sequences given in the present
invention, but which are not specifically mentioned within the
specification

XX Sequence 635 AA;

Query Match 1.9%; Score 10; DB 3; Length 635;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 334 DDEDEDEDD 343

|||||

Db 577 DDEDEDEDD 586

RESULT 57

ABB62471

ID ABB62471 standard; protein; 660 AA.

XX ABB62471;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 14205.

DE Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX WO200171042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EM;

XX WPI; 2001-656860/75.

XX N-ESDB; ABL06574.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from *Drosophila* and for elucidating cell signaling and cell-cell
interactions.

PS Disclosure; SEQ ID NO 14205; 2lpp + Sequence Listing; English.

relates to an isolated nucleic acid detection reagent detecting 1000 or more genes from Drosophila. The invention is supplemental biology and in elucidating cell signalling and interactions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention omic DNA sequences (ABL16176-ABL30511), expressed DNA (01840-ABL16175) and the encoded proteins (ABBS7737-01840-ABL16175) for this patent did not form part of the invention, but was obtained in electronic format directly from ftp.wipo.int/pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 660;

arity 100.0%; Pred. No. 8.5; conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 150

ard; protein; 660 AA.

(first entry)

ad by Prokaryotic essential gene #33095.

Prokaryotic essential gene; cell proliferation; drug design.

chi.

?

2002WO-US009107.

2001US-00815242.

2001US-00948993.

2001US-0342923P.

2002US-00072851.

2002US-0362699P.

A PHARM INC.

lio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

ck JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

26/02.

138.

nucleic acids, useful for identifying proteins or screening nucleic acids required for cellular proliferation to late molecules for rational drug discovery programs.

ID NO 75492; 1766pp; English.

relates to an isolated nucleic acid comprising any one of sense sequences given in the specification where expression acid inhibits proliferation of a cell. Also included are: comprising a promoter operably linked to the nucleic acid -peptide whose expression is inhibited by the antisense (2) a host cell containing the vector; (3) an isolated its fragment whose expression is inhibited by the nucleic acid; (4) an antibody capable of specifically binding le; (5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the act the gene product or that has an activity against a biological pat required for proliferation, or that inhibits cellular proliferati identifying a gene required for cellular proliferation or the bio pathway in which a proliferation-required gene or its gene produc or a gene on which the test compound that inhibits proliferation organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which t product is overexpressed or underexpressed; (12) determining the to which each of the strains is present in a culture or collectio strains; or (13) identifying the target of a compound that inhibi proliferation of an organism. The antisense nucleic acids are use identifying proteins or screening for homologous nucleic acids re for cellular proliferation to isolate candidate molecules for rat drug discovery programs, or for screening homologous nucleic acid required for proliferation in cells other than S. aureus, S. typh K. pneumoniae or P. aeruginosa. The present sequence is encoded b the target prokaryotic essential genes. Note: The sequence is encoded b patent did not form part of the printed specification, but was ob in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 660 AA;

Query Match 1.9%; Score 10; DB 6; Length 660;

Best Local Similarity 100.0%; Pred. No. 8.5; Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEED 342

|||||

Db 238 DDEDEDEED 247

RESULT 59

ABU47065

ID ABU47065 standard; protein; 660 AA.

XX AC ABU47065;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #32592.

XX Antisense; prokaryotic essential gene; cell proliferation; drug d

XX OS Salmomella typhimurium.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX FF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA50935.

XX PT New antisense nucleic acids, useful for identifying proteins or sc for homologous nucleic acids required for cellular proliferation t isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 74989; 1766pp; English.

Sequence 687 AA;

```

Query Match      1.9%; Score 10; DB 4; Length 697;
Best Local Similarity 100.0%; Pred.No. 8.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gc
QY 333 DDEDEDEED 342
      |||||
DB 132 DDEDEDEED 141

```

62/73.
97.

New isolated polynucleotide and encoded polypeptides, useful in

forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 48036; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polynucleotides are also used as expressed sequence tags for identifying expressed useful in gene therapy techniques to restore normal II) or to treat disease states involving (II). (II) is nerating antibodies against it, detecting or quantitating a n tissue, as molecular weight markers and as a food II) and its binding partners are useful in medical imaging essing (II). (I) and (II) are useful for treating disorders riant protein expression or biological activity. The nd polynucleotide sequences have applications in forensics, gene mapping, identification of mutations or genetic disorders or other traits to assess biodiversity e other types of data and products dependent on DNA and quences. ABG00010-ABG30377 represent novel human diagnostic quences of the invention. Note: The sequence data for this t appear in the printed specification, but was obtained in rmat directly from WIPO at pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 725;

arity 100.0%; Pred. No. 9.2; Indels 0; Gaps 0; Mismatches 0; Conservative 0;

DEDEED 342
|||||||
DEDEED 141

dard; protein; 806 AA.

(first entry)

lanogaster polypeptide SEQ ID NO 9390.

velopmental biology; cell signalling; insecticide; l.

lanogaster.

2.

2001WO-US009231.

2000US-0191637P.

2000US-00614150.

RP NY.

Jams M, Li PWD, Myers EW;

860/75.
969.

nucleic acid detection reagent for detecting 1000 or more osophila and for elucidating cell signaling and cell-cell

XX Disclosure; SEQ ID NO 9390; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reage
CC capable of detecting 1000 or more genes from Drosophila. The inve
CC useful in developmental biology and in elucidating cell signalin
CC cell-cell interactions in higher eukaryotes for the development c
CC insecticides, therapeutics and pharmaceutical drugs. The inventio
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DN
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC AB372072). The sequence data for this patent did not form part of
CC printed specification, but was obtained in electronic format dire
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 806 AA;

Query Match 1.9%; Score 10; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 20 AAASSSAASP 29

Db 214 AAASSSAASP 223

RESULT 63
ABB07036
ID ABB07036 standard; protein; 1101 AA.

AC ABB07036;

XX 21-JUN-2002 (first entry)

DE Mouse SRG3 (SWI3-related gene) protein sequence.

KW Mouse; SRG3; SWI3-related gene.

XX Mus sp.

OS Key Location/Qualifiers

FT Misc-difference 20 /note= "encoded by CGG"

XX KR191125-B1.

XX 15-JUN-1999.

XX 10-AUG-1996; 96KR-00033288.

XX 10-AUG-1996; 96KR-00033288.

XX (SUNG/) SUNG N.

XX Sung N, Park S, Chun S;

XX WPI; 2000-644520/62.

XX N-PSDB; ABL50888, ABL50889.

XX NEW SWI3-RELATED GENE PURIFIED FROM MOUSE AND THE PROTEIN EXPRESS
PT THAT.

XX Claim 2; Page 11-12; 15pp; Korean.

XX The present invention describes an SWI3-related gene, designated;
CC which is isolated from mouse. The present sequence represents the
CC SRG3 protein sequence

XX Sequence 1101 AA;

Query Match 1.9%; Score 10; DB 3; Length 1101;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QPPPP 229
 |||||
 QPPPP 1083

ard; protein; 1250 AA.

first entry)

anogaster retinal degeneration B polypeptide (DmrdgB).

/rosine kinase binding protein; 6-transmembrane domain;
 iron; Pyk2 binding domain; synaptic vesicles;
 ar signalling; myasthenia gravis; stroke; neuroblastoma;
 lia; Alzheimer's; Huntington's; Parkinson's; depression;
 pain epilepsy.

anogaster.

Location/Qualifiers

≥ 1055
 /note= "encoded by TA"
 ≥ 1133
 /note= "encoded by TCC"
 ≥ 1134
 /note= "encoded by ACC"
 ≥ 1149
 /note= "encoded by CA"

97WO-US017374.

96US-0027337P.

INC.

EW YORK MEDICAL CENT.

GD, Schlessinger J;

36/22.
 36.

id encoding human retinal degradation polypeptide - and
 vectors, transformed cells, proteins and antibodies, used
 neurological disease and to identify specific modulators with
 peutic activity.

je 48-50; 59pp; English.

quence represents the D.melanogaster retinal degeneration B
 3), which is a non-receptor tyrosine kinase binding
 VA that encodes this protein had previously been identified
 al, Journal of cell biology, volume 122: 1013-1022, 1993.
 is a false stop codon sequencing error in this reference,
 he sequence to be incorrectly interrupted as a member of the
 a domain family of proteins, thus the Pyk-2 binding domain
 identified. DmrdgB contains both a PIT domain, and a Pyk2
 and is thus concerned with PI transfer and regulating
 ar signalling respectively. This protein is seen to be
 gnalling transduction pathways and therefore would be
 nosis, treatment, and prevention of the following diseases:
 vis; neuroblastoma; thrombocytopaenia; stroke; Alzheimer's;
 parkinson's; depression; schizophrenia; pain epilepsy

AA;

Query Match 1.9%; Score 10; DB 2; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 329 EEEEDDEDE 338
 |||||
 Db 324 EEEEDDEDE 333

RESULT 65

ABB65508
 ID ABB65508 standard; protein; 1250 AA.

XX AC ABB65508;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 23316.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL09611.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or
 PT genes from Drosophila and for elucidating cell signalling and cell-
 PT interactions.

XX PS Disclosure; SEQ ID NO 23316; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The inven
 CC useful in developmental biology and in elucidating cell signalling
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB7072). The sequence data for this patent did not form part of
 CC printed specification, but was obtained in electronic format direc
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1250 AA;

Query Match 1.9%; Score 10; DB 4; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga

QY 329 EEEEDDEDE 338
 |||||
 Db 324 EEEEDDEDE 333

RESULT 66

ABB65470
 ID ABB65470 standard; protein; 1250 AA.

XX AC ABB65470;

(first entry)
lanogaster polypeptide SEQ ID NO 23202.
evolutional biology; cell signalling; insecticide;
1.
lanogaster.
2.
2001WO-US009231.
2000US-0191637P.
2000US-00614150.
3P NY.
iams M, Li PWD, Myers EW;
360/75.
573.
nucleic acid detection reagent for detecting 1000 or more
osophila and for elucidating cell signaling and cell-cell
EQ ID NO 23202; 21pp + Sequence Listing; English.
relates to an isolated nucleic acid detection reagent
ecting 1000 or more genes from Drosophila. The invention is
olopmental biology and in elucidating cell signalling and
ructions in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention
omic DNA sequences (AB116176-AB130511), expressed DNA
01840-AB116175) and the encoded proteins (AB1857737-
sequence data for this patent did not form part of the
fication, but was obtained in electronic format directly
ftp.wipo.int/pub/published_pct_sequences
AA;
arity 1.9%; Score 10; DB 4; Length 1250;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDDEDE 338
|||||
DDDEDE 333
iard; protein; 1277 AA.
(first entry)
m glutamicum MCT protein SEQ ID NO:54.
m glutamicum; brevibacterium lactofermentum; MCT;
struction and membrane transport protein; petroleum spill;
egradation; gram positive aerobic bacterium; marker;
a; microorganism; fine chemical production; transformation;
i; genetic engineering.
m glutamicum.
2.

XX 04-JAN-2001.
XX 23-JUN-2000; 2000WO-IB000926.
XX 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031454.
PR 08-JUL-1999; 99DE-01031478.
PR 08-JUL-1999; 99DE-01031563.
PR 09-JUL-1999; 99DE-01032122.
PR 09-JUL-1999; 99DE-01032124.
PR 09-JUL-1999; 99DE-01032125.
PR 09-JUL-1999; 99DE-01032128.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032182.
PR 09-JUL-1999; 99DE-01032190.
PR 09-JUL-1999; 99DE-01032191.
PR 09-JUL-1999; 99DE-01032209.
PR 09-JUL-1999; 99DE-01032212.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032228.
PR 09-JUL-1999; 99DE-01032229.
PR 09-JUL-1999; 99DE-01032230.
PR 14-JUL-1999; 99DE-01032927.
PR 14-JUL-1999; 99DE-01033005.
PR 14-JUL-1999; 99DE-01033006.
PR 27-AUG-1999; 99DE-01040764.
PR 27-AUG-1999; 99DE-01040765.
PR 27-AUG-1999; 99DE-01040766.
PR 27-AUG-1999; 99DE-01040830.
PR 27-AUG-1999; 99DE-01040831.
PR 27-AUG-1999; 99DE-01040832.
PR 27-AUG-1999; 99DE-01040833.
PR 31-AUG-1999; 99DE-01041378.
PR 31-AUG-1999; 99DE-01041379.
PR 31-AUG-1999; 99DE-01041395.
PR 03-SEP-1999; 99DE-01042077.
PR 03-SEP-1999; 99DE-01042078.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042088.
PA (BADI) BASF AG.
XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX WPI; 2001-071486/08.
XX N-PSDB; AAF67769.
XX Corynebacterium glutamicum nucleic acids encoding membrane constru
PT and membrane transport proteins or their portions, useful for typ
PT identifying C. glutamicum or related bacteria, and as markers for
PT transformation.
XX Claim 20; Page 242-246; 1119pp; English.
XX AAF67743 to AAF68080 encode the Corynebacterium glutamicum membra
CC construction and membrane transport (MCT) proteins given in AAB76
CC AAB76847. The MCT nucleic acids and proteins are useful in the
CC identification of microorganisms which can be used to produce fin
CC chemicals, for modulating fine chemical production in C. glutamic
CC related bacteria (e.g. Brevibacterium lactofermentum), the typing
CC identification of C. glutamicum or related bacteria, as reference
CC for mapping C. glutamicum genome, and as markers for transformati
CC AAF68082 and AAF68082 represent sequencing primers which are used
CC example from the present invention
XX Sequence 1277 AA;
SQ
Query Match 1.9%; Score 10; DB 4; Length 1277;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY 137 PAPVAAAPAA 146

|||||
AAAPA 993

ard; protein; 1301 AA.

first entry)

anogaster polypeptide SEQ ID NO 2179.

velopmental biology; cell signalling; insecticide;

anogaster.

001WO-US009231.

000US-0191637P.

000US-00614150.

P NY.

ams M, Li PWD, Myers EW;

60/75.

32.

nucleic acid detection reagent for detecting 1000 or more
sophila and for elucidating cell signaling and cell-cell

2 ID NO 2179; 21pp + Sequence Listing; English.

relates to an isolated nucleic acid detection reagent
acting 1000 or more genes from *Drosophila*. The invention is
developmental biology and in elucidating cell signalling and
reactions in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention
nic DNA sequences (ABL16176-ABL30511), expressed DNA
(1840-ABL16175) and the encoded proteins (ABB57737-
sequence data for this patent did not form part of the
ication, but was obtained in electronic format directly
p.wipo.int/pub/published_pct_sequences

AA;

1.9%; Score 10; DB 4; Length 1301;

city 100.0%; Pred.No. 15;

iservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 22

AAAAA 1276

ard; protein; 1390 AA.

first entry)

rotein.

KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vacc
KW human.
XX
OS Homo sapiens.
XX
PN WO200272757-A2.
XX
PD 19-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-US006908.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274845P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
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PR 13-MAR-2001; 2001US-0275601P.
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PR 16-MAR-2001; 2001US-0276776P.
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PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
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PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
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PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
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PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291130P.
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PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
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PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
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PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.

2002US-0345705P.
2002US-00092900.

EN CORP.

Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Gangolli E, Vernet CM, Guo X, Tchernev V;
Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Catterton E, Burgess C, Leite M, Zhong H, Alsbrook JP;
Ieger DK;

332/78.

119.

ides and polynucleotides, useful for preventing or treating
sociated with aberrant NOVX expression or activity e.g.,
tension, atherosclerosis, cardiomyopathy or bronchial

323; 1103pp; English.

n describes novel human NOVX polypeptides which have
aridant, antiarteriosclerotic, antiasthmatic and hypotensive
rmaceutical compositions comprising the NOVX proteins or
molecules or NOVX antibodies are useful for preventing or
sorder associated with aberrant NOVX expression or activity
ypertension, atherosclerosis, cardiomyopathy or bronchial
roducts of the invention can be used for gene therapy or in
J65041-ABU65218 represent the NOVX polypeptides encoded by
7185

AA;

arity 1.9%; Score 10; DB 5; Length 1390;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

QPQPPP 235
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QPQPPP 986

dard; protein; 1461 AA.

(first entry)

ans essential protein SEQ ID NO 7629.

; tetracyclin; promoter; GRACE strain; biosynthesis;
action; DNA replication; cell division; growth;
; Candida albicans; fungicide; antifungal.

ans.

2.

2001WO-US049486.

2000US-0259128P.

2001US-00792024.

2001US-0314050P.

A PHARM INC.

ang B, Boone C, Bussey H, Ohlsen KL;

DR

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CC

CC

CC

CC

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XX

SQ

Sequence 1461 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 5; Length 1461;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

OY

334 DDEDEDEDD 343

|||||

Db 1436 DDEDEDEDD 1445

RESULT 71

ABB08801

ID ABB08801 standard; protein; 1887 AA.

XX

AC ABB08801;

XX

DT 27-MAY-2002 (first entry)

XX

DE Yeast fatty acid synthetase SEQ ID NO 1.

XX

KW Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzym

XX

OS Saccharomyces cerevisiae.

XX

PN JP2002027989-A.

XX

PD 29-JAN-2002.

XX

PF 17-JUL-2000; 2000JP-00215908.

XX

PR 17-JUL-2000; 2000JP-00215908.

XX

PA (YAMA-) YAMAGUCHI KEN.

XX

DR WPI; 2002-248227/30.

XX

DR N-PSDB; ABL54551.

XX

ast for improved productivity of ethyl caproate, and for
, comprises a mutated fatty acid synthetase gene.

8-12; 28pp; Japanese.

relates to recombinant yeast with improved productivity of
by introducing mutations into fatty acid synthetase
e yeast is used for improved productivity of ethyl caproate
sing the fermentation characteristic features of yeast. The
ce is that of the yeast fatty acid synthetase gene

AA;

1.9%; Score 10; DB 5; Length 1887;

ity 100.0%; Pred. No. 20;

servative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

|||||

AAAPA 134

ard; protein; 1887 AA.

first entry)

id synthetase mutant G1250Q.

id synthetase; ethyl caproate; fermentation; enzyme;

cerevisiae.

Location/Qualifiers

a 1250

/note= "Wild-type Gly substituted by Gln"

000JP-00215908.

000JP-00215908.

CHI KEN.

CHI TLO YG.

27/30.

ast for improved productivity of ethyl caproate, and for
, comprises a mutated fatty acid synthetase gene.

28pp; Japanese.

relates to recombinant yeast with improved productivity of
by introducing mutations into fatty acid synthetase
e yeast is used for improved productivity of ethyl caproate
sing the fermentation characteristic features of yeast. The
ce is that of the yeast fatty acid synthetase mutant. Note:
quence is not shown in the specification but is derived
, fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAPVAAAAPA 146

|||||

Db 125 PAPVAAAAPA 134

RESULT 73

ABB08803

ID ABB08803 standard; protein; 1887 AA.

XX

AC ABB08803;

XX 27-MAY-2002 (first entry)

XX Yeast fatty acid synthetase mutant G1250A.

XX Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzyme
mutant; mutein.

XX Saccharomyces cerevisiae.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1250

XX /note= "Wild-type Gly substituted by Ala"

PN JP2002027989-A.

XX 29-JAN-2002.

PF 17-JUL-2000; 2000JP-00215908.

PR 17-JUL-2000; 2000JP-00215908.

XX (YAMA-) YAMAGUCHI KEN.

PA (YAMA-) YAMAGUCHI TLO YG.

XX WPI; 2002-248227/30.

XX Recombinant yeast for improved productivity of ethyl caproate, and
producing food, comprises a mutated fatty acid synthetase gene.

PS Claim 1; Page; 28pp; Japanese.

XX The invention relates to recombinant yeast with improved productiv
ethyl caproate by introducing mutations into fatty acid synthet
(ABB08801). The yeast is used for improved productivity of ethyl c
without decreasing the fermentation characteristic features of yea
CC present sequence is that of the yeast fatty acid synthetase mutant
CC The present sequence is not shown in the specification but is deri
CC from the yeast fatty acid synthetase sequence given as SEQ ID NO 1
CC 8-12 (ABB08801)

XX Sequence 1887 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 5; Length 1887;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAPVAAAAPA 146

|||||

Db 125 PAPVAAAAPA 134

RESULT 74

ABB08805

ID ABB08805 standard; protein; 1887 AA.

XX

AC ABB08805;

XX 27-MAY-2002 (first entry)

acid synthetase mutant G1250C.
acid synthetase; ethyl caproate; fermentation; enzyme;
a.
cerevisiae.
Location/Qualifiers
ce 1250
/note= "Wild-type Gly substituted by Cys"
A.
2000JP-00215908.
2000JP-00215908.
UCHI KEN.
UCHI TLO YG.
227/30.
east for improved productivity of ethyl caproate, and for
i, comprises a mutated fatty acid synthetase gene.
; 28pp; Japanese.
relates to recombinant yeast with improved productivity of
e By introducing mutations into fatty acid synthetase
ne yeast is used for improved productivity of ethyl caproate
asing the fermentation characteristic features of yeast. The
ace is that of the yeast fatty acid synthetase mutant. Note:
sequence is not shown in the specification but is derived
t, fatty acid synthetase sequence given as SEQ ID NO 1, Page
1)
AA;
1.9%; Score 10; DB 5; Length 1887;
arity 100.0%; Pred. No. 20;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAA 146
|||||
AAAAA 134
iard; protein; 1887 AA.
(first entry)
cid synthetase mutant G1250T SEQ ID NO 5.
acid synthetase; ethyl caproate; fermentation; enzyme;
n.
cerevisiae.
Location/Qualifiers
ce 1250
/note= "Wild-type Gly substituted by Thr"
A.
The invention relates to recombinant yeast with improved producti-

29-JAN-2002.
17-JUL-2000; 2000JP-00215908.
17-JUL-2000; 2000JP-00215908.
(YAMA-) YAMAGUCHI KEN.
(YAMA-) YAMAGUCHI TLO YG.
WPI; 2002-248227/30.
N-PSDB; ABL54554.
Recombinant yeast for improved productivity of ethyl caproate, an
producing food, comprises a mutated fatty acid synthetase gene.
Claim 1; Page 20-27; 28pp; Japanese.
The invention relates to recombinant yeast with improved producti
ethyl caproate by introducing mutations into fatty acid synthetase
(ABB08801). The yeast is used for improved productivity of ethyl
CC without decreasing the fermentation characteristic features of ye
CC present sequence is that of the yeast fatty acid synthetase mutan
XX
SQ Sequence 1887 AA;
Query Match 1.9%; Score 10; DB 5; Length 1887;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 137 PAPVAAAAPA 146
Db 125 PAPVAAAAPA 134
|||||
RESULT 76
ABB08806
ID ABB08806 standard; protein; 1887 AA.
XX ABB08806;
AC ABB08806;
XX
XX 27-MAY-2002 (first entry)
DT
DE Yeast fatty acid synthetase mutant G1250Y.
XX
XX Yeast; fatty acid synthetase; ethyl caproate; fermentation; enzym
KW mutant; mutsin.
XX
XX Saccharomyces cerevisiae.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1250
FT /note= "Wild-type Gly substituted by Tyr"
XX
XX JP2002027989-A.
XX
XX 29-JAN-2002.
XX
XX 17-JUL-2000; 2000JP-00215908.
XX
XX 17-JUL-2000; 2000JP-00215908.
PR
XX (YAMA-) YAMAGUCHI KEN.
PA (YAMA-) YAMAGUCHI TLO YG.
XX
XX WPI; 2002-248227/30.
DR
XX
PT Recombinant yeast for improved productivity of ethyl caproate, an
producing food, comprises a mutated fatty acid synthetase gene.
XX
XX Claim 1; Page; 28pp; Japanese.
XX
XX The invention relates to recombinant yeast with improved producti

by introducing mutations into fatty acid synthetase
 yeast is used for improved productivity of ethyl caproate
 sing the fermentation characteristic features of yeast. The
 ce is that of the yeast fatty acid synthetase mutant. Note:
 quence is not shown in the specification but is derived
) fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;
 rity 100.0%; Pred. No. 20;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
 |||||
 AAAPA 134

lard; protein; 1887 AA.

first entry)

id synthetase mutant G1250F.

cid synthetase; ethyl caproate; fermentation; enzyme;

cerevisiae.

Location/Qualifiers

e 1250

/note= "Wild-type Gly substituted by Phe"

000JP-00215908.

000JP-00215908.

CHI KEN.

CHI TLO YG.

27/30.

ast for improved productivity of ethyl caproate, and for
 , comprises a mutated fatty acid synthetase gene.

28pp; Japanese.

relates to recombinant yeast with improved productivity of
 by introducing mutations into fatty acid synthetase
 e yeast is used for improved productivity of ethyl caproate
 sing the fermentation characteristic features of yeast. The
 ce is that of the yeast fatty acid synthetase mutant. Note:
 quence is not shown in the specification but is derived
) fatty acid synthetase sequence given as SEQ ID NO 1, Page

AA;

1.9%; Score 10; DB 5; Length 1887;
 rity 100.0%; Pred. No. 20;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

Db 125 PAFVAAAAPA 134
 |||||

RESULT 78

ABR52621
 ID ABR52621 standard; protein; 1887 AA.

XX
 AC ABR52621;

DT 20-JUN-2003 (first entry)

DE Protein sequence #SEQ ID 107.

XX
 KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX
 OS Saccharomyces cerevisiae.

XX
 PN EP1258494-A1.

XX
 PD 20-NOV-2002.

XX
 PF 20-DEC-2001; 2001EP-00130253.

XX
 PR 15-MAY-2001; 2001EP-00111774.

XX
 PA (CELL-) CELLZONE AG.

XX
 PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 PI Marzioch M, Schultz JD, Superti-Furga GD;

XX
 DR WPI; 2003-250078/25.
 DR N-PSDB; ACC60663.

XX
 PT New isolated protein complexes useful for diagnosing a disease or
 PT disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease
 PT disorder.

XX
 PS Disclosure; SEQ ID NO 107; 17pp + Sequence Listing; English.

XX
 CC The invention relates to multiprotein complexes from eukaryotes. f
 CC of the invention and DNA sequences encoding them are given in rec
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complex
 CC obtainable by using a protein as a bait and isolating the set of f
 CC which is attached thereto from cells. Such protein complexes may c
 CC up to 30 distinct proteins. Protein complexes of the invention are
 CC for diagnosing a disease or disorder, or as a target for an active
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for t
 CC patent is not represented in the printed specification, but is bas
 CC sequence information supplied by the European Patent Office. The c
 CC document is available on CD-ROM

XX
 SQ Sequence 1887 AA;

Query Match

Best Local Similarity 1.9%; Score 10; DB 6; Length 1887;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 137 PAFVAAAAPA 146

Db 125 PAFVAAAAPA 134
 |||||

RESULT 79

ABU88253
 ID ABU88253 standard; protein; 1894 AA.

XX
 AC ABU88253;

XX
 DT 07-JUL-2003 (first entry)

XX

secreted and transmembrane PRO polypeptide #1.
ed and transmembrane protein: PRO; gene therapy;
is factor-alpha release; TNF-alpha release;
roliferation; chondrocyte differentiation; tumour;
ur; lung tumour; colon tumour; breast tumour;
ur; rectal tumour; cervical tumour; liver tumour.

A1.

2002US-00183012.

97US-0059263P.
97US-0059266P.
97US-0062250P.
97US-0063486P.
97US-0063120P.
97US-0063121P.
97US-0063540P.
97US-0063541P.
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97US-0063564P.
97US-0063734P.
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98US-0086392P.
98US-0086486P.

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PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088035P.
PR 04-JUN-1998; 98US-0088028P.
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PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
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PR 12-JUN-1998; 98US-0089090P.
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PR 18-JUN-1998; 98US-0089952P.
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PR 24-JUN-1998; 98US-0090429P.
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PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090678P.
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PR 26-JUN-1998; 98US-0090862P.
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PR 01-JUL-1998; 98US-0091359P.
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PR 02-JUL-1998; 98US-0091478P.
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PR 04-AUG-1998; 98US-0094006P.
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PR 18-AUG-1998; 98US-0097022P.

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98US-0097974P.
98US-0098014P.
98US-0098716P.
98US-0098723P.
98US-0098803P.
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98US-0098962P.
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1.9%; Score 10; DB 6; Length 1894;

ity	1.5%;	score 10;	DB
ity	100.0%;	Pred. No. 20;	

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    100.0%, Fred. NO. 20,
    nservative 0; Mismatches 0; Indels 0; Gaps 0;

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TAAAA 22

|||||TAAAA 1060

ard; protein; 1894 AA.

first entry)

creted and transmembrane PRO protein #1.

erapy; tissue typing; tumour; chondrocyte proliferation; differentiation; tumour necrosis factor-alpha release; differentiation.

XX	US2003036147-A1.	97US-00592663P.
XX		97US-00592666P.
XX		97US-00625250P.
XX	20-FEB-2003.	97US-0063486P.
XX		97US-0063120P.
XX		97US-0063121P.
XX	02-JUL-2002; 20C2US-00187741.	97US-0063540P.
		97US-0063541P.
		97US-0063544P.
		97US-0063564P.
		97US-0063734P.
		97US-0063870P.
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Query Match 1.9%; Score 10; DB 6; Length 1894;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

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Db 1051 AAAATTAAAA 1060

RESULT 81

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XX AC ABU96434;

XX DT 25-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein #1.

XX KW Human; secreted and transmembrane protein; PRO; transgenic animal
knockout; chromosome identification; tissue typing; tumour;
XX KW chondrocyte proliferation; chondrocyte differentiation;
tumor necrosis factor-alpha release stimulator.

XX OS Homo sapiens.

XX PN US2003036144-A1.

XX PD 20-FEB-2003.

XX PF 01-JUL-2002; 2002US-00187601.


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1.9%; Score 10; DB 6; Length 1894;
arity 100.0%; Pred. No. 20;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TTAAAA 1060

dard; protein; 1894 AA.

(first entry)

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timulator; tumour; adrenal tumour; lung tumour;
breast tumour; prostate tumour; rectal tumour;
ur; liver tumour; TNF-alpha release;
is factor alpha release; chondrocyte cell proliferation;
ell differentiation; pharmaceutical; diagnostic; biosensor;

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97US-0059266P.
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Query Match 1.9%; Score 10; DB 6; Length 1894;
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Db 1051 AAAATTAAAA 1060

RESULT 83
ABU98258
ID ABU98258 standard; protein; 1894 AA.
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DT 30-JUL-2003 (first entry)
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DE Novel human secreted and transmembrane protein #1.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; gene 1
KW chondrocyte stimulator; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome identification.
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OS Homo sapiens.
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US2003017544-A1.
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PD 23-JAN-2003.
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PF 21-JUN-2002; 2002US-00176915.
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1.9%; Score 10; DB 6; Length 1894;
urity 100.0%; Pred.No. 20;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

TAAAA 22

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TAAAA 1060

ard; protein; 1894 AA.

first entry)

creted and transmembrane PRO protein #1.

erapy; chromosome identification; tissue typing.

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002US-00176985.

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XX KW chondrocyte stimulator; chromosome mapping; gene mapping;
XX OS transgenic animal; knock-out animal; tumour.
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XX PD 13-FEB-2003.
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(first entry)

secreted and transmembrane PRO protein #1.

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stimulation; tumour; tissue typing.

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Db 1051 AAAATTAAAA 1060

lard; protein; 1894 AA.

first entry)

creted and transmembrane protein #1.

id and transmembrane protein; PRO; gene therapy;

imulatur; chromosome mapping; gene mapping;

mal; knockout animal; tissue typing;

oliferation; chondrocyte differentiation;

s factor-alpha stimulation; TNF-alpha stimulation.

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arity 100.0%; Pred. No. 20;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

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TTAAAA 1060

dard; protein; 1894 AA.

XX 24-JUL-2003 (first entry)
 DT Novel human secreted and transmembrane protein #1.
 XX
 DE Human; secreted and transmembrane protein; PRO; cytostatic; gene
 KW chromosome mapping; gene mapping; transgenic animal; knock-out ar
 KW tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003036117-A1.
 XX
 PD 20-FEB-2003.
 XX
 XX 21-JUN-2002; 2002US-00176751.
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Query Match 1.9%; Score 10; DB 6; Length 1894;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gc

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RESULT 90
ABU95204
ID ABU95204 standard; protein; 1894 AA.
XX
AC ABU95204;
XX
DT 24-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein #1.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; gene t
tumour.

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A1.

2002US-00180555.

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XX Human; gene therapy; chondrocyte stimulator; tumour; TNF-alpha;
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XX OS Homo sapiens.
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XX PD 13-FEB-2003.
XX PF 25-JUN-2002; 2002US-00180544.
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ECH INC.

n J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 V, Watanabe CK, Wood WI, Zhang Z;

73/32.

and five nucleic acids encoding PRO polypeptides, useful
 cure of a medicament for diagnosing or treating tumor or
 or detecting expression of an associated gene.

Q ID NO 613; 707pp; English.

XX The invention relates to three hundred and five nucleic acids encod
 CC PRO polypeptides (secreted and transmembrane). The PRO nucleic aci
 CC polypeptides are useful for the manufacture of a medicament for
 CC diagnosing or treating tumour in a mammal, for measuring or detect
 CC expression of an associated gene, for stimulation of chondrocytes
 CC stimulating the release of tumour necrosis factor alpha (TNF-alpha)
 CC human blood. The present sequence represents the amino acid sequen
 CC secreted and transmembrane PRO protein. Note: The sequence data fr
 CC patent did not form part of the printed specification but was obtai
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030032199
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 Best Local Similarity 100.0%; Pred. No. 20;
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 AC ABUS6188;
 XX 01-JUL-2003 (first entry)
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 KW Human; secreted and transmembrane protein; PRO; chromosome mapping
 KW gene mapping; transgenic animal; knockout animal; tissue typing; t
 KW chondrocyte cell proliferation; gene therapy;
 KW chondrocyte cell differentiation; tumour necrosis factor-alpha rel
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first entry)

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XX PD 20-FEB-2003.
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(first entry)

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; prostate tumour; rectal tumour; cervical tumour;
bone disorder; cartilage disorder; sport injury; arthritis.

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ITAAAA 1060

hard; protein; 1894 AA.

(first entry)

secreted and transmembrane protein #1.

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 Breast tumour; prostate tumour; rectal tumour;
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Query Match 1.9%; Score 10; DB 6; Length 1894;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gz

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Db 1051 AAAATTAAAA 1060

RESULT 100
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ID ABU90442 standard; protein; 1894 AA.

XX AC ABU90442;
XX DT 11-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane PRO protein #1.
XX KW Human; gene therapy; tumour necrosis factor-alpha release; TNF;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
XX tissue typing.
XX OS Homo sapiens.
XX US2003036153-A1.
XX PN 20-FEB-2003.
XX PD 02-JUL-2002; 2002US-00187754.
XX PF 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.

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1.9%; Score 10; DB 6; Length 1894;

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nservative 0; Mismatches 0; Indels 0; Gaps 0;

TAAAA 22

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TAAAA 1060

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first entry)

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typing; tumour; chondrocyte stimulator; gene therapy;
s factor-alpha release; affinity purification.

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002US-00199464.

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PR 18-SEP-1998; 98US-0101068P.
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Query Match 1.9%; Score 10; DB 6; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
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RESULT 102

ABO5229
 ID ABO5229 standard; protein; 1894 AA.
 XX AC ABO5229;
 XX DT 12-AUG-2003 (first entry)
 XX DE Novel human secreted and transmembrane PRO protein #1.
 XX DE Human; gene therapy; tumour necrosis factor-alpha; tumour;
 KW chondrocyte stimulation; tissue typing.
 XX OS Homo sapiens.
 XX PN US2003008352-A1.
 XX PD 09-JAN-2003.
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 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 23-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 11-DEC-1997; 97US-0069335P.

97US-0069425P.
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 98US-0084414P.
 98US-0084639P.
 98US-0084640P.
 98WO-US019330.
 98WO-US021141.
 98WO-US025108.
 99WO-US005028.
 99WO-US010733.
 99WO-US012252.
 99WO-US020111.
 99WO-US021090.
 99WO-US028301.
 99WO-US028551.
 99WO-US031274.
 00WO-US000219.
 00WO-US004341.
 00WO-US004342.
 00WO-US004414.
 00WO-US005004.
 00WO-US005601.
 00WO-US005841.
 00WO-US006884.
 00WO-US008439.
 00WO-US013705.
 00WO-US014042.
 00WO-US014941.
 00WO-US015264.
 00WO-US020710.
 00WO-US023328.
 00WO-US030952.
 00WO-US032678.
 00WO-US034956.
 00WO-US006520.
 00WO-US017800.
 00WO-US019692.
 00WO-US021066.
 00WO-US021735.
 00WO-US027099.
 002US-00052586.

ECH INC.

u J. Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 V, Watanabe CK, Wood WI, Zhang Z;

DR WPI; 2003-341327/32.
 XX New PRO polypeptides and nucleic acids encoding the polypeptides,
 PT in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX Disclosure; SEQ ID NO 613; 708pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide. The PRO nuc
 CC sequences are useful as hybridisation probes in chromosome and ge
 CC mapping, for stimulating the release of tumour necrosis factor- α
 CC stimulating proliferation or differentiation of chondrocyte cells
 CC detecting the presence of tumour in a mammal, or in generating an
 CC RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules i
 CC in binding reaction, to generate transgenic animals or knockout a
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification an
 CC typing. The PRO polypeptides and nucleic acid molecules are also
 CC in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies may be used in
 CC diagnostic assays for PRO, or for the affinity purification of PR
 CC recombinant cell culture or natural sources. The present sequence
 CC represents the amino acid sequence of a secreted and transmembran
 CC polypeptide
 XX
 XX Sequence 1894 AA;
 SQ
 Query Match 1.9%; Score 10; DB 6; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G;
 QY 13 AAAATTAAAA 22
 Db 1051 AAAATTAAAA 1060
 RESULT 103
 AAB76534
 ID AAB76534 standard; protein; 2012 AA.
 XX AC AAB76534;
 XX DT 11-APR-2001 (first entry)
 XX DE Corynebacterium glutamicum MCT protein SEQ ID NO:50.
 XX KW Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
 KW membrane construction and membrane transport protein; petroleum s
 KW hydrocarbon degradation; gram positive aerobic bacterium; marker;
 KW identification; microorganism; fine chemical production; transform
 KW genome mapping; genetic engineering.
 XX OS Corynebacterium glutamicum.
 XX PN WO200100805-A2.
 XX PD 04-JAN-2001.
 XX PF 23-JUN-2000; 2000WO-IB000926.
 XX PR 25-JUN-1999; 99US-0141031P.
 PR 08-JUL-1999; 99DE-01031454.
 PR 08-JUL-1999; 99DE-01031478.
 PR 08-JUL-1999; 99DE-01031563.
 PR 09-JUL-1999; 99DE-01032122.
 PR 09-JUL-1999; 99DE-01032124.
 PR 09-JUL-1999; 99DE-01032125.
 PR 09-JUL-1999; 99DE-01032128.
 PR 09-JUL-1999; 99DE-01032180.
 PR 09-JUL-1999; 99DE-01032182.
 PR 09-JUL-1999; 99DE-01032190.
 PR 09-JUL-1999; 99DE-01032191.

99DE-01032209.
99DE-01032212.
99DE-01032227.
99DE-01032228.
99DE-01032229.
99DE-01032230.
99DE-01032927.
99DE-01033005.
99DE-01033006.
99DE-01040764.
99DE-01040765.
99DE-01040766.
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99DE-01041379.
99DE-01041395.
99DE-01042077.
99DE-01042078.
99DE-01042079.
99DE-01042088.

AG.

Kroeger B, Schroeder H, Zelder O, Haberhauer G;

486/08.
767.

A glutamicum nucleic acids encoding membrane construction transport proteins or their portions, useful for typing or glutamicum or related bacteria, and as markers for a.

a 224-231; 1119pp; English.

AF68080 encode the Corynebacterium glutamicum membrane and membrane transport (MCT) proteins given in AAB76510 to MCT nucleic acids and proteins are useful in the a of microorganisms which can be used to produce fine r modulating fine chemical production in C. glutamicum or cia (e.g. Brevibacterium lactofermentum), the typing or i of C. glutamicum or related bacteria, as reference points i glutamicum genome, and as markers for transformation. iAF68082 represent sequencing primers which are used in an the present invention

AA;

1.9%; Score 10; DB 4; Length 2012;
arity 100.0%; Pred. No. 21;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 1675

iard; protein; 2993 AA.

(first entry)

protein fragment SEQ ID NO: 6239.

terium; amino acid synthesis; vitamin; saccharide; synthesis.

Corynebacterium glutamicum.
EP1108790-A2.
20-JUN-2001.
18-DEC-2000; 2000EP-00127688.
16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
(KYOW) KYOWA HAKKO KOGYO KK.
Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi
Tateishi N, Senoh A, Ikeda M, Ozaki A;
WPI; 2001-376931/40.
N-FSDB; AAH67704.

Novel polynucleotides derived from Coryneform bacteria, for ident mutation point of a gene, measuring expression of a gene, analyzi expression profile or pattern of a gene and identifying homologou Claim 17; SEQ ID NO 6239; 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicu are useful for identifying the mutation point of a gene derived f mutant of coryneform bacterium, measuring expression amount and a the expression profile or expression pattern of a gene derived fr Coryneform bacterium, and identifying a homologue of a gene deriv Coryneform bacterium. Coryneform bacteria are useful for produc acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein describe exemplification of the invention. Note: The sequence data for thi did not form part of the printed specification, but was obtained electronic format directly from the European Patent Office

Sequence 2993 AA;

Query Match 1.9%; Score 10; DB 4; Length 2993;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 137 PAPVAAAAPA 146
|||||
Db 1696 PAPVAAAAPA 1705

RESULT 105
AAG34648

ID AAG34648 standard; protein; 43 AA.

XX AAG34648;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 42193.

XX Protein identification; signal transduction pathway; metabolic pat hybridisation assay; genetic mapping; gene expression control; pr termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
99US-0131449P.
99US-0132048P.
99US-0132407P.
99US-0132484P.
99US-0132485P.
99US-0132486P.
99US-0132487P.
99US-0132863P.
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99US-0138540P.
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99US-0142390P.
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PR 99US-0159637P.
PR 99US-0159638P.
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PR 99US-0160770P.
PR 99US-0160814P.
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PR 99US-0160989P.
PR 99US-0161404P.
PR 99US-0161405P.
PR 99US-0161408P.
PR 99US-0161359P.
PR 99US-0161360P.
PR 99US-0161361P.
PR 99US-0161920P.
PR 99US-0161922P.
PR 99US-0161933P.
PR 99US-0162142P.

1.7%; Score 9; DB 3; Length 43;
arity 100.0%; Pred. No. 6.8;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 35

dard; protein; 49 AA.

(first entry)
haliana protein fragment SEQ ID NO: 66991.
ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
equence.
haliana.

2000EP-00301439.

99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
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99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160770P.
99US-0160814P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0161404P.
99US-0161405P.
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99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161922P.
99US-0161993P.
99US-0162142P.

1.7%; Score 9; DB 3; Length 51;
city 100.0%; Pred. No. 7.8;
servative 0; Mismatches 0; Indels 0; Gaps 0;

APA 146
|||||
APA 35

ard; protein; 52 AA.

(first entry)

erived DKFzphutel_22n2 homologue #2.

arapy; vaccine; disease treatment; detection.

000WO-IB001495.
99US-0149499P.
99US-0156503P.

HUMAN GENOME PROJECT.

40/34.

having the sequences of clones isolated from libraries of
n tissues, useful in recombinant DNA methodologies.

age 519; 1095pp; English.

A library of polynucleotides and polypeptides isolated
polynucleotides which can be used for gene therapy or in
ed in the prevention, diagnosis and treatment of diseases
h inappropriate polypeptide expression. The products of the
also be used to identify modulators of expression and
o down regulate expression and activity. The antibodies of
may also be used as diagnostic agents for detecting the
lpeptides in samples. This sequence represents a homologue
de described in the disclosure of the invention

XX
SQ Sequence 52 AA;

Query Match 1.7%; Score 9; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.9; 0; Indels 0; Ga
Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 330 EEEDEDEDE 338
|||||
Db 3 EEEDEDEDE 11

RESULT 109

AAG01387
ID AAG01387 standard; protein; 66 AA.

XX
AC AAG01387;

XX
DT 06-OCT-2000 (first entry)

XX
DE Human secreted protein, SEQ ID NO: 5468.

XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isol
KW gene therapy; chromosome mapping.

XX
OS Homo sapiens.

XX
PN EP1033401-A2.

XX
PD 06-SEP-2000.

XX
PF 21-FEB-2000; 2000EP-00200610.

XX
PR 26-FEB-1999; 99US-0122487P.

XX
PA (GEST) GENSET.

XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX
DR WPI; 2000-500381/45.

XX
DR N-PSDB; AAC01393.

XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedur

XX
PS Claim 13; SEQ ID NO 5468; 71pp + Sequence Listing; English.

XX
CC The present sequence is a polypeptide encoded by one of a large nu
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC prepared from total human RNAs or polyA+ RNAs derived from 30 diff
CC tissues. EST sequences usually correspond mainly to the 3' untrans
CC region (UTR) of the mRNA because they are often obtained from olig
CC primed cDNA libraries. Such ESTs are not well suited for isolating
CC sequences derived from the 5' ends of mRNAs and even in those case
CC longer cDNA sequences have been obtained, the full 5' UTR is rarel
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and c
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5'
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory se
CC and to design expression and secretion vectors

XX
SQ Sequence 66 AA;

Query Match 1.7%; Score 9; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 221 PQQQQPPPP 229
|||||
Db 22 PQQQQPPPP 30

dard; protein; 68 AA.

(first entry)

haliana protein fragment SEQ ID NO: 42272.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126284P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
99US-0128714P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130510P.
99US-0130891P.
99US-0131449P.
99US-0132048P.
99US-0132407P.
99US-0132484P.
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PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140351P.
PR 24-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 29-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 01-JUL-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
PR 06-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 09-JUL-1999; 99US-0142803P.
PR 12-JUL-1999; 99US-0142920P.
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Query Match 1.7%; Score 9; DB 3; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; C

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RESULT 112

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ID AAG52668 standard; protein; 68 AA.

XX
AC AAG52668;

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DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 66977.

XX Protein identification; signal transduction pathway; metabolic pa
XX hybridisation assay; genetic mapping; gene expression control; pr
XX termination sequence.

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AAAAA 146

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AAAAA 35

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(first entry)

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ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

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2000EP-00301439.

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Best Local Similarity 100.0%; Pred. No. 9.9;		
Matches 9; Conservative 0; Mismatches 0; Indels 0; G		
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XX	17-OCT-2000 (first entry)	
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DE	Protein identification; signal transduction pathway; metabolic p:	
XX	hybridisation assay; genetic mapping; gene expression control; p:	
KW	termination sequence.	
KW	Arabidopsis thaliana.	
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OS	Arabidopsis thaliana.	
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PN	EP1033405-A2.	
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PD	06-SEP-2000.	
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(first entry)

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ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
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RESULT 116

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XX DT 18-OCT-2000 (first entry)

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XX KW Protein identification; signal transduction pathway; metabolic p
hybridisation assay; genetic mapping; gene expression control; p
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XX OS Arabidopsis thaliana.

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(first entry)

thaliana protein fragment SEQ ID NO: 42192.
fication; signal transduction pathway; metabolic pathway;
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thaliana.

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XX AC AAR22394;
XX 25-MAR-2003 (revised)
DT 17-AUG-1992 (first entry)
XX Antigen tc-10a.
XX Oocysts; MAB 12-07; sporozoite.
XX Eimeria tenella.
XX WO9204460-A.
XX 19-MAR-1992.
XX 05-SEP-1991; 91WO-US006430.
XX 12-SEP-1990; 90US-00581693.
XX (GEMX) GENEX CORP.
XX Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SI
PI Ruff MD, Augustine PC, Danforth HD;
XX WPI; 1992-114365/14.
XX N-PSDB; AAQ23094.
XX Vaccine against avian coccidiosis - comprising recombinant eimer.
PT antigen ac-18 or ac-6b gene, or microorganisms expressing them.
XX Claim 10; Page 39 + Fig 10; 56pp; English.
XX To identify antigens of E. tenella, expression libraries were pri
CC lambda vector, lambda gt11, using cDNA prep. from polyA mRNA is:
CC from E. tenella oocysts. The cDNA expression library was screened
CC monoclonal antibody (MAB) 12-07 which was raised against the spo
CC stage of E. tenella. The library to be screened was plated on a l
CC allows lysis and plaque formation. During induction of the anti
CC encoded by the phage, the plaques were identified by screening t
CC filters with Mab 12-07. The cDNA inserts from the MAB 12-07 posi
CC phage were cloned into bacteriophage M13 and subjected to sequen
CC analysis. Following sequence analysis, E. tenella antigen tc-10a
CC identified. (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 76 AA;
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
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AAAAA 31

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(first entry)

haliana protein fragment SEQ ID NO: 41809.

ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

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 DE Arabidopsis thaliana.
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 KW hybridisation assay; genetic mapping; gene expression control; pr
 KW termination sequence.
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 XX EP1033405-A2.
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DT 18-OCT-2000 (first entry)
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(first entry)

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n assay; genetic mapping; gene expression control; promoter;
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Db 58 APVAAAAPA 66

RESULT 123

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XX AAG34371;

XX 18-OCT-2000 (first entry)

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KW termination sequence.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

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 AAAPA 35

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(first entry)

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 owth; cell differentiation; cell death.

A2.

2002WO-US031095.
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 2001US-0327380P.
 2001US-0328186P.
 2001US-0329690P.
 2001US-0345384P.
 2001US-0348165P.
 2001US-0350219P.
 2001US-034518P.

PR 09-NOV-2001; 2001US-0345143P.
 PR 16-NOV-2001; 2001US-0332375P.
 PR 03-DEC-2001; 2001US-0336908P.
 PR 07-DEC-2001; 2001US-0340747P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Chawla NK;
 PI Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Gorvad AB;
 PI Griffin JA, Hafalia AJA, Ison CH, Kable AE, Kalafus DP;
 PI Lehr-Mason PM, Lu DAM, Marquis JP, Nguyen DB, Ramkumar J;
 PI Richardson TW, Sapperstein SK, Swarnakar A, Tang YI, Tran UK
 PI Warren BA, Xu Y, Yao MG, Yue H, Yue H;
 XX WPI; 2003-421159/39.
 DR N-PSDB; ACC90601.
 XX New human proteins associated with cell growth, differentiation,
 PT death (CGDD), useful for diagnosing, treating and preventing dis
 PT conditions associated with the aberrant CGDD expression e.g. can
 PT AIDS, or epilepsy.
 XX Claim 1; Page 274; 350pp; English.
 XX The invention relates to an isolated polypeptide associated with
 CC growth, differentiation and death (CGDD). Also disclosed are the
 CC polynucleotides encoding the polypeptides. The polypeptides and
 CC polynucleotides are useful in diagnosing, treating and preventing
 CC diseases or conditions associated with the decreased expression
 CC expression of CGDD. Such diseases include cell proliferative (e.
 CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington
 CC disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and
 CC reproductive disorders, or disorders of the placenta. They are a
 CC useful in assessing the effects of exogenous compounds on the ex
 CC of nucleic acid and amino acid sequences of CGDD. The CGDD or it
 CC fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the ex
 CC of the target polynucleotide and compounds that specifically bin
 CC modulate the activity of the polypeptide. Microarrays consist
 CC polynucleotides of the invention are useful in monitoring or mea
 CC protein-protein interactions, drug-target interactions, and gene
 CC expression profiles. Sequences given in records AAR69601-AAR6965.
 CC represent CGDD polypeptides of the invention
 XX SQ Sequence 84 AA;
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pa
 KW hybridisation assay; Genetic mapping; gene expression control; pr
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 OS Arabidopsis thaliana.
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AAAAA 79
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Query Match 1.7%; Score 9; DB 3; Length 93;
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PD 06-SEP-2000.
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1.7%; Score 9; DB 3; Length 95;
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AAAAA 146
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AAAAA 79

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(first entry)

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sequence.

thaliana.

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Query Match 1.7%; Score 9; DB 3; Length 96;
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RESULT 129

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DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 23548.

XX KW Protein identification; signal transduction pathway; metabolic pa
hybridisation assay; genetic mapping; gene expression control; pr
termination sequence.

XX OS Arabidopsis thaliana.

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(first entry)

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ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

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AAAPA 146
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standard; protein; 99 AA.

(first entry)

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ification; signal transduction pathway; metabolic pathway;
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AAAPA 66

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XX KW Protein identification; signal transduction pathway; metabolic pa
XX KW hybridisation assay; genetic mapping; gene expression control; pr
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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Query Match 1.7%; Score 9; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

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RESULT 134

ID AAG41927 standard; protein; 100 AA.

XX AC AAG41927;

XX DT 18-OCT-2000 (first entry)

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fication; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
quence.

alialana.

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AAAPA 146

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AAAPA 66

standard; protein; 101 AA.

(first entry)

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ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.

haliana.

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99US-0144884P.
99US-0144814P.
99US-0145086P.
99US-0145088P.
99US-0145085P.
99US-0145087P.
99US-0145089P.
99US-0145192P.
99US-0145145P.
99US-0145218P.
99US-0145224P.
99US-0145276P.
99US-0145913P.
99US-0145918P.
99US-0145919P.
99US-0145951P.
99US-0146386P.
99US-0146388P.
99US-0146399P.
99US-0147038P.
99US-0147204P.
99US-0147302P.
99US-0147320P.
99US-0147260P.
99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
99US-0148171P.
99US-0148319P.
99US-0148341P.
99US-0148565P.
99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149426P.
99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
99US-0150884P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153758P.
99US-0154018P.

PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 21-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.7%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAPA 146
Db 58 APVAAAAPA 66

RESULT 136
ABG25320
ID ABG25320 standard; protein; 105 AA.
XX AC ABG25320;
XX 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #25311.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PF 31-MAR-2000; 2000US-00540217.

2000US-00649167.
} INC.
Liu C, Tang YT;
1362/73.
1507.
polynucleotide and encoded polypeptides, useful in
forensics, gene mapping, identification of mutations
for genetic disorders or other traits and to assess
} ID NO 55679; 103pp; English.
} relates to isolated polynucleotide (I) and polypeptide (II)
(I) is useful as hybridisation probes, polymerase chain
} primers, oligomers, and for chromosome and gene mapping.
} inant production of (II). The polynucleotides are also used
as expressed sequence tags for identifying expressed
} useful in gene therapy techniques to restore normal
(II) or to treat disease states involving (II). (II) is
generating antibodies against it, detecting or quantitating a
in tissue, as molecular weight markers and as a food
(II) and its binding partners are useful in medical imaging
} (II). (I) and (II) are useful for treating disorders
} errant protein expression or biological activity. The
and polynucleotide sequences have applications in
} forensics, gene mapping, identification of mutations
for genetic disorders or other traits to assess biodiversity
} for other types of data and products dependent on DNA and
sequences. AB00010-AB03077 represent novel human diagnostic
} sequences of the invention. Note: The sequence data for this
} appear in the printed specification, but was obtained in
} format directly from WIPO at
} /pub/published_pct_sequences
AA;
1.7%; Score 9; DB 4; Length 105;
arity 100.0%; Pred. No. 14;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
} PAPAA 186
} PAPAA 55
} idard; protein; 109 AA.
(first entry)
} ein fragment SEQ ID NO: 41779.
} ification; signal transduction pathway; metabolic pathway;
} assay; genetic mapping; gene expression control; promoter;
sequence; corn.
sp. mays.
2000EP-00301439.
99US-0121825P.
99US-0123180P.

09-MAR-1999; 99US-0123548P.
23-MAR-1999; 99US-0125788P.
25-MAR-1999; 99US-0126264P.
29-MAR-1999; 99US-0126785P.
01-APR-1999; 99US-0127462P.
06-APR-1999; 99US-0128234P.
08-APR-1999; 99US-0128714P.
16-APR-1999; 99US-0129845P.
19-APR-1999; 99US-0130077P.
21-APR-1999; 99US-0130449P.
23-APR-1999; 99US-0130510P.
23-APR-1999; 99US-0130891P.
28-APR-1999; 99US-0131445P.
30-APR-1999; 99US-0132048P.
04-MAY-1999; 99US-0132484P.
05-MAY-1999; 99US-0132485P.
06-MAY-1999; 99US-0132486P.
06-MAY-1999; 99US-0132487P.
07-MAY-1999; 99US-0132863P.
11-MAY-1999; 99US-0134256P.
14-MAY-1999; 99US-0134218P.
14-MAY-1999; 99US-0134219P.
14-MAY-1999; 99US-0134221P.
14-MAY-1999; 99US-0134370P.
18-MAY-1999; 99US-0134768P.
19-MAY-1999; 99US-0134941P.
20-MAY-1999; 99US-0135124P.
21-MAY-1999; 99US-0135353P.
24-MAY-1999; 99US-0135629P.
25-MAY-1999; 99US-0136021P.
27-MAY-1999; 99US-0136392P.
28-MAY-1999; 99US-0136782P.
01-JUN-1999; 99US-0137222P.
03-JUN-1999; 99US-0137528P.
04-JUN-1999; 99US-0137502P.
07-JUN-1999; 99US-0137724P.
08-JUN-1999; 99US-0138094P.
10-JUN-1999; 99US-0138540P.
14-JUN-1999; 99US-0138847P.
16-JUN-1999; 99US-0139452P.
16-JUN-1999; 99US-0139453P.
17-JUN-1999; 99US-0139492P.
18-JUN-1999; 99US-0139454P.
18-JUN-1999; 99US-0139455P.
18-JUN-1999; 99US-0139456P.
18-JUN-1999; 99US-0139463P.
18-JUN-1999; 99US-0139457P.
18-JUN-1999; 99US-0139458P.
18-JUN-1999; 99US-0139459P.
18-JUN-1999; 99US-0139460P.
18-JUN-1999; 99US-0139461P.
18-JUN-1999; 99US-0139462P.
18-JUN-1999; 99US-0139463P.
18-JUN-1999; 99US-0139750P.
18-JUN-1999; 99US-0139763P.
21-JUN-1999; 99US-0139817P.
22-JUN-1999; 99US-0139899P.
23-JUN-1999; 99US-0140353P.
23-JUN-1999; 99US-0140354P.
24-JUN-1999; 99US-0140695P.
28-JUN-1999; 99US-0140823P.
29-JUN-1999; 99US-0140991P.
30-JUN-1999; 99US-0141287P.
01-JUL-1999; 99US-0141842P.
01-JUL-1999; 99US-0142154P.
02-JUL-1999; 99US-0142055P.
06-JUL-1999; 99US-0142390P.
08-JUL-1999; 99US-0142803P.
09-JUL-1999; 99US-0142920P.
12-JUL-1999; 99US-0142977P.
13-JUL-1999; 99US-0143542P.
14-JUL-1999; 99US-0143624P.

99US-0144005P.
99US-0144085P.
99US-0144086P.
99US-0144325P.
99US-0144331P.
99US-0144332P.
99US-0144333P.
99US-0144334P.
99US-0144335P.
99US-0144352P.
99US-0144632P.
99US-0144844P.
99US-0144814P.
99US-0145086P.
99US-0145088P.
99US-0145085P.
99US-0145087P.
99US-0145089P.
99US-0145192P.
99US-0145145P.
99US-0145218P.
99US-0145224P.
99US-0145276P.
99US-0145913P.
99US-0145918P.
99US-0145919P.
99US-0145951P.
99US-0146386P.
99US-0146388P.
99US-0146389P.
99US-0147038P.
99US-0147204P.
99US-0147302P.
99US-0147192P.
99US-0147260P.
99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
99US-0148171P.
99US-0148319P.
99US-0148341P.
99US-0148565P.
99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149426P.
99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
99US-0149930P.
99US-0150566P.
99US-0150884P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-0151438P.
99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
99US-0155486P.
99US-0155659P.
99US-0156458P.
99US-0156596P.
99US-0157117P.
99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 1.7%; Score 9; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAPA 146
| | | | | | | | | |
Db 69 APVAAAAPA 77

RESULT 138

AAAM19703
ID AAAM19703 standard; protein; 111 AA.
AC AAAM19703;
XX
XX 12-OCT-2001 (first entry)
DT
XX
XX Peptide #6137 encoded by probe for measuring cervical gene expres
DE
XX
XX Probe; human; microarray; gene expression; cervical epithelial ce
KW cervical cancer.
XX
XX Homo sapiens.
OS
XX WO200157278-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX

12el DK, Chen W, Rank DR;
1901/53.
derived single exon nucleic acid probes useful for analyzing
on in human cervical epithelial cells.
ID NO 24529; 487pp; English.
vention relates to human single exon nucleic acid probes
110068-AA128459). The present sequence is a peptide encoded
probe. The SNPs are derived from human HeLa cells. The SNPs
o produce a single exon microarray, which can be used for
an gene expression in a sample derived from human cervical
ills. By measuring gene expression, the probes are therefore
iding and/or staging of diseases of the cervix, notably
er. Note: The sequence data for this patent did not form
printed specification, but was obtained in electronic format
a WIPO at ftp.wipo.int/pub/published_pct_sequences
AA;
1.7%; Score 9; DB 4; Length 111;
arity 100.0%; Pred. No. 15;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAA 126
|||||
AAAAA 29
idard; protein; 111 AA.
(first entry)
lanogaster polypeptide SEQ ID NO 39846.
evelopmental biology; cell signalling; insecticide;
il.
lanogaster.
A2.
2001WO-US009231.
2000US-0191637P.
2000US-00614150.
DRP NY.
Adams M, Li PWD, Myers EW;
5860/75.
5121.
nucleic acid detection reagent for detecting 1000 or more
rosophila and for elucidating cell signalling and cell-cell
SEQ ID NO 39846; 21pp + Sequence Listing; English.
a relates to an isolated nucleic acid detection reagent
etecting 1000 or more genes from Drosophila. The invention is
velopmental biology and in elucidating cell signalling and
eractions in higher eukaryotes for the development of
therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed D
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737
CC ABB72072). The sequence data for this patent did not form part o
CC printed specification, but was obtained in electronic format dir
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 111 AA;
SQ
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 131 PAPPPPPPAP 139
DB 68 PAPPPPPPAP 76
|||||
RESULT 140
ABB39430
ID ABB39430 standard; peptide; 111 AA.
XX
AC ABB39430;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #6936 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid p
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for
PT gene expression in human foetal liver.
XX
XX Claim 27; SEQ ID NO 32065; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for me
CC human gene expression in a sample derived from human foetal live
CC single exon nucleic acid probes may be used for predicting, meas
CC displaying gene expression in samples derived from human foetal l
CC present sequence is a peptide encoded by a single exon nucleic a
CC of the invention. Note: The sequence data for this patent did not
CC part of the printed specification, but was obtained in electroni
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 111 AA;
SQ
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 118 AAAAAAAA 126
|||||

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84
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86
87
88
89
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100

AAAAA 29

iard; protein; 111 AA.

(first entry)

encoded by probe for measuring placental gene expression.

cray; human; placenta; antenatal diagnosis;
fer.

2.

2001WO-US000663.

2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.

ULAR DYNAMICS INC.

zel DK, Chen W, Rank DR;
397/53.

derived single exon nucleic acid probes useful for analyzing
on in human placenta.

ID NO 33222; 654pp; English.

vention relates to single exon nucleic acid probes (SENP:
A157546). The present sequence is a peptide encoded by one
ie probes are useful for producing a microarray for
asuring and displaying gene expression in samples derived
acenta. The probes are useful for antenatal diagnosis of
disorders

AA;

1.7%; Score 9; DB 4; Length 111;
arity 100.0%; Pred. No. 15;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 29

iard; protein; 111 AA.

(first entry)

encoded by probe for measuring heart cell gene expression.

xpression; heart; microarray; vascular system;
c disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX MPI; 2001-488899/53.
XX
DR
XX Single exon nucleic acid probes for analyzing gene expression in
PT hearts.
PT
XX
XX Claim 15; SEQ ID NO 25972; 530pp; English.
PS
XX The present invention relates to single exon nucleic acid probes
CC measuring human gene expression in a sample derived from human he
CC ABA21535-ABA41305). The present sequence is a protein encoded by
CC probe. The probes may be used for predicting, measuring and displ
CC gene expression in samples derived from the human heart via micro
CC By measuring gene expression, the probes are useful for predictin
CC diagnosing, grading, staging, monitoring and prognosing diseases
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. N
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly fro
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 111 AA;
SQ
Query Match 1.7%; Score 9; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 118 AAAAAAAAAA 126
Db 21 AAAAAAAAAA 29
RESULT 143
AAW72722
ID AAW72722 standard; protein; 111 AA.
XX
AC AAW72722;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 3302
XX
XX Human; bone marrow expressed exon; gene expression analysis; prob
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
OS
XX WO200157276-A2.
PN
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000668.

2000US-0180312P.
 2000US-0207456P.
 2000US-00608408.
 2000US-00632366.
 2000US-0234687P.
 2000US-0236359P.
 2000GB-00024263.
 TULAR DYNAMICS INC.
 12el DK, Chen W, Rank DR;
 3900/53.
 -derived single exon nucleic acid probes useful for analyzing
 ion in human bone marrow.
 3Q ID NO 33028; 658pp + Sequence Listing; English.
 invention provides a number of single exon nucleic acid
 are derived from genomic sequences expressed in the human
 they can be used to measure gene expression in bone marrow
 h may enable the improved diagnosis and treatment of cancers
 mona, leukaemia and myeloma. The present sequence is a
 led by one of the probes of the invention
 AA;
 1.7%; Score 9; DB 4; Length 111;
 1arity 100.0%; Pred. No. 15;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAA 126
 |||||
 AAAAA 29
 dard; protein; 111 AA.
 (first entry)
 xpressed single exon probe encoded protein SEQ ID NO: 32215.
 expressed exon; Gene expression analysis; probe: microarray;
 disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 12.
 2001WO-US000667.
 2000US-0180312P.
 2000US-0207456P.
 2000US-00608408.
 2000US-00632366.
 2000US-0234687P.
 2000US-0236359P.
 2000GB-00024263.
 TULAR DYNAMICS INC.
 12el DK, Chen W, Rank DR;
 3446/52.

PT Single exon nucleic acid probes for analyzing gene expression in
 PT brains.
 XX
 PS Example 4; SEQ ID NO 32215; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic a
 CC probes which are derived from genomic sequences expressed in the
 CC brain. They can be used to measure gene expression in brain cell
 CC which may enable the diagnosis and improved treatment of nervous
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizo
 CC epilepsy and cancers. The present sequence is a protein encoded
 CC the probes of the invention
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 1.7%; Score 9; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 118 AAAAAAAAA 126
 Db 21 AAAAAAAAA 29
 |||||
 |||||
 RESULT 145
 ID ABG54420 standard; peptide; 111 AA.
 XX AC ABG54420;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human liver peptide, SEQ ID No 33068.
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488898/53.
 DR Human genome-derived single exon nucleic acid probes useful for
 XX gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 33068; 658pp; English.
 CC The invention relates to a single exon nucleic acid probe (SENP)
 CC measuring human gene expression in a sample derived from human a
 CC liver, comprising one of 13109 defined nucleotide sequences giv
 CC specification (or complements/ fragments). The probe hybridises
 CC stringency to a nucleic acid molecule expressed in the human adu
 CC (I) may be used for predicting, measuring and displaying gene exp
 CC in samples derived from human adult liver. The genes identified
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia

h coronary heart disease. ABG47348-ABG59930 represent human exon encoded peptides of the invention. Note: The sequence or this patent does not appear in the printed specification in electronic format directly from WIPO at pub/published_pct_sequences

AA;

arity 1.7%; Score 9; DB 4; Length 111;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
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AAAA 29

ard; peptide; 111 AA.

(first entry)

encoded by genome-derived single exon probe SEQ ID 32211.

exon probe; asthma; lung cancer; COPD; ILD;
active pulmonary disease; interstitial lung disease;
pathic pulmonary fibrosis; neurofibromatosis;
rosis; Gaucher's disease; Niemann-Pick disease;
lak syndrome; sarcoidosis; pulmonary haemosiderosis;
tiocytosis; lymphangioleiomyomatosis; Karagen syndrome;
solar proteinosis; fibrocystic pulmonary dysplasia;
ry dyskinesia; pulmonary hypertension;
ane disease.

2.

2001WO-US000665.

2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.

JLAR DYNAMICS INC.

zel DK, Chen W, Rank DR;

183/15.

ressable set of single exon nucleic acid probes, used to expression in human lung samples.

ID NO 32211; 634pp; English.

relates to a spatially-addressable set of single exon probes for measuring gene expression in a sample derived ng comprising single exon nucleic acid probes having one of acid sequences mentioned in the specification, or their r the 12387 open reading frames derived from the 12614 included are a microarray comprising the novel set of probes et of probes which hybridise at high stringency to a nucleic d in the human lung; measuring gene expression in a sample human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human
CC mRNA, and (b) measuring the label detectably bound to each probe
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequenc
CC the eukaryote; and (b) detecting specific hybridisation of detect
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon
CC having a fragment identical to the predicted exon, the probe is i
CC in the above mentioned microarray; assigning exons to a single ge
CC comprising (a) identifying exons from genomic sequence by the met
CC above and (b) measuring the expression of each of the exons in se
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern
CC expression of the exons in the tissues and/or cell types indicate
CC the exons should be assigned to a single gene; a peptide comprisi
CC of 12011 sequences, mentioned in the specification, or encoded by
CC probes/open reading frames (ORF). The probes are used for gene ex
CC analysis, and for identifying exons in a gene, particularly using
CC lung derived mRNA and for the study of lung diseases such as asth
CC cancer, chronic obstructive pulmonary disease (COPD), interstitia
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibro
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Herm
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmona
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar protei
CC Karagen syndrome, fibrocystic pulmonary dysplasia, primary cili
CC dyskinesia, pulmonary hypertension and hyaline membrane disease.
CC present sequence is a peptide/protein encoded by a single exon pr
CC the invention. Note: The sequence data for this patent did not fc
CC of the printed specification, but was obtained in electronic form
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 111 AA;

Query Match 1.7%; Score 9; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Oy 118 AAAAAAAAA 126
Db 21 AAAAAAAAA 29

RESULT 147

AAAY18127
ID AAAY18127 standard; protein; 112 AA.

XX AC AAAY18127;

XX DT 11-AUG-1999 (first entry)

XX DE Clone 1 of A. thaliana strong light adapting protein.

XX KW Strong light adapting condition; light-resistant plant; transgeni

XX OS Arabidopsis thaliana.

XX FN JP11137253-A.

XX PD 25-MAY-1999.

XX PF 07-NOV-1997; 97JP-00306044.

XX PR 07-NOV-1997; 97JP-00306044.

XX PA (SUMO) SUMITOMO CHEM CO LTD.

XX DR WPI; 1999-364702/31.

XX DR N-PSDB; AAX77096.

XX PT Induction of gene to be expressed in plant under a strong light a
XX condition - useful for enabling plant to grow in desert.

XX PS Claim 3; Page 9; 16pp; Japanese.

XX

represents a clone of the protein of the invention. The
ates to a gene that is induced and expressed in a plant
g light adapting conditions, and is prepared by a procedure
of the following light irradiations (1) to (3) is made on a
, irradiated by a light of a light intensity of 60-100 mu
sisting of a continuous wave length component of a wave
i of 300-800 nm at 15 to 38 degrees C and the gene expression
induced in the cell of said plant: (1) A light of a light
300-700 nm E/sq. m s consisting of a continuous wave length
a wave length region of 300-800 nm at 15-38 degrees C for 1
al days; (2) a light of a light intensity of 200-600 mu
sisting of a continuous wave length component of a wave
i of 350-560 nm at 15-38 degrees C for several hours to
(3) a light of intensity 75-270 mu E/sq. m s consisting of
wave length component of a wave length region of 300-800 nm
es C for several hours to several days. The method can be
rating a transgenic plant that is able to grow in the desert

AA;

1.7%; Score 9; DB 2; Length 112;

arity 100.0%; Pred. No. 15;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146

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AAAPA 79

dard; protein; 112 AA.

(first entry)

haliana protein fragment SEQ ID NO: 42270.

ification; signal transduction pathway; metabolic pathway;
assay; Genetic mapping; gene expression control; promoter;
sequence.

haliana.

2000EP-00301439.

99US-0121825P.

99US-0123180P.

99US-0123548P.

99US-0125788P.

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arity 100.0%; Pred.No.15;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAPA 146
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AAAPA 79
dard; protein; 112 AA.
(first entry)
aliana protein fragment SEQ ID NO: 23547.
ification; signal transduction pathway; metabolic pathway;
assay; genetic mapping; gene expression control; promoter;
sequence.
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1.7%; Score 9; DB 3; Length 112;

Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 138 APVAAAAPA 146
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Db 71 APVAAAAPA 79

Search completed: March 30, 2004, 15:00:42
Job time : 69 secs

11:33:41 2004

us-09-976-740-43.olig.rpr

GenCore version 5.1.6
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in search, using sw model

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listing first 150 summaries

[R 78.*

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pir2.*

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SUMMARIES

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5.0	301	2	S62087	hrpf protein - pse
6.0	436	2	T01652	zinc finger protei
7.0	469	2	T37451	HBFG-2 (HFK-2) pro
8.0	544	2	T17547	proline-rich prote
9.0	557	2	S12359	nicotinic acetylch
10.0	613	1	RNECS	transcription init
11.0	613	2	F91122	RNA polymerase sig
12.0	613	2	E85967	RNA polymerase sig
13.0	615	1	RNEBST	transcription init
14.0	635	2	A71620	hypothetical prote
15.0	660	2	AB0893	RNA polymerase sig
16.0	678	2	A54514	glutamic acid-rich
17.0	762	2	H87302	chemotaxis protein
18.0	1054	2	A61221	probable calcium t
19.0	1100	2	T30967	transcription acti
20.0	1887	2	S61703	fatty-acid synthas
21.0	100	2	T17126	hypothetical prote
22.0	109	1	R6UTP1	acidic ribosomal p
23.0	109	2	T02716	acidic ribosomal p
24.0	109	2	T02039	acidic ribosomal p
25.0	112	2	E86141	protein T25K16.9
26.0	172	2	F86176	protein F19P19.9
27.0	178	2	AH1394	B. subtilis RNA po
28.0	183	2	F84636	hypothetical prote
29.0	217	2	T04353	DNA binding protei

achae-sc
late 33K pr
traw protei
probable tr
phage SF01
protein F22
ectodermal
hypothetica
nucleosome
segmentatio
hypothetica
probable pp
hypothetica
hypothetica
evx1 protei
hypothetica
probable ph
basic helix
homeotic pr
HMS1 protei
hypothetica
SIS2 protei
hypothetica
F12K8.13 pr
hypothetica
hypothetica
elastin pre
hypothetica
clathrin as
phosphoprot
clathrin as
hypothetica
mineralocor
hypothetica
IrH1 protei
hypothetica
immediate-e
Gt1 protein
antifreeze
antifreeze
tyrosine 3-
tyrosine 3-
antifreeze
antifreeze
antifreeze
antifreeze
antifreeze
cystatin -
antifreeze
ribosomal p
acidic ribo
LSU ribosom
hypothetica
non-histone
acidic ribo
anther-spec
anther-spec
anther-spec
secretin pr
hypothetica
SSU ribosom
Alu RNA-bin
signal reco
hexon-associ
hexon-associ
large condu
ribonucleas
barwin homo
barwin homo

1.5 149 2 S39556 high mobility grou
1.5 165 2 B87702 ribosomal protein
1.5 172 2 S35568 sex-determining pr
1.5 176 2 I48752 gene RXRbeta1 prot
1.5 177 2 AB3269 outer membrane lip
1.5 178 2 S26481 calcium-binding pr
1.5 180 2 C61600 segmentatation prote
1.5 184 2 S77928 exoskeletal protei
1.5 205 2 JQ2247 photosystem I chai
1.5 205 2 S41002 hypothetical prote
1.5 207 2 T51567 hypothetical prote
1.5 208 2 T05859 hypothetical prote
1.5 209 2 JC4244 heat-shock 27K pro
1.5 209 2 A86455 hypothetical prote
1.5 211 2 B89716 protein F45B8.3 [i
1.5 213 2 T03931 DNA binding protei
1.5 214 2 B34503 small nuclear ribo
1.5 215 2 I51067 gene HMG-T2 protei
1.5 231 1 RDNCUF ubiquinol-cytochro
1.5 231 2 I53659 Sm-B protein - mou
1.5 233 2 D95860 probable transcript
1.5 234 2 AI3168 transcription regu
1.5 236 2 PQ0806 glycinin A3B4 - so
1.5 238 2 PQ0809 glycinin A3B4 (pla
1.5 239 2 AG3553 transcription regu
1.5 240 2 S09377 small nuclear ribo
1.5 240 2 H69932 hypothetical prote
1.5 241 2 T22216 hypothetical prote
1.5 243 2 PQ0807 glycinin A3B4 - so
1.5 243 2 A28993 auxin-induced prot
1.5 244 2 A98330 sporulation transc
1.5 244 2 AD2953 transcription regu
1.5 247 2 AG3513 channel protein vi
1.5 249 2 T35724 cobalt transport i
1.5 249 2 A37280 C/EBP-related prot
1.5 249 2 S59404 hypothetical prote
1.5 249 2 A41497 36K antigen pra -
1.5 251 1 RNBY3C DNA-directed RNA p
1.5 251 2 PQ0808 glycinin A3B4 (pla
1.5 253 2 T19129 hypothetical prote
1.5 255 2 A70758 hypothetical prote
1.5 257 2 T03825 myb protein homolo
1.5 257 2 T03646 probable zinc fing
1.5 258 2 H88130 protein F10G7.3 [i
1.5 261 2 S34604 homeobox protein G
1.5 271 2 S34666 glycine-rich prote
1.5 271 2 JC6553 transcription fact
1.5 274 2 T52103 GATA-binding trans

ALIGNMENTS

in 3L - Molluscum contagiosum virus 1
MC003L
um contagiosum virus 1
#sequence_revision 05-Nov-1999 #text_change 11-May-2000
14
Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
16, 1996
sequence of a human tumorigenic poxvirus: Prediction of specific host re
220876; MUID:96325459; PMID:8670425
14
ary; translated from GB/EMBL/DBDJ
DNA
<SEN>
s: EMBL:U60315; PIDN:AAC55131.1

2.0%; Score 11; DB 2; Length 445;

Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0;
Matches 11; Conservative 0; Mismatches 0;
QY 127 PPTTAPPPPP 137
DB 353 PPTTAPPPPP 363
RESULT 2
C72858
AcOrf-66 protein - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear
A:Reference number: A72850; MUID:94303173; PMID:8030224
A:Accession: C72858
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-808 <AYR>
A:Cross-references: GB:L22858; NID:g510708; PIDN:AAA66696.1; PID:g559
C:Genetics:
A:Gene: AcOrf-66

Query Match 2.0%; Score 11; DB 2; Length 808;
Best Local Similarity 100.0%; Pred. No. 0.45; Indels 0;
Matches 11; Conservative 0; Mismatches 0;

QY 212 PPPQPAPPQ 222
DB 108 PPPQPAPPQ 118

RESULT 3
T09193
ataxin 7 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jun-1999
C:Accession: T09193
R:Del-Favero, J.; Krois, L.; Michalik, A.; Theuns, J.; Lofgren, A.; G
Hum. Mol. Genet. 7, 177-186, 1998
A:Title: Molecular genetic analysis of autosomal dominant cerebellar
A:Reference number: Z16604; MUID:98087568; PMID:9425224
A:Accession: T09193
A:Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-892
A:Cross-references: EMBL:AF032105; NID:g3192953; PIDN:AAC39765.1; PID
A:Experimental source: cell type lymphoblast
C:Genetics:
A:Gene: SCA7
A:Map position: 3

Query Match 2.0%; Score 11; DB 2; Length 892;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0;
Matches 11; Conservative 0; Mismatches 0;

QY 222 QQQQPPPPQ 232
DB 36 QQQQPPPPQ 46

RESULT 4
S32101
PHLPSA protein - common timothy (fragment)
C:Species: Phleum pratense (common timothy)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995
C:Accession: S32101
R:Sufer, A.; Becker, W.M.; Petersen, A.; Schramm, G.; Schlaak, M.


```

RESULT 11
F91122
RNA polymerase sigma 70 factor RpoD [imported] - Escherichia coli (st
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Au
R:Accession: F91122
C:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yoko
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shima
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia co
A:Reference number: A39629; MUID:21156231; PMID:11258796
A:Accession: F91122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-613 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837373.1; PID:ig13363423; GSPD
A:Experimental source: strain O157:H7, substrain RIMD 050952
C:Genetics:
A:Gene: EC83950
C:Superfamily: transcription initiation factor sigma 70; transcrip
Query Match 1.9%; Score 10; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 333 DDEDEDED 342
|||||
DB 191 DDEDEDED 200
|||||
RESULT 12
E85967
RNA polymerase sigma 70 factor RpoD [imported] - Escherichia coli (st
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-No
C:Accession: E85967
R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.;
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potam
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-613 <STO>
A:Cross-references: GB:AB005174; NID:g12517649; PIDN:AAG58201.1; GSPD
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: rpoD
C:Superfamily: transcription initiation factor sigma 70; transcrip
Query Match 1.9%; Score 10; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 333 DDEDEDED 342
|||||
DB 191 DDEDEDED 200
|||||
RESULT 13
RNE827
transcription initiation factor sigma 70 - Salmonella typhimurium
N:Alternate names: DNA-directed RNA polymerase sigma chain; major sig
C:Species: salmonella typhimurium
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 11-Ju
C:Accession: C23985
R:Ericksen, B.D.; Burton, Z.F.; Watanabe, K.K.; Burgess, R.R.
Gene 40, 67-78, 1985
A:Title: Nucleotide sequence of the rpsU-dnaG-rpoD operon from Salmon
A:Reference number: A31542; MUID:86137422; PMID:3005129

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5  <ARI>
6  : GB:M14427; NID:g154402; PIDN:AAA27242.1; PID:g154406
7
8  ascription initiation factor sigma 70; transcription initiation factor
9  nding; sigma factor; transcription initiation
10 ascription initiation factor sigma region 1 homology <SR1>
11 transcription initiation factor sigma katF homology <KTF>
12
13     1.9%; Score 10; DB 1; Length 615;
14 arity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;
15 conservative 0; Mismatches 0;
16
17 DEDEED 342
18 |||||
19 DEDEED 202
20
21
22 in PF80250w - malaria parasite (Plasmodium falciparum)
23 ium falciparum
24 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
25
26 steelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
27 zberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
28 1132, 1998
29 e 2 sequence of the human malaria parasite Plasmodium falciparum.
30 : A71600; MUID:95021743; PMID:9804551
31
32 ary; nucleic acid sequence not shown; translation not shown
33 NA
34 <GAR>
35 : GB:AB001382; GB:AE001362; NID:g3845130; PIDN:AACT1839.1; PID:g384513
36 rce: clone 3D7
37
38     1.9%; Score 10; DB 2; Length 635;
39 arity 100.0%; Pred. No. 2.6;
40 conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 EDEDD 343
43 |||||
44 EDEDD 586
45
46 na-70 factor [imported] - Salmonella enterica subsp. enterica serovar
47 la enterica subsp. enterica serovar Typhi
48 es has also been called Salmonella typhi
49 l #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
50
51 gan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
52 P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
53 Gaora, P.
54 2, 2001
55 C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
56 genome sequence of a multiple drug resistant Salmonella enterica serov
57 : AB0502; MUID:21534947; PMID:11677608
58
59 ary
60 NA
61 <PAR>
62 : GB:AL513382; PIDN:CAD07736.1; PID:g16504288; GSPDB:GN00176
63
64 ascription initiation factor sigma 70; transcription initiation factor
65
66     1.9%; Score 10; DB 2; Length 660;

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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 333 DDEDEDEED 342
Db 238 DDEDEDEED 247
RESULT 16
A54514
glutamic acid-rich protein precursor - malaria parasite (Plasmodium fa
N; Alternate names: GARP
C; Species: Plasmodium falciparum
C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 21-Jul
C; Accession: A54514
R; Triglia, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; K
Mol. Biochem. Parasitol. 31, 199-202, 1988
A; Title: Structure of a Plasmodium falciparum gene that encodes a glut
A; Reference number: A54514; MUID:89040048; PMID:2903445
A; Accession: A54514
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-678 <TRI>
A; Cross-references: GB:J03998; NID:g160298; PIDN:AAA29605.1; PID:g1602
C; Genetics:
A; Introns: 25/3
C; Superfamily: histone H1
C; Keywords: tandem repeat
Query Match
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 331 EEDDEDEDE 340
Db 640 EEDDEDEDE 649
RESULT 17
H87302
chemotaxis protein CheA [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May
C; Accession: H87302
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.;
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter,
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: AB7249; MUID:21173698; PMID:11259647
A; Accession: H87302
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-762 <STO>
A; Cross-references: GB:AE005673; NID:g13421600; PIDN:AAK22420.1; GSPDB
C; Genetics:
A; Superfamily: chemotaxis protein cheA
Query Match
Best Local Similarity 100.0%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 118 APAAAAAAP 127
Db 338 APAAAAAAP 347
RESULT 18
A61221
probable calcium transporter rdgB - fruit fly (Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 03-May-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jul

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21 Hyde, D.R.; O'Tousa, J.E.
-768, 1991
A; Experimental source: strain S288C (AB972)
A; Reference number: S65202
A; Accession: S65250
A; Molecule type: DNA
A; Residues: 1567-1887 <RIE>
A; Cross-references: EMBL:Z73587; MIPS:YPL231w
R; Mohamed, A.H.; Chirala, S.S.; Mody, N.H.; Huang, W.Y.; Wakil, S.J.
J. Biol. Chem. 263, 12315-12325, 1988
A; Title: Primary structure of the multifunctional alpha subunit prote
A; Reference number: A31107; MUID:88315020; PMID:2900835
A; Accession: A31107
A; Molecule type: DNA
A; Residues: 1-310, 'TTGTGG', 311-593, 'I', 595-940, 'CINCVKSMKLKLERPPSK
A; Cross-references: EMBL:J03936; NID:gi71501; PIDN:AAA34601.1; PID:gi
C; Genetics:
A; Gene: SGD: FAS2
A; Cross-references: SGD: S0006152; MIPS: YPL231w
A; Map position: 16L
C; Superfamily: yeast fatty-acid synthase
C; Keywords: acyltransferase; coenzyme A

Query Match 1.9%; Score 10; DB 2; Length 1887;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAPVAAAPAA 146
Db 125 PAPVAAAPAA 134
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RESULT 21
T17126
hypothetical protein T30A10.30 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct
C; Accession: T17126
R; Revan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.
submitted to the Protein Sequence Database, September 1999
A; Reference number: Z18708
A; Accession: T17126
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-100 <BEV>
A; Cross-references: EMBL: A1117386
C; Genetics:
A; Map position: 4
A; Introns: 30/3
A; Note: T30A10.30

Query Match 1.7%; Score 9; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQPPPP 229
Db 65 PQQQPPPP 73
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RESULT 22
R6UTP1
acidic ribosomal protein P1 - Trypanosoma cruzi
C; Species: Trypanosoma cruzi
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Ju
C; Accession: S22644; S19924
R; Vazquez, M.P.; Schijman, A.G.; Levin, M.J.
Nucleic Acids Res. 20, 2599, 1992
A; Title: Nucleotide sequence of a cDNA encoding a Trypanosoma cruzi a

21 FlyBase: FBgn0003218
um binding; calcium transport; glycoprotein; transmembrane protein
calcium binding #status predicted <CAL>
, 852,928/Binding site: carbohydrate (Asn) (covalent) #status predicted
1.9%; Score 10; DB 2; Length 1054;
arity 100.0%; Pred. No. 4;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
EDDDEDE 338
|||||
EDDDEDE 333

ivator SRG3 - mouse
sculus (house mouse)
99 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
57
Z. M.G.; Kim, Y.H.; Lee, C.; Park, S.D.; Seong, R.H.
EMBL Data Library, January 1997
new mouse gene, SRG3, related to the SWI3 of Saccharomyces cerevisiae.
r: Z20948
57
nary; translated from GB/EMBL/DBJ
mRNA
0 <JEO>
s: EMBL:U85614; NID:gl816634; PID:gl816635; PIDN:AAB42085.1

olved in glucocorticoid-induced apoptosis in the thymoma cell line; ma
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arity 100.0%; Pred. No. 4.1;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QQQPPPP 229
|||||
QQQPPPP 1082

se (EC 2.3.1.85) alpha chain - yeast (Saccharomyces cerevisiae)
: Protein P1409; protein YPL211w
romyces cerevisiae
96 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
03; S65256; S65250; A31107
A.
EMBL Data Library, December 1995
r: S61699
03
DNA
7 <URR>
s: EMBL: X94561; NID:gl181252; PIDN:CAA64256.1; PID:gl181257
A.; Vissers, S.
Protein Sequence Database, May 1996
r: S65251
56
DNA

A; Residues: 1-1887 <URW>
A; Cross-references: EMBL:Z73587; NID:gi370477; PIDN:CAA97948.1; PID:g
A; Experimental source: strain S288C (AB972)
R; Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S65202
A; Accession: S65250
A; Molecule type: DNA
A; Residues: 1567-1887 <RIE>
A; Cross-references: EMBL:Z73587; MIPS:YPL231w
R; Mohamed, A.H.; Chirala, S.S.; Mody, N.H.; Huang, W.Y.; Wakil, S.J.
J. Biol. Chem. 263, 12315-12325, 1988
A; Title: Primary structure of the multifunctional alpha subunit prote
A; Reference number: A31107; MUID:88315020; PMID:2900835
A; Accession: A31107
A; Molecule type: DNA
A; Residues: 1-310, 'TTGTGG', 311-593, 'I', 595-940, 'CINCVKSMKLKLERPPSK
A; Cross-references: EMBL:J03936; NID:gi71501; PIDN:AAA34601.1; PID:gi
C; Genetics:
A; Gene: SGD: FAS2
A; Cross-references: SGD: S0006152; MIPS: YPL231w
A; Map position: 16L
C; Superfamily: yeast fatty-acid synthase
C; Keywords: acyltransferase; coenzyme A

Query Match 1.9%; Score 10; DB 2; Length 1887;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAPVAAAPAA 146
Db 125 PAPVAAAPAA 134
|||||

RESULT 21
T17126
hypothetical protein T30A10.30 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct
C; Accession: T17126
R; Revan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.
submitted to the Protein Sequence Database, September 1999
A; Reference number: Z18708
A; Accession: T17126
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-100 <BEV>
A; Cross-references: EMBL: A1117386
C; Genetics:
A; Map position: 4
A; Introns: 30/3
A; Note: T30A10.30

Query Match 1.7%; Score 9; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQPPPP 229
Db 65 PQQQPPPP 73
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RESULT 22
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acidic ribosomal protein P1 - Trypanosoma cruzi
C; Species: Trypanosoma cruzi
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Ju
C; Accession: S22644; S19924
R; Vazquez, M.P.; Schijman, A.G.; Levin, M.J.
Nucleic Acids Res. 20, 2599, 1992
A; Title: Nucleotide sequence of a cDNA encoding a Trypanosoma cruzi a

: S22644; MUID:92285148; PMID:1598221
 acid sequence not shown
 RNA
 <VAZ>
 : EMBL:X65025; NID:gl0629; PIDN:CAA46159.1; PID:gl0630
 acidic ribosomal protein P1
 protein; protein biosynthesis; ribosome
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 100.0%; Pred. No. 4.1;
 Mismatches 0; Indels 0; Gaps 0;
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 WAAA 85
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 ribosomal protein L12
 (maize)
 #sequence_revision 24-Mar-1999 #text_change 13-Aug-1999
 urcich, M.P.; Bokhari-Riza, A.; Mascarenhas, J.P.
 IBL Data Library, November 1995
 Z14703
 ry; translated from GB/EMBL/DBJ
 NA
 :HAM>
 EMBL:U40147; NID:gl209700; PIDN:AAA91168.1; PID:gl209701
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 acidic ribosomal protein P1
 biosynthesis; ribosome
 1.7%; Score 9; DB 2; Length 109;
 100.0%; Pred. No. 4.1;
 Mismatches 0; Indels 0; Gaps 0;
 AAPA 146
 ||||
 AAPA 77
 ry; translated from GB/EMBL/DBJ
 NA
 : (maize)
 #sequence_revision 26-Feb-1999 #text_change 13-Aug-1999
 ; Vangala, S.; Szick, K.; Lee, C.H.
 1293-1305, 1997
 aphoprotein complex of the 60S ribosomal subunit of maize seedling ro
 Z14507; MUID:97422884; PMID:9276949
 ry; translated from GB/EMBL/DBJ
 NA
 :BAL>
 EMBL:U62752; NID:g2431768; PIDN:AAB71079.1; PID:g2431769
 ce: strain B73
 acidic ribosomal protein P1
 biosynthesis; ribosome
 1.7%; Score 9; DB 2; Length 109;
 100.0%; Pred. No. 4.1;
 Mismatches 0; Indels 0; Gaps 0;
 AAPA 146
 ||||

Db 69 APVAAAAAPA 77
 RESULT 25
 E86141
 protein T25K16.9 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar
 C;Accession: E86141
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: E86141
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-112 <STO>
 A;Cross-references: GB:AE005172; NID:g6715644; PIDN:AAF26471.1; GSPDB:
 C;Genetics:
 A;Gene: T25K16.9
 A;Map position: 1
 C;Superfamily: rat acidic ribosomal protein P1
 Query Match 1.7%; Score 9; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 138 APVAAAAAPA 146
 |||||
 Db 71 APVAAAAAPA 79
 RESULT 26
 F86176
 protein F19P19.9 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar
 C;Accession: F86176
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F86176
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-172 <STO>
 A;Cross-references: GB:AE005172; NID:g2341030; PIDN:AAB70430.1; GSPDB:(
 C;Genetics:
 A;Gene: F19P19.9
 A;Map position: 1
 Query Match 1.7%; Score 9; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 119 PAAVAAAAAP 127
 |||||
 Db 42 PAAVAAAAAP 50

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RE polymerase delta chain homolog lmo2560 [imported] - Listeria monocytogenes
AB 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C1 34
C2 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C3 34
C4 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C5 34
C6 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C7 34
C8 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C9 34
C10 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C11 34
C12 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C13 34
C14 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C15 34
C16 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C17 34
C18 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C19 34
C20 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C21 34
C22 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C23 34
C24 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C25 34
C26 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C27 34
C28 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C29 34
C30 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C31 34
C32 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C33 34
C34 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C35 34
C36 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C37 34
C38 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C39 34
C40 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C41 34
C42 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C43 34
C44 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C45 34
C46 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C47 34
C48 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C49 34
C50 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C51 34
C52 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C53 34
C54 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
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C57 34
C58 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C59 34
C60 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C61 34
C62 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C63 34
C64 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C65 34
C66 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C67 34
C68 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C69 34
C70 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C71 34
C72 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C73 34
C74 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
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C76 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
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C79 34
C80 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C81 34
C82 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C83 34
C84 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C85 34
C86 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C87 34
C88 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C89 34
C90 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C91 34
C92 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C93 34
C94 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C95 34
C96 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C97 34
C98 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C99 34
C100 1 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003

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A:Reference number: Z14889
A:Accession: T04353
A>Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-217 <HS>
A:Cross-references: EMBL:U25283; NID:gi753084; PIDN:AAB39320.1; PID:g
A:Experimental source: cv. Tainung 67, seed

Query Match 1.7%; Score 9; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0;
Matches 9; Conservative 0;

QY 119 PAAAAAAPP 127
DB 52 PAAAAAAPP 60

RESULT 30
I51382
A:Title: A chicken achae-scute homolog (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Ju
C:Accession: I51382
R:Jasani, C.D.; Walker, M.B.; Morris, M.D.; Reh, T.A.
Development 120, 769-783, 1994
A:Reference number: I51382; MUID:95324365; PMID:7600956
A:Accession: I51382
A>Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-219 <JAS>
A:Cross-references: EMBL:U01339; NID:g401726; PIDN:AAC59658.1; PID:g4

Query Match 1.7%; Score 9; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0;
Matches 9; Conservative 0;

QY 120 AAAAAAAPP 128
DB 28 AAAAAAAPP 36

RESULT 31
WMAD51
A:Title: late 33K protein - human adenovirus 5
C:Species: Mastadenovirus h5 (human adenovirus 5)
A:Notes: host Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 04-Ma
C:Accession: F39449
R:Chroboczek, J.; Bieher, F.; Jacrot, B.
Virology 186, 280-285, 1992
A:Title: The sequence of the genome of adenovirus type 5 and its comp
A:Reference number: A39449; MUID:92087470; PMID:1727603
A:Accession: F39449
A:Molecule type: DNA
A:Residues: 1-229 <CHR>
A:Cross-references: GB:M73260
C:Superfamily: adenovirus late 33K protein
C:Keywords: late protein

Query Match 1.7%; Score 9; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.7; Mismatches 0; Indels 0;
Matches 9; Conservative 0;

QY 118 AAAAAAAPP 126
DB 109 AAAAAAAPP 117

RESULT 32
T31231
A:Title: traw protein homolog - Sphingomonas aromaticivorans plasmid pML1
C:Species: Sphingomonas aromaticivorans

```

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) #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
llwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
4BL Data Library, July 1998
plete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
: Z20992
try; translated from GB/EMBL/DBJ
VA
: EMBL:AF079317; NID:g3378261; PID:g3378372; PIDN:AAD03955.1
DNL1
erichia coli plasmid F F-pilus assembly periplasmic protein traw
1.7%; Score 9; DB 2; Length 231;
arity 100.0%; Pred. No. 7.8;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
PARAP 149
|||||
PARAP 222

in - Mycobacterium tuberculosis (strain H37RV)
erium tuberculosis
) #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
sh, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
s, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
t, 1998
R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
g the biology of Mycobacterium tuberculosis from the complete genome
: A70500; MUID:9829598; PMID:9634230
try; nucleic acid sequence not shown; translation not shown
VA
COL>
: GB:295554; GB:AL123456; NID:g3261771; PIDN:CAB08905.1; PID:g2113895
ce: strain H37RV

le-3-glycerol-phosphate synthase; trpC homology
C homology <TRC>
1.7%; Score 9; DB 2; Length 272;
arity 100.0%; Pred. No. 8.9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
VAPP 129
|||||
VAPP 40

merase-related protein [imported] - Caulobacter crescentus
ter crescentus
) #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
ldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
Boy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
ici, U.S.A. 98, 4136-4141, 2001
genome Sequence of Caulobacter crescentus.
: A87249; MUID:21173698; PMID:11259647
try
VA

```

A;Residues: 1-273 <STO>
A;Cross-references: GB:AE005673; NID:g13422678; PIDN:AAK23314.1; GSPDB
C;Genetics:
A;Gene: CCI333

Query Match 1.7%; Score 9; DB 2; Length 273;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 133 PPPPPAPVA 141
|||||
Db 47 PPPPPAPVA 55

RESULT 35
D86208
protein F22G5.34 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug
C;Accession: D86208
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Ma
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86208
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <STO>
A;Cross-references: GB:AE005172; NID:g8778555; PIDN:AAF79563.1; GSPDB:
C;Genetics:
A;Gene: F22G5.34
A;Map position: 1
C;Superfamily: Escherichia coli ribosomal protein L4

Query Match 1.7%; Score 9; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 330 EEDDDDEDE 338
|||||
Db 267 EEDDDDEDE 275

RESULT 36
A61047
ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Feb
C;Accession: A61047
R;Raha, D.; Nguyen, Q.D.; Garen, A.
Dev. Genet. 11, 310-317, 1990
A;Title: Molecular and developmental analyses of the protein encoded b;
A;Reference number: A61047; MUID:91215866; PMID:2090376
A;Accession: A61047
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-280 <RAH>
A;Note: in the nucleotide sequence codons for residues 25-28 are not s
A;Note: the authors' translation is shown for the codon GAG at residue
C;Genetics:
A;Gene: FlyBase:ect
A;Cross-references: FlyBase:FBgn0000451

Query Match 1.7%; Score 9; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 338
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 DDEDE 87

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ed from GB/EMBL/DBJ
RNA
<HSI>
: EMBL:U25430; NID:G818848; PID:G818849
urce: strain Tainung 67

an phosphodiesterase I / nucleotide pyrophosphatase 4
me A; metalloprotein; phosphoric diester hydrolase

1.7%; Score 9; DB 2; Length 479;
arity 100.0%; Pred. No. 14;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPP 128
|||||
AAAPP 10

helix protein, DEC2 - human
piens (man)
l1 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
33
en, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E.
Res. Commun. 280, 164-171, 2001
: cloning and characterization of DEC2, a new member of basic helix-loop
: JC7583; MUID:21092582; PMID:11162494
33
RNA
<PUJ>
: DDBJ:AB044088
rotein, a novel member of the DEC subfamily of basic helix-loop-helix p
ppl1-23-pl2.1
ription factor
ghly conserved #status predicted
Orange #status predicted <ORA>
alanine and glycine-rich #status predicted

1.7%; Score 9; DB 2; Length 482;
arity 100.0%; Pred. No. 14;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 402

HLX1 - human
piens (man)
5 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
10; I54180
ayner, J.C.; Morris, C.M.
55, 1994
structure, promoter sequence, and revised translation of human homeobox
: A55180; MUID:95104845; PMID:7806220
10
ary; not compared with conceptual translation
DNA
<KEN>
: Purchio, A.F.; Murray, J.C.
164, 1993
localization of TGF2 and the human homeobox gene HLX1 to chromosome 1q
: I54180; MUID:93194183; PMID:8095486
30
ary; translated from GB/EMBL/DBJ
DNA
59 <RES>

A;Cross-references: GB:S56767; NID:g298601; PIDN:AD13883.1; PID:g426;
C;Genetics:
A;Gene: GDB:HLX1
A;Cross-references: GDB:128988; OMIM:142995
A;Map position: 1q41-1q42.1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:277-333/Domain: homeobox homology <HOX>

Query Match 1.7%; Score 9; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQQPPPP 229
|||||
DB 133 PQQQQPPPP 141

RESULT 49
S52830
HMS1 protein - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM9916.09; protein YMR070w
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct
C;Accession: S52830; S59820
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S52814
A;Accession: S52830
A;Molecule type: DNA
A;Residues: 1-490 <PEA>
A;Cross-references: EMBL:Z48952; NID:g763008; PIDN:CAA88795.1; PID:g7f
A;Experimental source: strain AB972
R;Madison, J.; Winston, F.
submitted to the EMBL Data Library, April 1995
A;Reference number: S59820
A;Accession: S59820
A;Molecule type: DNA
A;Residues: 1-490 <MAD>
A;Cross-references: EMBL:U25279; NID:g805129; PIDN:AAC49982.1; PID:g8f
C;Genetics:
A;Gene: SGD:MOT3; HMS1
A;Cross-references: MIPS:YMR070w; SGD:S0004674
A;Map position: 13R

Query Match 1.7%; Score 9; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAAATAP 159
|||||
DB 443 AAAAAATAP 451

RESULT 50
C85435
Hypothetical protein AT4G36860 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb
C;Accession: C85435
R;anonymous, The European Union Arabidopsis Genome Sequencing Consorti
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsi
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <STO>
A;Cross-references: GB:NC_001268; NID:g720635; PIDN:CAB80352.1; GSPDI
C;Genetics:
A;Gene: AT4G36860
A;Map position: 4
```

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1.7%; Score 9; DB 2; Length 542;
arity 100.0%; Pred. No. 16;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDE 341
|||||
DEDE 114

it (Saccharomyces cerevisiae)
protein YKR072c
#sequence_revision 03-May-1994 #text_change 21-Jul-2000
#S4982; S43078
F.M.
rotein Sequence Database, March 1994
S37897

IA
:POH>
EMBL:Z28297; NID:g486544; PID:g486545; MIPS:YKR072c
ce: strain S288C
se, R.; Arndt, K.T.
17, 1995
ision of S152, which contains an extremely acidic region, increases th
S54982; MUID:95220693; PMID:7705654

IA
:DIW>
EMBL:U01878; NID:g430983; PIDN:AAA80000.1; PID:g430984

SGD:S0001780; MIPS:YKR072c

1.7%; Score 9; DB 2; Length 562;
arity 100.0%; Pred. No. 16;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDE 338
|||||
DEDE 504

n KIAA0616 - human (fragment)
iens (man)
#sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
ase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
, 1998
i of the coding sequences of unidentified human genes. X. The complete
214142; MUID:98403880; PMID:9734811
ay; translated from GB/EMBL/DBJ
RNA
:ISH>
ce: EMBL:AB014516; NID:g3327045; PIDN:BA31591.1; PID:g3327046
ce: brain

1.7%; Score 9; DB 2; Length 634;
arity 100.0%; Pred. No. 18;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPPP 235
|||||
PQPPP 371

```

```

RESULT 53
T22002
hypothetical protein F39H11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-
C;Accession: T22002
R;White, S.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19500
A;Accession: T22002
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-650 <WIL>
A;Cross-references: EMBL:Z81079; PIDN:CAB03084.1; GSPDB:GN00019; CBSP:1
A;Experimental source: clone F39H11
C;Genetics:
A;Gene: CBSP:F39H11.4
A;Map position: 1
A;Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3

Query Match 1.7%; Score 9; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 128 PPTPAPPPP 136
|||||
DB 136 PPTPAPPPP 144

RESULT 54
E86358
F12K8.13 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov
C;Accession: E86358
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kh
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86358
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-683 <STO>
A;Cross-references: GB:AE005172; NID:g6587836; PIDN:AAF18525.1; GSPDB:
C;Genetics:
A;Map position: 1

Query Match 1.7%; Score 9; DB 2; Length 683;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 132 APPPPAPV 140
|||||
DB 116 APPPPAPV 124

RESULT 55
T40168
hypothetical protein SPBC30B4.02c - fission yeast (Schizosaccharomyces
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec
C;Accession: T40168
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft
submitted to the EMBL Data Library, August 1998

```


A: Gene: SGD:IFH1; RRP3
A: Cross-references: SGD:S0004213; MIPS:YLR223c
A: Map position: 12R

Query Match 1.7%; Score 9; DB 2; Length 1085;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEEEDDED 337
Db 133 EEEEEEDDED 141

RESULT 66
A33507
hypothetical protein DUC-1 - human
C: Species: Homo sapiens (man)
C: Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 05-Nov-1989
C: Accession: A33507
R: Fujii, H.; Shimada, T.
J. Biol. Chem. 264, 10057-10064, 1989
A: Title: Isolation and characterization of cDNA clones derived from the
A: Reference number: A33507; MUID: 89255490; PMID: 2722860
A: Accession: A33507
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-1137 <FUJ>
A: Cross-references: GB:J04810; NID:G181841; PIDN: AAB47281.1; PID: G181841

Query Match 1.7%; Score 9; DB 2; Length 1137;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAPP 128
Db 56 AAAAAAAPP 64

RESULT 67
EDBEIF
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Fur)
C: Species: suid herpesvirus 1
C: Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1990
C: Accession: S04713
R: Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A: Title: DNA nucleotide sequence analysis of the immediate-early gene
A: Reference number: S04713; MUID: 89315207; PMID: 2546124
A: Accession: S04713
A: Molecule type: DNA
A: Residues: 1-1460 <CHE>
C: Superfamily: herpesvirus immediate-early protein regulation
C: Keywords: DNA binding; early protein; transcription regulation

Query Match 1.7%; Score 9; DB 1; Length 1460;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 118 AAAAAA 126
Db 377 AAAAAA 385

RESULT 68
T30250
GTL protein - mouse
C: Species: Mus musculus (house mouse)
C: Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-1999
C: Accession: T30250
R: Imai, Y.; Suzuki, Y.; Matsui, T.; Tohyama, M.; Wanaka, A.; Takagi, J.
Brain Res. Mol. Brain Res. 31, 1-9, 1995
A: Title: Cloning of a retinoic acid-induced gene, GTL, in the embryonal
A: Reference number: Z20788; MUID: 96078271; PMID: 7476016

A: Gene: GB:ML6801; NID:G187460; PIDN:AAA59571.1; PID:G307166

A: GDB:120188; OMIM:264350

31-4q31
assigned erba-related proteins; erba transforming protein homology
binding; transcription regulation; zinc finger
erba transforming protein homology <ERBA>
zinc finger
zinc finger

1.7%; Score 9; DB 2; Length 984;
arity 100.0%; Pred. No. 26;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPP 229
QPPPP 697

in F25E4.40 - Arabidopsis thaliana
psis thaliana (mouse-ear cress)
9 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
2
rd, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft
rotein Sequence Database, June 1999
2
NA
<BEV>
: EMBL:AL050399; GSPDB:GNO0062; ATSP:F25E4.40
rce: cultivar Columbia; BAC clone F25E4
.40

76/3; 248/3; 371/3; 381/3; 457/3; 511/3; 585/3; 654/3; 723/3; 750/3; 8

1.7%; Score 9; DB 2; Length 987;
arity 100.0%; Pred. No. 27;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
AAAAA 899

st (Saccharomyces cerevisiae)
protein L8083.9; protein YLR223c; RRP3 protein
omyces cerevisiae
5 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
2; S51446; S47477
iaux, P.
1995
gene product interacts with a fork head protein in Saccharomyces cerev
S55352; MUID:95304839; PMID:7785326

acid sequence not shown
DNA
3: <CHE>
3: EMBL:Z29488; NID:G531491; PIDN:CAA82624.1; PID:G531492

EMBL Data Library, December 1994
sequence of S. cerevisiae cosmid 8083.
S51443
16
DNA
3: <HAL>
3: EMBL:U19027; NID:G609363; PID:G609372; MIPS:YLR223c

ry; translated from GB/EMBL/DBJ
NA
<INA>
EMBL:D29801; NID:g475015; PIDN:BAA06184.1; PID:g475016
was specifically localized in neurons but not in glial cells
ce: brain
ity 1.7%; Score 9; DB 2; Length 1840;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
QPQP 233
|||||
QPQP 126

3 - winter flounder
euronectes americanus (winter flounder)
#sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
n, Y.
cta 495, 388-392, 1977
of a peptide antifreeze and mechanism of adsorption to ice.
A03192; MUID:78060969; PMID:588591

otein
EV>
freeze protein
eze

ity 1.5%; Score 8; DB 1; Length 37;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
|||||
ATA 36

enase (EC 1.14.16.2) type 1 and 2 - orangutan (fragment)
oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
gmaeus (orangutan)
#sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
e, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
es. Commun. 195, 158-165, 1993
heterogeneity of tyrosine hydroxylase in humans.
PN0575; MUID:93371398; PMID:7689834

omic RNA
ICH>
GB:U14800
ce: lymphocytes of peripheral blood
yme catalyzes the first and rate-limiting step of catecholamine biosy
ylalanine 4-monooxygenase
lin; monooxygenase; oxidoreductase

ity 1.5%; Score 8; DB 2; Length 45;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAP 127
|||||
AAP 31

tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - common gibbon (f
N; Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine
C; Species: Hylobates lar (common gibbon, white-handed gibbon)
C; Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-
C; Accession: PN0592
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A; Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A; Reference number: PN0575; MUID:93371398; PMID:7689834
A; Accession: PN0592
A; Molecule type: Genomic RNA
A; Residues: 1-45 <ICH>
A; Cross-references: GB:U14794
A; Experimental source: lymph nodes
C; Comment: This enzyme catalyzes the first and rate-limiting step of c
C; Superfamily: phenylalanine 4-monooxygenase
C; Keywords: biopterin; monooxygenase; oxidoreductase

Query Match 1.5%; Score 8; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
Db 24 AAAAAAAP 31

RESULT 72

PN0593
tyrosine 3-monooxygenase (EC 1.14.16.2) type 1 and 2 - Japanese macaque
N; Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine
C; Species: Macaca fuscata (Japanese macaque)
C; Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-
C; Accession: PN0593
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A; Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A; Reference number: PN0575; MUID:93371398; PMID:7689834
A; Accession: PN0593
A; Molecule type: Genomic RNA
A; Residues: 1-45 <ICH>
A; Experimental source: kidney
C; Comment: This enzyme catalyzes the first and rate-limiting step of c
C; Superfamily: phenylalanine 4-monooxygenase
C; Keywords: biopterin; monooxygenase; oxidoreductase

Query Match 1.5%; Score 8; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
Db 24 AAAAAAAP 31

RESULT 73

FDLAW
antifreeze protein A precursor - winter flounder
C; Species: Pseudopleuronectes americanus (winter flounder)
C; Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 22-Jun
C; Accession: JS0704; A03194
R; Davies, P.L.
Gene 112, 163-170, 1992
A; Title: Conservation of antifreeze protein-encoding genes in tandem r
A; Reference number: JH0627; MUID:92209995; PMID:1555765
A; Accession: JS0704
A; Molecule type: DNA
A; Residues: 1-82 <DAL>
R; Davies, P.L.; Roach, A.H.; Hew, C.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 335-339, 1982
A; Title: DNA sequence coding for an antifreeze protein precursor from
A; Reference number: A03194; MUID:82197490; PMID:6952188

RNA
DA2>
ce: clones 4-2b and 2A-7c
s translated the codon AGC for residue 24 as Arg

ifreeze protein
eeze; plasma; tandem repeat
nal sequence #status predicted <SIG>
opeptide #status predicted <PRO>
ntifreeze protein A #status predicted <MAT>

1.5%; Score 8; DB 1; Length 82;
arity 100.0%; Pred. No. 23;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATA 158
|||||
AAATA 80

A - winter flounder
neuronectes americanus (winter flounder)
#sequence_revision 30-Sep-1989 #text_change 24-Oct-2000
6; JH0627
ies, P.L.; Kao, M.H.; Fletcher, G.L.
29-35, 1988
al amplification of antifreeze protein genes in the Pleuronectinae.
6
S02326; MUID:88259236; PMID:3133486
DNA
SCO>
: EMBL:X07506; NID:g64211; PIDN:CAA30389.1; PID:g64212

1992
ion of antifreeze protein-encoding genes in tandem repeats.
: JH0627; MUID:92209995; PMID:1555765
7
DNA
DAV>
: GB:M62415

ifreeze protein
eeze

1.5%; Score 8; DB 2; Length 82;
arity 100.0%; Pred. No. 23;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATA 158
|||||
AAATA 80

1 (clone 4-2c) - winter flounder
neuronectes americanus (winter flounder)
2 #sequence_revision 17-Aug-1992 #text_change 24-Oct-2000
06

1992
ion of antifreeze protein-encoding genes in tandem repeats.
r: JH0627; MUID:92209995; PMID:1555765
06
DNA
<DAV>

3: GB:M62417; NID:g213594; PIDN:AAA49472.1; PID:g213595
rs translated the codon AGC for residue 24 as Arg

C;Genetics:
A;Introns: 19/2
C;Superfamily: antifreeze protein
C;Keywords: antifreeze

Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAATA 158
|||||
Db 73 AAAAATA 80

RESULT 76
A05161
antifreeze protein B precursor - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 24-Oct-1987
C;Accession: A05161
R;Davies, P.L.; Hough, C.; Scott, G.K.; Ng, N.; White, B.N.; Hew, C.L.
J. Biol. Chem. 259, 9241-9247, 1984
A;Reference number: A05161; MUID:84264559; PMID:6086629
A;Accession: A05161
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:L00138; GB:J00929; NID:g343126; PIDN:AAAB59964.1
C;Genetics:
A;Introns: 19/2
C;Superfamily: antifreeze protein
C;Keywords: antifreeze

Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAATA 158
|||||
Db 73 AAAAATA 80

RESULT 77
JS0705
antifreeze protein (clones 1A-1a and 3-3a) - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Oct-1992
C;Accession: JS0705
R;Davies, P.L.
Gene 112, 163-170, 1992
A;Title: Conservation of antifreeze protein-encoding genes in tandem
A;Reference number: JH0627; MUID:92209995; PMID:1555765
A;Accession: JS0705
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M62413; NID:g213586; PIDN:AAA49468.1; PID:g213586
C;Genetics:
A;Introns: 19/2
C;Superfamily: antifreeze protein
C;Keywords: antifreeze

Query Match 1.5%; Score 8; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAATA 158
|||||
Db 73 AAAAATA 80

RESULT 78
IS1125
antifreeze protein - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)

```

1 #sequence_revision 13-Sep-1996 #text_change 24-Oct-2000
2
3 t, G.; Davies, P.; Wang, N.; Joshi, S.; Hew, C.
4 43, 35-38, 1984
5 of an antifreeze protein precursor.
6 : IS1125; MUID:84285392; PMID:6547905
7
8 ary; translated from GB/EMBL/DBJ
9 RNA
10 PIC>
11 : GB:M28337; NID:g2l3581; PIDN:AAA49466.1; PID:g2l3582
12
13 ifreeze protein
14 seze
15
16 1.5%; Score 8; DB 2; Length 82;
17 arity 100.0%; Pred.No.23;
18 nservative 0; Mismatches 0; Indels 0; Gaps 0;
19
20 AATA 158
21 ||||
22 AATA 80
23
24 4 precursor - winter flounder
25 leuronectes americanus (winter flounder)
26 l #sequence_revision 01-Sep-1981 #text_change 25-Apr-1997
27 }
28 J.K.
29 Sci. U.S.A. 78, 2825-2829, 1981
30 cloning and characterization of winter flounder antifreeze cdna.
31 : A03193; MUID:81247379; PMID:6265915
32 }
33 RNA
34 JIN>
35 ifreeze protein
36 seze
37 al sequence #status predicted <SIG>
38 ntifreeze protein 4 #status predicted <MAT>
39
40 1.5%; Score 8; DB 1; Length 85;
41 arity 100.0%; Pred.No.24;
42 nservative 0; Mismatches 0; Indels 0; Gaps 0;
43
44 AATA 158
45 ||||
46 AATA 35
47
48 IIA7 precursor - winter flounder
49 leuronectes americanus (winter flounder)
50 ; #sequence_revision 05-Oct-1988 #text_change 24-Oct-2000
51 ?; SI2604
52 Y.; Price, J.; De Vries, A.L.; Powers, D.; Huang, R.C.C.
53 14960-14965, 1984
54 under antifreeze proteins: a multigene family.
55 : A22592; MUID:85054933; PMID:6548752
56 }
57 RNA
58 300>
59 : GB:M10148; NID:g2l3579; PIDN:AAA49465.1; PID:g2l3580
60 Y.; Davies, P.L.
61 18, 5303, 1990
62 sequence of a variant antifreeze protein gene.
63 : SI2604; MUID:90384854; PMID:2402466
64 }
65 RNA
66 65-91 <GAU>

```

A;Cross-references: EMBL:X53718; NID:G64213; PIDN:CAA37754.1; PID:G9380

C:Genetics:
A:Introns: 19/2
C:Superfamily: antifreeze protein
C:Keywords: antifreeze; tandem repeat
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-91/Product: antifreeze protein IIA7 #status predicted <MAT>

Query Match 1.5%; Score 8; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAAATA 158
| | | | | | | |
DB 45 AAAAAATA 52

RESULT 81

S58341
cystatin - Trypanosoma cruzi
C:Species: Trypanosoma cruzi
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Sep
C:Accession: S58341
R:Stock, R.P.; Moro, A.; Ruiz-Cabello, F.; Gonzalez, A.
submitted to the EMBL Data Library, January 1995
A:Description: Cloning and sequence of a cystatin-like gene from Trypa
A:Reference number: S58341
A:Accession: S58341
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A;Cross-references: EMBL:Z47798; NID:G940939; PID:G940940

Query Match 1.5%; Score 8; DB 2; Length 91;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 10 PETAAAT 17
| | | | | | | |
DB 27 PETAAAT 34

RESULT 82

S02376
antifreeze protein precursor - yellowtail flounder
C:Species: Limanda ferruginea (yellowtail flounder)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 24-Oct
C:Accession: S02376
R:Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L.
Eur. J. Biochem. 168, 629-633, 1987
A:Title: Structural variations in the alanine-rich antifreeze proteins
A:Reference number: S02376; MUID:88029483; PMID:3665937
A:Accession: S02376
A:Molecule type: mRNA
A:Residues: 1-97 <SC>
A;Cross-references: EMBL:X06356; NID:G64041; PIDN:CAA29655.1; PID:G640
A>Note: part of this sequence, including the amino end of the mature p
C:Superfamily: antifreeze protein
C:Keywords: antifreeze
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-48/Domain: propeptide #status predicted <PRO>
F:49-96/Product: antifreeze protein #status predicted <MAT>

Query Match 1.5%; Score 8; DB 2; Length 97;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 119 PAAAAAAA 126
| | | | | | | |
DB 39 PAAAAAAA 46

RESULT 83

A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69436
A:Status: preliminary; nucleic acid sequence not shown; translation n
A:Molecule type: DNA
A:Residues: 1-106 <KLE>
A:Cross-references: GB:AE000999; GB:AE000782; NID:g2689322; PIDN:AA8
C:Superfamily: rat acidic ribosomal protein P1

Query Match 1.5%; Score 8; DB 2; Length 106;
Best Local Similarity 100.0%; Pred.No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 118 APAAAAAA 125
|||||
Db 66 APAAAAAA 73

RESULT 86
S20693
hypothetical protein, 12.3K (early region E3) - human adenovirus 41
C:Species: Mastadenovirus h41 (human adenovirus 41)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Au
C:Accession: S20693
R:Pienaziek, N.J.; Slemenda, S.B.; Pienazek, D.; Velarde Jr., J.; Luf
submitted to the EMBL Data Library, March 1990
A:Description: Characterisation of the early region E3 of the human e
A:Reference number: S20688
A:Accession: S20693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <PIE>
A:Cross-references: EMBL:X52198; NID:g58660; PIDN:CAA36448.1; PID:g58
C:Superfamily: adenovirus early E3B 14.5K protein

Query Match 1.5%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 133 PPPPPAPV 140
|||||
Db 83 PPPPPAPV 90

RESULT 87
T38936
non-histone chromosomal protein high mobility group - fission yeast ((
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Ja
C:Accession: T38936
R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z21818
A:Accession: T38936
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-108 <BAD>
A:Cross-references: EMBL:Z94864; PIDN:CA08172.1; GSPDB:GN000066; SPDB:
A:Experimental source: strain 972h-; cosmid c57A10
C:Genetics:
A:Gene: SPDB:SPAC57A10.09c
A:Map position: 1
A:Introns: 44/1; 63/3
C:Superfamily: unassigned HMG box proteins; HMG box homology

Query Match 1.5%; Score 8; DB 2; Length 108;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 118 APAAAAAA 125
|||||
Db 98 APAAAAAA 105

```

RES 1
REF 1
A: ribosomal protein P1 - fruit fly (Drosophila melanogaster)
A: ribosomal protein A; ribosomal protein DL12EII; ribosomal protein rp2
A: melanogaster
C: #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
Q 3
R: 15, 10064, 1987
R: reduced amino acid sequence of Drosophila rp21C, another 'A'-type ribo
R: S00659; MUID:88096510; PMID:3122177
RNA
<WT>
: EMBL:Y00504; NID:98475; PIDN:CAA68557.1; PID:g8476
2) 21C
: FlyBase:FBgn0002593
:
: acidic ribosomal protein P1
: protein; protein biosynthesis; ribosome
Q 1.5%; Score 8; DB 1; Length 112;
R 100.0%; Pred. No. 30;
M conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y AAA 125
Y |||||
Y AAA 83
:
: stein - common sunflower
: us annuus (common sunflower)
: #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
: J.L.; Pillay, D.T.N.; Steinmetz, A.
: 9, 238-244, 1991
: ntron separates the signal peptide coding sequence of an anther-speci
: S17718; MUID:92017657; PMID:1921973
:
: ry
: A
: DOM>
:
: 1.5%; Score 8; DB 2; Length 121;
: rity 100.0%; Pred. No. 32;
: nservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: ppp 137
: |||||
: ppp 89
:
: tein SP2 precursor - common sunflower
: proline-rich protein
: us annuus (common sunflower)
: #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
: S13373
: J.L.; Herdenberger, F.; Pillay, D.T.N.; Steinmetz, A.
: , 643-646, 1990
: sequence of two anther-specific cDNAs from sunflower (Helianthus ann
: S12245; MUID:91338702; PMID:2102380
:
: NA
: DOM>
: EMBL:X53374; NID:g18814; PIDN:CAA37454.1; PID:g18815
: o, C.; Saint-Guilly, A.; Weil, J.H.; Kuntz, M.
: , 271-281, 1991
: cific, developmentally regulated expression of genes encoding a new d

```

```

A:Reference number: S13373; MUID:91370869; PMID:1716499
A:Accession: S13373
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-121 <EVR>
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-121/Product: anther-specific protein SP2 #status predicted <MAT>
Query Match 1.5%; Score 8; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 130 TPAPPPPP 137
DB 82 TPAPPPPP 89
RESULT 91
T03603
anther specific protein - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul
C:Accession: T03603
R:Tsuchiya, T.; Toriyama, K.; Ejiri, S.; Hinata, K.
Plant Mol. Biol. 26, 1737-1746, 1994
A:Title: Molecular characterization of rice genes specifically express
A:Reference number: Z14972; MUID:95161699; PMID:7858214
A:Accession: T03603
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-128 <TSU>
A:Cross-references: EMBL:D21160; NID:g736717; PIDN:BAA04696.1; PID:g16
A:Experimental source: subsp. Japonica
C:Genetics:
A:Introns: 110/3; 125/3
A:Note: g8B
Query Match 1.5%; Score 8; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 18 TAAASSS 25
DB 7 TAAASSS 14
RESULT 92
SEPG
secretin precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-
C:Accession: B35094; A01544; A36052
R:Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 2299-2303, 1990
A:Title: Secretin: structure of the precursor and tissue distribution
A:Reference number: A35094; MUID:90192795; PMID:2315322
A:Accession: B35094
A:Molecule type: mRNA
A:Residues: 1-131 <KOP>
A:Cross-references: GB:M31496; NID:gl64670; PIDN:AAA31121.1; PID:gl6467
R:Mutt, V.; Jorpes, J.E.; Magnusson, S.
Eur. J. Biochem. 15, 513-519, 1970
A:Title: Structure of porcine secretin. The amino acid sequence.
A:Reference number: A91147; MUID:70282334; PMID:5465996
A:Accession: A01544
A:Molecule type: protein
A:Residues: 30-56 <MUT>
A:Note: tryptic peptides were sequenced
R:Gafvelin, G.; Joernvall, H.; Mutt, V.
Proc. Natl. Acad. Sci. U.S.A. 87, 6781-6785, 1990
A:Title: Processing of prosecretin: isolation of a secretin precursor f
A:Reference number: A36052; MUID:90370867; PMID:2395872
A:Accession: A36052

```

A: protein
 A: R'92-131 <GAP>
 A: Indetti, M.A.; Levine, S.D.; Narayanan, V.L.; Saltza, M.V.; Sheehan, J.
 A: 757-1758, 1966
 A: of a heptacosapeptide amide with the hormonal activity of secretin.
 A: A90916
 A: tion
 A: confirmed the proposed structure of the natural hormone
 A: agon
 A: ed carboxyl end; duodenal mucosa; duplication; hormone; secretagogue
 A: mal sequence #status predicted <SIG>
 A: secretin #status experimental <MAT>
 A: : amidated carboxyl end (Val) (amide in mature form from following gly
 A: 1.5%; Score 8; DB 1; Length 131;
 A: arity 100.0%; Pred. No. 34;
 A: onservative 0; Mismatches 0; Indels 0; Gaps 0;
 A: RAPR 116
 A: |||||
 A: RAPR 29
 A: in CC3490 [imported] - Caulobacter crescentus
 A: cter crescentus
 A: 1 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 A: eldbylum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 A: eBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 A: M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 A: Sci. U.S.A. 98, 4136-4141, 2001
 A: Genome Sequence of Caulobacter crescentus.
 A: : A87249; MUID:21173698; PMID:11259647
 A: 1
 A: lary
 A: NA
 A: <STO>
 A: : GB:AE005673; NID:g13425216; PIDN:AAK25452.1; GSPDB:GN00148
 A: 1.5%; Score 8; DB 2; Length 133;
 A: arity 100.0%; Pred. No. 34;
 A: onservative 0; Mismatches 0; Indels 0; Gaps 0;
 A: PAPV 140
 A: |||||
 A: PAPV 75
 A: ein S16P [imported] - Brucella melitensis (strain 16M)
 A: 2 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
 A: 0
 A: : Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 A: sman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
 A: Sci. U.S.A. 99, 443-448, 2002
 A: e sequence of the facultative intracellular pathogen Brucella melitens
 A: : AB3252; PMID:11756688
 A: 0
 A: lary
 A: NA
 A: <KUR>
 A: : GB:AE008917; PIDN:AAL51409.1; PID:g17982114; GSPDB:GN00190
 A: rce: strain 16M

C:Superfamily: Escherichia coli ribosomal protein S16
 Query Match 1.5%; Score 8; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAAP 127
 Db 120 AAAAAAAP 127
 |||||
 RESULT 95
 AS6062
 Alu RNA-binding protein - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 07-May
 C:Accession: AS6062
 R:Chang, D.Y.; Nelson, B.; Bilyeu, T.; Hsu, K.; Darlington, G.J.; Marz
 Mol. Cell. Biol. 14, 3949-3959, 1994
 A:Title: A human Alu RNA-binding protein whose expression is associat
 A:Reference number: AS6062; MUID:94254852; PMID:8196634
 A:Accession: AS6062
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <CH>
 A:Cross-references: GB:U07857; NID:g469048; PID:g468209
 C:Keywords: RNA binding
 Query Match 1.5%; Score 8; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAAP 127
 Db 110 AAAAAAAP 117
 |||||
 RESULT 96
 S34196
 signal recognition particle 14K chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar
 C:Accession: S34196
 R:Leifers, H.
 A:Submitted to the EMBL Data Library, June 1993
 A:Description: The human signal recognition particle subunit (SRP14) n
 A:Reference number: S34196
 A:Accession: S34196
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-136 <LEF>
 A:Cross-references: EMBL:X73459; NID:g313660; PIDN:CAA51838.1; PID:g31
 Query Match 1.5%; Score 8; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 120 AAAAAAAP 127
 Db 110 AAAAAAAP 117
 |||||
 RESULT 97
 SXAD97
 hexon-associated protein - human adenovirus 7
 N:Alternate names: polypeptide IX
 C:Species: Mastadenovirus h7 (human adenovirus 7)
 C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 05-Jun
 C:Accession: A03854
 R:Dijkema, R.; Maat, J.; Dekker, B.M.M.; van Ormondt, H.; Boyer, H.W.
 Gene 13, 375-385, 1981
 A:Title: The gene for polypeptide IX of human adenovirus type 7.
 A:Reference number: A91480; MUID:81261948; PMID:6266923

```

A: ribonuclease Sa (EC 3.1.27.-) precursor - Streptomyces aureofaciens (s
N: Alternate names: guanyloribonuclease; ribonuclease Sa3
C: Species: Streptomyces aureofaciens
C: Date: 30-Sep-1993 #sequence_revision 02-Dec-1994 #text_change 06-Dec
C: Accession: JCI1287
R: Homeroova, D.; Hollaenderova, Z.; Kormanec, J.; Sevcik, J.
Gene 119, 147-148, 1992
A: Title: Cloning and sequencing of the gene encoding a ribonuclease fr
A: Reference number: JCI1287; MUID: 93012968; PMID: 1398084
A: Accession: JCI1287
A: Molecule type: DNA
A: Residues: 1-141 <ROM>
A: Cross-references: GB:M82920
A: Experimental source: strain CCM3239
C: Superfamily: ribonuclease Sa
C: Keywords: extracellular protein; hydrolase
F: 1-28/Domain: (or 1-34) signal sequence #status predicted <SIG>
F: 29-141/Product: (or 35-141) ribonuclease #status predicted <MAT>

Query Match 1.5%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; G

QY 139 PVAAAAPA 146
Db 24 PVAAAAPA 31

RESULT 101
T06485
barwin homolog wheatwin1 precursor - wheat
N: Alternate names: barwin homolog PR4a
C: Species: Triticum aestivum (common wheat)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C: Accession: T06485
R: Caruso, C.
submitted to the EMBL Data Library, May 1998
A: Reference number: Z15711
A: Accession: T06485
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-146 <CAR>
A: Cross-references: EMBL:AJ006098; PIDN:CAA06856.1
A: Experimental source: cv. S. Pastore, endosperm
C: Genetics:
A: Gene: PR4a
C: Superfamily: pathogenesis-related protein 4a; barwin homolog
F: 1-21/Domain: signal sequence #status predicted <SIG>
F: 22-146/Product: barwin homolog wheatwin1 #status predicted <MAT>
F: 22-146/Domain: barwin homolog <BAR>

Query Match 1.5%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; G

QY 151 AAAAAATA 158
Db 14 AAAAAATA 21

RESULT 102
T06486
barwin homolog wheatwin2 precursor - wheat
N: Alternate names: barwin homolog PR4b
C: Species: Triticum aestivum (common wheat)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C: Accession: T06486
R: Caruso, C.
submitted to the EMBL Data Library, May 1998
A: Reference number: Z15711
A: Accession: T06486
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA

```

```

A: ribonuclease Sa (EC 3.1.27.-) precursor - Streptomyces aureofaciens (s
N: Alternate names: guanyloribonuclease; ribonuclease Sa3
C: Species: Streptomyces aureofaciens
C: Date: 30-Sep-1993 #sequence_revision 02-Dec-1994 #text_change 06-Dec
C: Accession: JCI1287
R: Homeroova, D.; Hollaenderova, Z.; Kormanec, J.; Sevcik, J.
Gene 119, 147-148, 1992
A: Title: Cloning and sequencing of the gene encoding a ribonuclease fr
A: Reference number: JCI1287; MUID: 93012968; PMID: 1398084
A: Accession: JCI1287
A: Molecule type: DNA
A: Residues: 1-141 <ROM>
A: Cross-references: GB:M82920
A: Experimental source: strain CCM3239
C: Superfamily: ribonuclease Sa
C: Keywords: extracellular protein; hydrolase
F: 1-28/Domain: (or 1-34) signal sequence #status predicted <SIG>
F: 29-141/Product: (or 35-141) ribonuclease #status predicted <MAT>

Query Match 1.5%; Score 8; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; G

QY 139 PVAAAAPA 146
Db 24 PVAAAAPA 31

RESULT 101
T06485
barwin homolog wheatwin1 precursor - wheat
N: Alternate names: barwin homolog PR4a
C: Species: Triticum aestivum (common wheat)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C: Accession: T06485
R: Caruso, C.
submitted to the EMBL Data Library, May 1998
A: Reference number: Z15711
A: Accession: T06485
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-146 <CAR>
A: Cross-references: EMBL:AJ006098; PIDN:CAA06856.1
A: Experimental source: cv. S. Pastore, endosperm
C: Genetics:
A: Gene: PR4a
C: Superfamily: pathogenesis-related protein 4a; barwin homolog
F: 1-21/Domain: signal sequence #status predicted <SIG>
F: 22-146/Product: barwin homolog wheatwin1 #status predicted <MAT>
F: 22-146/Domain: barwin homolog <BAR>

Query Match 1.5%; Score 8; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; G

QY 151 AAAAAATA 158
Db 14 AAAAAATA 21

RESULT 102
T06486
barwin homolog wheatwin2 precursor - wheat
N: Alternate names: barwin homolog PR4b
C: Species: Triticum aestivum (common wheat)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun
C: Accession: T06486
R: Caruso, C.
submitted to the EMBL Data Library, May 1998
A: Reference number: Z15711
A: Accession: T06486
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA

```

```

<CAR>
: EMBL:AJ006099; PIDN:CAA06857.1
: cv: S. Pastore, endosperm

: hogenesis-related protein 4A; barwin homology
: inal sequence #status predicted <SIG>
: barwin homology wheatwin2 #status predicted <MAT>
: barwin homology <BAR>

      1.5%; Score 8; DB 2; Length 148;
      arity 100.0%; Pred. No. 38;
      onservative 0; Mismatches 0; Indels 0; Gaps 0;

AATA 158
|||||
AATA 23

P protein HMG - fava bean
aba (fava bean)
4 #sequence_revision 03-Aug-1995 #text_change 21-May-1999
6
: ohlfarth, T.; Baumelein, H.; Feix, G.
: 3, 619-625, 1993
: ve analysis of chromosomal HMG proteins from monocotyledons and dicoty
: : S39556; MUID:94033341; PMID:8219095
6
ary
RNA
<GRA>
assigned HMG box proteins; HMG box homology
nding; nucleus
MG box homology <HMG1>

      1.5%; Score 8; DB 2; Length 149;
      arity 100.0%; Pred. No. 38;
      onservative 0; Mismatches 0; Indels 0; Gaps 0;

DEED 342
|||||
DEED 142

S16 [imported] - Caulobacter crescentus
cter crescentus
1 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
2
eldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
eBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Sci. U.S.A. 98, 4136-4141, 2001
Genome Sequence of Caulobacter crescentus.
: A87249; MUID:21173698; PMID:11259647
2
ary
NA
<STO>
: GB:AE005673; NID:g13425408; PIDN:AAK25614.1; GSPDB:GN00148

      1.5%; Score 8; DB 2; Length 165;
      arity 100.0%; Pred. No. 41;
      onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAP 127
|||||
AAP 142

```

```

RESULT 105
S35568
sex-determining protein Sry - multimammate rat (Mastomys hildebrandtii);
C:Species: Mastomys hildebrandtii
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep
C:Accession: S35568
R:Tucker, P.K.; Lundrigan, B.L.
Nature 364, 715-717, 1993
A:Title: Rapid evolution of the sex determining locus in Old World mic
A:Reference number: S35565; MUID:93361118; PMID:8355784
A:Accession: S35568
A:Molecule type: DNA
A:Residues: 1-172 <TUC>
A:Cross-references: GB:L29542; NID:g496161; PIDN:AAA40587.1; PID:g4961
C:Genetics:
A:Gene: Sry
A:Map position: Y
C:Superfamily: unassigned HMG box proteins; HMG box homology
C:Keywords: DNA binding
F:2-77/Domain: HMG box homology <HMG1>

      Query Match      1.5%; Score 8; DB 2; Length 172;
      Best Local Similarity 100.0%; Pred. No. 43;
      Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 120 AAAAAAAAAAP 127
Db 151 AAAAAAAAAAP 158

RESULT 106
I48752
gene RXRbeta protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct
C:Accession: I48752
R:Nagata, T.; Kanno, Y.; Ozato, K.; Taketo, M.
Gene 142, 183-189, 1994
A:Title: The mouse Rxb gene encoding RXR beta: genomic organization a
A:Reference number: I48752; MUID:94252565; PMID:8194750
A:Accession: I48752
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <RES>
A:Cross-references: EMBL:X72017; NID:g510152; PIDN:CAA50896.1; PID:g51
C:Genetics:
A:Gene: RXRbeta
A:Introns: 76/1; 137/2
C:Superfamily: mouse gene RXRbeta protein

      Query Match      1.5%; Score 8; DB 2; Length 176;
      Best Local Similarity 100.0%; Pred. No. 44;
      Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 119 PAAAAAAA 126
Db 45 PAAAAAAA 52

RESULT 107
AB3269
outer membrane lipoprotein [imported] - Brucella melitensis (strain 16
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb
C:Accession: AB3269
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.;
; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Cal
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3269

```

```

ary
NA
<KUR>
: GB:AE008917; PIDN:AA151317.1; PID:g17982013; GSPDB:GN00190
rce: strain 16M

1.5%; Score 8; DB 2; Length 177;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PAPV 140
|||||
PAPV 41

tein, 57K - mouse
culus (house mouse)
5 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
1
Patrick, D.
MEL Data Library, September 1990
accural analysis of mouse placental 57-KD Calcium-binding protein.
: S26481
1
ary
RNA
<TUA>
: EMBL:X56603; NID:g53597; PIDN:CAA39940.1; PID:g53598
n binding

1.5%; Score 8; DB 2; Length 178;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

DEED 342
|||||
DEED 24

in knirps - house fly (fragment)
mestica (house fly)
: #sequence_revision 06-Jan-1995 #text_change 07-May-1999
), D.
: 9-430, 1991
on gene expression in the housefly Musca domestica.
A61600; MUID:92146255; PMID:1685986
),
ary; not compared with conceptual translation
IA
: SOM>

1.5%; Score 8; DB 2; Length 180;
arity 100.0%; Pred.No. 44;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 126
|||||
AAA 173

HACPI88 - American lobster (fragment)
americanus (American lobster)
: #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997

```

```

C;Accession: S77928
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the Ameri
A;Reference number: S77925
A;Accession: S77928
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-184 <NOU>
C;Keywords: blocked amino end; pyroglutamic acid
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimer

Query Match 1.5%; Score 8; DB 2; Length 184;
Best Local Similarity 100.0%; Pred.No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 120 AAAAAAAP 127
|||||
Db 175 AAAAAAAP 182

RESULT 111
JQ2247
Photosystem I chain D precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 28-May
C;Accession: JQ2247
R;Kjarulff, S.; Okkels, J.S.
Plant Physiol. 101, 335-336, 1993
A;Title: Cloning and sequencing of a full-length cDNA clone encoding t
A;Reference number: JQ2247; MUID:94105296; PMID:8278501
A;Accession: JQ2247
A;Molecule type: mRNA
A;Residues: 1-205 <KTA>
A;Cross-references: GB:M98254; NID:g167084; PIDN:AAA18567.1; PID:g1670
C;Superfamily: photosystem I chain II
C;Keywords: chloroplast; photosystem I
P;1-43/Domain: transit peptide (chloroplast) #status predicted <TNP>
P;44-205/Product: photosystem I chain D #status predicted <MAT>

Query Match 1.5%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 182 PAPAAPPA 189
|||||
Db 50 PAPAAPPA 57

RESULT 112
S41002
hypothetical protein T05G5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep
C;Accession: S41002
R;Thomas, K.
submitted to the EMBL Data Library, October 1993
A;Reference number: S41001
A;Accession: S41002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <THO>
A;Cross-references: EMBL:Z27079; NID:g414641; PID:g414643
C;Genetics:
A;Introns: 21/3

Query Match 1.5%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 132 APPPPAP 139
|||||
Db 176 APPPPAP 183

```

RE ein F2K13_270 - Arabidopsis thaliana
 DE opsis thaliana (mouse-ear cress)
 CY 00 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C1 67
 C2 ura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
 C3 Protein Sequence Database, August 2000
 C4 r: Z25394
 C5 67
 C6 nary
 C7 DNA
 C8 <SAT>
 C9 s: EMBL:AL391141
 C0 irce: cultivar Columbia; BAC clone F2K13
 C1 141/3
 C2
 C3 1.5%; Score 8; DB 2; Length 207;
 C4 larity 100.0%; Pred. No. 50;
 C5 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C6
 C7 EDDDE 336
 C8 |||||
 C9 EDDDE 38
 C0
 C1 in T29A15.30 - Arabidopsis thaliana
 C2 opsis thaliana (mouse-ear cress)
 C3 19 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
 C4 19
 C5 der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; H
 C6 Protein Sequence Database, March 1999
 C7 s: Z15455
 C8 NA
 C9 <BEV>
 C0 s: EMBL:AL035602
 C1 irce: cultivar Columbia; BAC clone T29A15
 C2
 C3 bidopsis thaliana hypothetical protein T29A15.30
 C4
 C5 1.5%; Score 8; DB 2; Length 208;
 C6 arity 100.0%; Pred. No. 50;
 C7 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C8
 C9 SSSA 26
 C0 |||||
 C1 SSSA 45
 C2
 C3 tein - dog
 C4 HSP27 protein
 C5 upus familiaris (dog)
 C6 5 #sequence_revision 08-Feb-1996 #text_change 13-Aug-1999
 C7 4
 C8 rthoffer, W.T.; Hickey, E.; Weber, L.A.
 C9 1995
 C0 nd sequencing of a cDNA encoding the canine HSP27 protein.
 C1 : J04244; MUID:93394379; PMID:7665102
 C2 4
 C3 RNA

A;Residues: 1-209 <IAR>
 A;Cross-references: GB:U19368; NID:G624684; PIDN:AAA87172.1; PID:G624
 A;Experimental source: smooth muscle
 C;Comment: This protein is synthesized in a wide range of tissues in
 entiation, modulation of actin microfilament dynamics and smooth musc
 C;Superfamily: alpha-crystallin
 C;Keywords: heat shock; phosphoprotein; stress-induced protein
 F;66-75/Region: alanine-rich
 F;15,82,86/Binding site: phosphate (Ser) (covalent) (by MAP kinase II
 Query Match 1.5%; Score 8; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 119 PAAAAAAA 126
 DB 66 PAAAAAAA 73
 RESULT 116
 A86455
 hypothetical protein F9L11.19 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-De
 C;Accession: A86455
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.;
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creas
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; K
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; M
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidops
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86455
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-209 <STO>
 A;Cross-references: GB:AB005172; NID:G6910577; PIDN:AAF31282.1; GSPDB
 C;Genetics:
 A;Map position: 1
 Query Match 1.5%; Score 8; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 330 EEEDEDED 337
 DB 37 EEEDEDED 44
 RESULT 117
 B89716
 protein F45B8.3 [imported] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov
 C;Accession: B89716
 R;anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode C. elegans: a platform for in
 A;Reference number: A75000; MUID:9069613; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac
 A;Note: published errata appeared in Science 283, 35, 1999; Science 28
 A;Accession: B89716
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <STO>
 A;Cross-references: GB:chr_X; PIDN:CAB05726.1; PID:G3877144; GSPDB:GNO
 C;Genetics:
 A;Gene: F45B8.3
 A;Map position: X

1.5%; Score 8; DB 2; Length 211;
arity 100.0%; Pred. No. 51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PAAP 187
PAAP 119
a PFL - rice
ativa (rice)
9 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
l
; Ichida, A.; Quail, P.H.
301, 1994
-T hook containing DNA binding protein from rice that interacts with a
; Z15142; MUID:94198599; PMID:8148649
l
ary; translated from GB/EMBL/DBDJ
RNA
>NIE>
: EMBL:L24390; NID:g453691; PIDN:AAA33914.1; PID:g453692
ce: cv. Nipponbare, shoot
one H1
iding
1.5%; Score 8; DB 2; Length 213;
arity 100.0%; Pred. No. 51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAP 127
AAP 117
nucleoprotein-associated protein Sm11, cardiac - rat (fragment)
orvegicus (Norway rat)
#sequence_revision 22-Jun-1990 #text_change 26-May-2000
S.; Russo, A.F.; Simmons, D.M.; Rosenfeld, M.G.
ci. U.S.A. 86, 9778-9782, 1989
of cDNA clones encoding small nuclear ribonucleoparticle-associated H
A34503; MUID:90093348; PMID:2532363
ry
NA
LIS>
GB:M29295; NID:g207009; PIDN:AAA42159.1; PID:g207010
ine-rich protein
muscle; heart
1.5%; Score 8; DB 2; Length 214;
arity 100.0%; Pred. No. 51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
ATA 158
ATA 142
- rainbow trout
chus mykiss (rainbow trout)
#sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
R;Stros, M.; Retief, J.D.; Dixon, G.H.
Gene 158, 181-187, 1995
A:Title: cDNA sequence and structure of a trout HMG-2 gene. Evidence f
A:Reference number: 151067; MUID:95331614; PMID:7607539
A:Accession: 151067
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-215 <STR>
A:Cross-references: GB:L32954; NID:g609552; PIDN:AAA74556.1; PID:g6095
C:Genetics;
A:Gene: HMG-T2
A:Introns: 50/3; 101/2; 159/3
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;94-168/Domain: HMG box homology <HMG2>
Query Match 1.5%; Score 8; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 330 EEEEDDED 337
Db 206 EEEEDDED 213
RESULT 121
RDNCUF
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur prot
C:Species: Neurospora crassa
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 03-Jun
C:Accession: A24612
R;Harnisch, U.; Weiss, H.; Seibald, W.
Eur. J. Biochem. 149, 95-99, 1985
A:Title: The primary structure of the iron-sulfur subunit of ubiquinol
A:Reference number: A24612; MUID:85203899; PMID:2986972
A:Accession: A24612
A:Molecule type: DNA
A:Residues: 1-231 <HAR>
A:Cross-references: GB:X02472; NID:g3001; PIDN:CAA26308.1; PID:g3002
C:Genetics;
A:Introns: 92/1; 121/3; 172/1
C:Superfamily: ubiquinol-cytochrome-c reductase iron-sulfur protein; R;
C:Keywords: 2Fe-2S; electron transfer; membrane-associated complex; me
F;164-211/Domain: Rieske [2Fe-2S] homology <RSK>
F;174-176,193,196/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (c
F;179-195/Disulfide bonds: #status predicted
F;196/Active site: His #status predicted
Query Match 1.5%; Score 8; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 141 AAAAPARA 148
Db 14 AAAAPARA 21
RESULT 122
I53659
Sm-B protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-
C:Accession: I53659
R;Griffith, A.J.; Schmauss, C.; Craft, J.E.
Gene 114, 195-201, 1992
A:Title: The murine gene encoding the highly conserved Sm B protein cor
A:Reference number: I53659; MUID:92290275; PMID:1376292
A:Accession: I53659
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-231 <REG>
A:Cross-references: GB:M58761; NID:g200991; PIDN:AAA40119.1; PID:g20099
C:Superfamily: proline-rich protein

```

1.5%; Score 8; DB 2; Length 231;
arity 100.0%; Pred. No. 55;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AATA 158
|||||
AATA 159

tion regulator protein [imported] - Sinorhizobium meliloti (strain 102
zobium meliloti.
1 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
30
idner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Sci. U.S.A. 98, 9889-9894, 2001
lete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
: A95842; MUID:21396508; PMID:11481431
30
ary
DNA
<KUR>
: GB:AL591985; PIDN:CAC48548.1; PID:gl15140020; GSPDB:GN00167
urce: strain 1021, megaplasmid pSymB
nan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
: Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Jones, T.
572, 2001
); Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
mbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
site genome of the legume symbiont Sinorhizobium meliloti.
: A96039; MUID:21368234; PMID:11474104
ition

1.5%; Score 8; DB 2; Length 233;
arity 100.0%; Pred. No. 55;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AATA 126
|||||
AATA 114

lator, GntR family pdhR [imported] - Agrobacterium tumefaciens (strain
erium tumefaciens
12 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
18
bal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
), P.; Zhang, S.
2323, 2001
; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ve of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
: AB2577; MUID:21608550; PMID:11743193
18
ary
DNA
<KUR>
: GB:AE008687; PIDN:AAL45767.1; PID:gl7743501; GSPDB:GN00188
urce: strain C58 (Dupont)

1.5%; Score 8; DB 2; Length 234;

```

```

Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAA 126
|||||
DB 107 PAAAAAA 114

RESULT 125
PQ0806
Glycinin A3B4 - soybean (cv. Mandarin) (fragment)
N:Alternate names: 11S globulin; basic and acidic chains
C:Species: Glycine max (soybean)
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-
C:Accession: PQ0806
R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
A:Title: An attempt to elucidate the origin of cultivated soybean via
genitor, Glycine soja.
A:Reference number: PQ0806
A:Accession: PQ0806
A:Molecule type: mRNA
A:Residues: 1-236 <ZAK>
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:84-236/Product: glycinin, B4 chain #status predicted <GB4>

Query Match 1.5%; Score 8; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEEE 341
|||||
DB 26 DDEDEEE 33

RESULT 126
PQ0809
Glycinin A3B4 (plasmid pSGL1) - Glycine soja (strain 123) (fragment)
N:Alternate names: 11S globulin; basic and acidic chains
C:Species: Glycine soja
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-
C:Accession: PQ0809
R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A:Title: An attempt to elucidate the origin of cultivated soybean via
genitor, Glycine soja.
A:Reference number: PQ0806
A:Accession: PQ0809
A:Molecule type: mRNA
A:Residues: 1-238 <ZAK>
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:99-238/Product: glycinin B4 chain #status predicted <GLB>

Query Match 1.5%; Score 8; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEEE 341
|||||
DB 41 DDEDEEE 48

RESULT 127
AG3553
transcription regulator, gntR family BMEI10352 [imported] - Brucella m
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Jul
C:Accession: AG3553
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.;
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Cal

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A;Reference number: S10594
A;Accession: S10594
A;Status: translation not shown
A:Molecule type: mRNA
A;Residues: 1-229, 'LL' <SCH>
A;Cross-references: EMBL:X15893; NID:g29409; PIDN:CAA33902.1.; PID:g294
A;Note: This is a revision to the sequence from reference S07641
R;Schmaus, C.; McAllister, G.; Ohosone, Y.; Hardin, J.A.; Lerner, M.F.
Nucleic Acids Res. 17, 1733-1743, 1989
A;Title: A comparison of snRNP-associated Sm-autoantigens: human N, ra
A;Reference number: S07641; MUID:189160326; PMID:2522186
A;Contents: annotation
A;Note: translation of nucleotide sequence is not given
A;Note: The nucleotide sequence contains several frameshift errors that
R;Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
Proc. Natl. Acad. Sci. U.S.A. 86, 4249-4253, 1989
A;Title: Molecular cloning of cDNA encoding Sm autoantigen: derivation
A;Reference number: A32909; MUID:89264596; PMID:2524838
A;Accession: A32909
A:Molecule type: mRNA
A;Residues: 1-171, 'L', 173, 175-201, 203-216, 'S', 219-226, 'CEAFFDPWQSMVEVA
A;Cross-references: GB:J04564; NID:G190246; PIDN:AAG60151.1.; PID:G1902
A;Note: this sequence has been corrected in reference A36189
R;Ohosone, Y.; Mimori, T.; Griffith, A.; Akizuki, M.; Homma, M.; Craft
Proc. Natl. Acad. Sci. U.S.A. 86, 8392, 1989
A;Reference number: A36189
A;Accession: A36189
A:Molecule type: mRNA
A;Residues: 170-229, 'LL' <OH2>
A;Note: this is a revision to reference A32909
C;Comment: snRNP proteins B and B' result from alternative splicing of
C;Genetics:
A;Gene: GDB:SNRPB; SNRPB1
A;Cross-references: GDB:I18877; OMIM:182282
A;Map position: 20pter-20qter
A;Introns: 229/1
A;Note: the list of introns may be incomplete
C;Superfamily: proline-rich protein
C;Keywords: alternative splicing; nucleus; splicing protein

Query Match 1.5%; Score 8; DB 2; Length 240;
Best local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 151 AAAAATA 158
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Db 152 AAAAATA 159

RESULT 129
H69932
hypothetical protein ypbE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct
C;Accession: H69932
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; A
C.; Bron, S.; Bouilliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.;
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabre
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; G
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holeappel, S.; Hoson
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapid
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; I
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; S
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; S
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstap, K.; Togonoi, A.; To
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ya
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Ba
A;Reference number: A65980; MUID:98044033; PMID:9384377
A;Accession: H69932
A;Status: preliminary; nucleic acid sequence not shown; translation not

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A28993
auxin-induced protein aux28 - soybean
C:Species: Glycine max (soybean)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Au
C:Accession: A28993
R:Ainley, W.M.; Walker, J.C.; Nagao, R.T.; Key, J.L.
J. Biol. Chem. 263, 10658-10666, 1988
A:Title: Sequence and characterization of two auxin-regulated genes f
A:Reference number: A92658; MUID:88273183; PMID:2899079
A:Accession: A28993
A:Molecule type: mRNA
A:Residues: 1-243 <AIN>
A:Cross-references: GB:J03919; NID:gl69920; PIDN:AAA33945.1; PID:gl69
C:Genetics:
A:Gene: aux28
C:Superfamily: auxin-induced protein aux28
C:Keywords: nucleus

Query Match 1.5%; Score 8; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 15 AATTAAAA 22
DB 54 AATTAAAA 61

RESULT 133
A98330
sporulation transcription factor (AF096293) [imported] - Agrobacteriu
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov
C:Accession: A98330
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qu
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappa
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98330
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-244 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90163.1; PID:gl5160164; GSPDI
C:Genetics:
A:Gene: AGR_L_3177
A:Map position: linear chromosome
C:Superfamily: transcription regulator, GntR family

Query Match 1.5%; Score 8; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126
DB 118 PAAAAAAA 125

RESULT 134
AD2953
transcription regulator, GntR family Atu3226 [imported] - Agrobacteriu
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov
C:Accession: AD2953
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, F
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Rao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tume
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2953
A:Status: preliminary

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zo
zp
zq
zr
zs
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zu
zv
zw
zx
zy
zz

```

NA
<KUR>
: GB:AF008689; PIDN:AAL44042.1; PID:gl7741604; GSPDB:GN00187
rce: strain C58 (Dupont)

near chromosome
nscription regulator, GntR family

1.5%; Score 8; DB 2; Length 244;
arity 100.0%; Pred. No. 57;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
|||||
AAAA 125

rB9 homolog [imported] - Brucella melitensis (strain 16M)
a melitensis
2 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
3
; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
sman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Sci. U.S.A. 99, 443-448, 2002
e sequence of the facultative intracellular pathogen Brucella melitensis
: AD3252; PMID:11756688
3
ay
ay
NA
<KUR>
: GB:AF008918; PIDN:AAL53274.1; PID:gl7984156; GSPDB:GN00191
rce: strain 16M

or-inducing plasmid pTic58 virB9 protein

1.5%; Score 8; DB 2; Length 247;
arity 100.0%; Pred. No. 58;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
|||||
AAAA 110

integral membrane protein - Streptomyces coelicolor
myces coelicolor
; #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
i
is, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
4BL Data Library, January 1998
: Z21548
i
ary; translated from GB/EMBL/DBJ
NA
<MUR>
: EMBL:AL021411; PIDN:CAA16216.1; GSPDB:GN00070; SCOEDB:SC7H1.29C
rce: strain A3(2)

DB:SC7H1.29C
ult transport protein Q homolog

1.5%; Score 8; DB 2; Length 249;
arity 100.0%; Pred. No. 58;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

UAGG 244

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Db
97 GGAVRAGG 104
|||||
RESULT 137
A37280
C/EBP-related protein CRP1 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 13-Sep
C/Accession: A37280
R/Williams, S.C.; Cantwell, C.A.; Johnson, P.F.
Genes Dev. 5, 1553-1567, 1991
A/Title: A family of C/EBP-related proteins capable of forming covaler
A/Reference number: A37280; MUID:91357471; PMID:1884998
A/Accession: A37280
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <WIL>
A/Cross-references: GB:M85143
C/Superfamily: CCAAT/enhancer-binding protein alpha
Query Match 1.5%; Score 8; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Oy 138 APVAAAAP 145
|||||
Db 139 APVAAAAP 146
|||||
RESULT 138
S59404
hypothetical protein YLR435w - Yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein L9753.3
C/Species: Saccharomyces cerevisiae
C/Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr
C/Accession: S59404
R/Du, Z.
submitted to the EMBL Data Library, February 1995
A/Description: The sequence of S. cerevisiae cosmid 9753.
A/Reference number: S59401
A/Accession: S59404
A/Molecule type: DNA
A/Residues: 1-249 <DUZ>
A/Cross-references: EMBL:U21094; NID:g665967; PIDN:AAB67515.1; PID:g66
A/Experimental source: strain S288C (AB972)
C/Genetics:
A/Gene: MIPS:YLR435w
A/Cross-references: SGD:S0004427
A/Map position: 12R
Query Match 1.5%; Score 8; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Oy 334 DDEDEEE 341
|||||
Db 209 DDEDEEE 216
|||||
RESULT 139
A41497
36K antigen pra - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jun-
C/Accession: A41497
R/Thole, J.E.R.; Stabel, L.F.B.M.; Suykerbuyk, M.B.G.; de Wit, M.Y.L.;
Infect. Immun. 58, 80-87, 1990
A/Title: A major immunogenic 36,000-molecular-weight antigen from Mycol
A/Reference number: A41497; MUID:90093489; PMID:1688422
A/Accession: A41497
A/Molecule type: DNA
A/Residues: 1-249 <THO>

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A: GB:X65546
1.5%; Score 8; DB 2; Length 249;
arity 100.0%; Pred. No. 58;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
APPP 136
|||||
APPPP 19

polymyrase (EC 2.7.7.6) III chain C31 - yeast (*Saccharomyces cerevisiae*)
: DNA-directed RNA polymerase C chain C31; DNA-directed RNA polymerase
omyces cerevisiae
1 #sequence revision 31-Dec-1991 #text change 21-Jul-2000
5; A33811; A33656; S42275; S60976; S63103; S63823; S12321
M.; Beltrame, M.; Cassar, E.; Sentenac, A.; Thuriaux, P.
0, 4737-4743, 1990
t gene of *Saccharomyces cerevisiae* encodes a subunit of RNA polymerase
: A36465; MUID:90355990; PMID:2201900
5
acid sequence not shown
NA
<MOS>
: EMBL:X51498; NID:G4376; PIDN:CAA35866.1; PID:G4377
1
rotein
58-63 <MOS2>
odrubetz, D.
, 1282-1289, 1988
aromyces cerevisiae ACP2 gene encodes an essential HMGI-like protein.
: A33656; MUID:88216604; PMID:2835668
6
NA
<HAG>
: EMBL:M20315
odrubetz, D.
MBL Data Library, February 1989
: S42275
5
NA
R', 13-204, 'H', 206-251 <HA2>
: EMBL:M20315; NID:G170983; PIDN:AAA34390.1; PID:G170984
A.M.; Herbert, C.J.
MBL Data Library, October 1995
: sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 co
nase.
: S60958
6
NA
<NAS>
: EMBL:X92517; NID:G1050783; PIDN:CAA63288.1; PID:G1050801
A.M.; Herbert, C.
rotein Sequence Database, April 1996
: S62967
3
NA
<NAW>
: EMBL:E71427; NID:G1302107; PIDN:CAA96038.1; PID:G1302108; GSPDB:GN00
ice: strain S288C
A.M.; Herbert, C.J.
1996
nce of 36.8 kb from the left arm of chromosome XIV reveals 24 complete
: S63805; MUID:96287653; PMID:8686380
3
acid sequence not shown; translation not shown
NA
<NAF>
: EMBL:X92517; NID:G1050783; PIDN:CAA63288.1; PID:G1050801
ide sequence was submitted to the EMBL Data Library, October 1995

C:Genetics:
A:Gene: SGD:RPC31; APC2; RPC8; MIPS:YNL151C
A:Cross-references: SGD:S0005095; MIPS:YNL151C
A:Map position: 14L
C:Superfamily: DNA-directed RNA polymerase III chain C31
C:Keywords: DNA binding; nucleotidyltransferase; transcription
F:202-248/Region: acidic

Query Match 1.5%; Score 8; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 336 EDEDEDD 343
DB 215 EDEDEDD 222

RESULT 141
PQ0808
glycinin A3B4 (plasmid pSG204) - soybean (cv. Rannaya-10) (fragment)
N:Alternate names: 11S globulin; basic and acidic chains
M:Contains: glycinin B4 chain
C:Species: Glycine max (soybean)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: PQ0808
R:Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A:Title: An attempt to elucidate the origin of cultivated soybean via
genitor, Glycine soja
A:Reference number: PQ0806
A:Accession: PQ0808
A:Molecule type: mRNA
A:Residues: 1-251 <ZAK>
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:99-251/Product: glycinin B4 chain #status predicted <GB4>

Query Match 1.5%; Score 8; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 334 DDEDEDE 341
DB 41 DDEDEDE 48

RESULT 142
TI9129
hypothetical protein C09F9.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: TI9129
R:Smve, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19078
A:Accession: TI9129
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-253 <WIL>
A:Cross-references: EMBL:Z81465; PIDN:CA03860.1; GSPDB:GN000020; CESP:
A:Experimental source: clone C09F9
C:Genetics:
A:Gene: CESP:C09F9.4
A:Map position: 2
A:Introns: 111/3; 128/1; 189/3

Query Match 1.5%; Score 8; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 220 PPQQQQPP 227
DB 203 PPQQQQPP 210

```

in Rv1995 - Mycobacterium tuberculosis (strain H37RV)
terium tuberculosis
8 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
8
ch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
es, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
4, 1998
R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
ng the biology of Mycobacterium tuberculosis from the complete genome
8 : A70500; MUID:98295987; PMID:9634230
ary; nucleic acid sequence not shown; translation not shown
NA
<COL>
: GB:274025; GB:AL123456; NID:g3261586; PIDN:CAA98391.1; PID:e248805;
rce: strain H37RV
bacterium tuberculosis hypothetical protein Rv1995
1.5%; Score 8; DB 2; Length 255;
arity 100.0%; Pred. No. 60;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 22
|||||
AAAA 166
} - rice
ativa (rice)
} #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
MBL Data Library, February 1997
: Z15103
ary; translated from GB/EMBL/DBJ
RNA
:COR>
EMBL:Y11414; PIDN:CAA72217.1
ce: cv. Arborio, coleoptile
idopsis 28K leaf-specific myb-related protein; myb DNA-binding repeat
DNA-binding repeat homology <MYB1>
b DNA-binding repeat homology <MYB>
1.5%; Score 8; DB 2; Length 257;
arity 100.0%; Pred. No. 60;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
APP 128
|||
APP 150
r protein - alfalfa (fragment)
sativa (alfalfa)
#sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
681-682, 1993
ing putative zinc finger motifs from salt-tolerant alfalfa (Medicago

```

A:Reference number: Z16794; MUID:94151444; PMID:8108516
A:Accession: T09646
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-257 <WIN>
A:Cross-references: EMBL:L07291; NID:gl66409; PID:gl66410
A:Experimental source: strain HG2; callus
C:Keywords: zinc finger

Query Match 1.5%; Score 8; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDDE 336
|||||
Db 191 EEEEDDDE 198

RESULT 146
H88130
protein F10G7.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May
C:Accession: H88130
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for in
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac
A>Note: published errata appeared in Science 283, 35, 1999; Science 28
A:Accession: H88130
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: GB:chr_II; PIDN:AA81128.1; PID:g1055159; GSPDB:GNO
C:Genetics:
A:Gene: F10G7.3
A:Map position: 2

Query Match 1.5%; Score 8; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDDE 336
|||||
Db 173 EEEEDDDE 180

RESULT 147
S63604
homeobox protein Gsh-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov-
C:Accession: S63604; S66126; A37290; A38809
R:Li, H.; Zeitler, F.S.; Valerius, M.T.; Small, K.; Potter, S.S.
EMBO J. 15, 714-724, 1996
A>Title: Gsh-1, an orphan hox gene, is required for normal pituitary de
A:Reference number: S63604; MUID:96181350; PMID:8631293
A:Accession: S63604
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-261 <LHA>
R:Valerius, M.T.; Li, H.; Stock, J.L.; Weinstein, M.; Kaur, S.; Singh,
Dev. Dyn. 203, 337-351, 1995
A>Title: Gsh-1: A novel murine homeobox gene expressed in the central i
A:Reference number: S66126; MUID:96172995; PMID:8589431
A:Accession: S66126
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <VAL>
A:Cross-references: EMBL:U21224; NID:g836957; PIDN:AAA96814.1; PID:g836
R:Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copel
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991

11:33:41 2004

us-09-976-740-43.Orig.rpr

```

A: cation of 10 murine homeobox genes.
A: r: A37290; MUID:92073356; PMID:1683707
A: 90
A: nary
A: DNA
A: 05 <SIN>
A: assigned homeobox proteins; homeobox homology
A: inding; homeobox; nucleus; transcription regulation
A: homeobox homology <HOX>
A: 1.5%; Score 8; DB 2; Length 261;
A: larity 100.0%; Pred.No. 61;
A: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:
A: AAAAA 126
A: |||||
A: AAAAA 116
A:
A:
A: sin - common tobacco
A: ina tabacum (common tobacco)
A: 95 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
A: 56
A: illi, A.G.; Albersheim, P.
A: EMBL Data Library, July 1993
A: ivation of a tobacco glycine-rich protein gene by a fungal glucan prep
A: : S34666
A: 56
A: nary
A: DNA
A: <BRA>
A: : EMBL:X74106; NID:G395146; PIDN:CAA52208.1; PID:G395147
A: iseculus glycine-rich protein 1.0
A: 1.5%; Score 8; DB 2; Length 271;
A: arity 100.0%; Pred.No. 63;
A: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:
A: XGAGG 266
A: |||||
A: XGAGG 261
A:
A: or hoxa-9 - mouse
A: culus (house mouse)
A: 8 #sequence_revision 05-Dec-1998 #text_change 15-Oct-1999
A: 3
A: aki, K.; Chisaka, O.; Araki, M.; Takagi, K.; Yamamura, K.
A: 998
A: of the murine Hoxa-9 cDNA: An alternatively spliced transcript encodes
A: : JC6553; MUID:98192518; PMID:9524228
A: 3
A: RNA
A: <FUG>
A: : DDBJ:AB008914
A:
A: assigned homeobox proteins; homeobox homology
A: nding; homeobox; metal binding; nucleus; transcription regulation
A: homeobox homology <HOX>
A: 1.5%; Score 8; DB 2; Length 271;
A: arity 100.0%; Pred.No. 63;
A: conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:
A: AAP 145
A: |||||
A: AAP 102

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RESULT 150

T52103

GATA-binding transcription factor homolog 1 [imported] - Arabidopsis
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Ma
C;Accession: T52103
R;Teakle, G.R.; Gilmartin, P.M.
submitted to the EMBL Data Library, June 1997
A;Description: Two types of GATA factor are found in fungi but are un
A;Reference number: Z25956
A;Accession: T52103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-274 <TEA>
A;Cross-references: EMBL:Y13648; PIDN:CAA73999.1
A;Experimental source: ecotype Columbia
C;Genetics:
A;Gene: GATA-1
C;Superfamily: Arabidopsis thaliana GATA transcription factor 4

Query Match 1.5%; Score 8; DB 2; Length 274;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDDE 336

|||||

Db 17 EEEEDDDE 24

Search completed: March 30, 2004, 15:02:39

Job time : 25 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.
 in search, using sw model
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 (without alignments)
 3060.305 Million cell updates/sec

-09-976-740-43
 8
 MAGPALPPPTAAATTA.....HIKVLQGHEDDDPGFLG 538

IGO
 pop 60.0 , Gapext 60.0

65169 seqs, 261661801 residues

ts satisfying chosen parameters: 1065169

gth: 0

gth: 2000000000

isting first 150 summaries

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 t than or equal to the score of the result being printed,
 id by analysis of the total score distribution.

SUMMARIES

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1.0	538	12	US-10-671-242-43	Sequence 43, Appl
1.0	538	13	US-10-023-529-43	Sequence 43, Appl
1.0	538	13	US-10-023-523-43	Sequence 43, Appl
1.0	538	15	US-10-616-187-43	Sequence 43, Appl
1.3	217	9	US-09-962-055-7	Sequence 7, Appl
1.3	217	9	US-09-976-740-7	Sequence 7, Appl
1.3	217	12	US-10-671-242-7	Sequence 7, Appl
1.3	217	13	US-10-023-529-7	Sequence 7, Appl
1.3	217	13	US-10-023-523-7	Sequence 7, Appl
1.3	217	15	US-10-616-187-7	Sequence 7, Appl
1.8	241	14	US-10-102-806-665	Sequence 665, App
1.4	550	9	US-09-976-740-47	Sequence 47, Appl
1.4	550	12	US-10-671-242-47	Sequence 47, Appl
1.4	550	13	US-10-023-529-47	Sequence 47, Appl

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17	99	18.4	550	15	US-10-616-187-47	Sequence
18	76	14.1	232	9	US-09-962-055-3	Sequence
19	76	14.1	232	9	US-09-976-740-3	Sequence
20	76	14.1	232	12	US-10-671-242-3	Sequence
21	76	14.1	232	13	US-10-023-529-3	Sequence
22	76	14.1	232	13	US-10-023-523-3	Sequence
23	76	14.1	232	15	US-10-616-187-3	Sequence
24	76	14.1	252	9	US-09-962-055-4	Sequence
25	76	14.1	252	9	US-09-976-740-4	Sequence
26	76	14.1	252	12	US-10-671-242-4	Sequence
27	76	14.1	252	13	US-10-023-529-4	Sequence
28	76	14.1	252	13	US-10-023-523-4	Sequence
29	76	14.1	252	15	US-10-616-187-4	Sequence
30	76	14.1	317	9	US-09-962-055-2	Sequence
31	76	14.1	317	9	US-09-976-740-2	Sequence
32	76	14.1	317	12	US-10-671-242-2	Sequence
33	76	14.1	317	13	US-10-023-529-2	Sequence
34	76	14.1	317	13	US-10-023-523-2	Sequence
35	76	14.1	317	15	US-10-616-187-2	Sequence
36	26	4.8	26	9	US-09-962-055-20	Sequence
37	26	4.8	26	9	US-09-976-740-20	Sequence
38	26	4.8	26	12	US-10-671-242-20	Sequence
39	26	4.8	26	13	US-10-023-529-20	Sequence
40	26	4.8	26	13	US-10-023-523-20	Sequence
41	26	4.8	26	15	US-10-616-187-20	Sequence
42	15	2.8	15	9	US-09-962-055-19	Sequence
43	15	2.8	15	9	US-09-976-740-19	Sequence
44	15	2.8	15	12	US-10-671-242-19	Sequence
45	15	2.8	15	13	US-10-023-529-19	Sequence
46	15	2.8	15	13	US-10-023-523-19	Sequence
47	15	2.8	15	15	US-10-616-187-19	Sequence
48	15	2.8	102	12	US-10-221-625-66	Sequence
49	15	2.8	116	15	US-10-094-749-2857	Sequence
50	11	2.0	11	9	US-09-962-055-21	Sequence
51	11	2.0	11	9	US-09-976-740-21	Sequence
52	11	2.0	11	12	US-10-671-242-21	Sequence
53	11	2.0	11	13	US-10-023-529-21	Sequence
54	11	2.0	11	13	US-10-023-523-21	Sequence
55	11	2.0	11	15	US-10-616-187-21	Sequence
56	11	2.0	12	9	US-09-962-055-27	Sequence
57	11	2.0	12	9	US-09-976-740-27	Sequence
58	11	2.0	12	12	US-10-671-242-27	Sequence
59	11	2.0	12	13	US-10-023-529-27	Sequence
60	11	2.0	12	13	US-10-023-523-27	Sequence
61	11	2.0	12	15	US-10-616-187-27	Sequence
62	11	2.0	28	9	US-09-962-055-26	Sequence
63	11	2.0	28	9	US-09-976-740-26	Sequence
64	11	2.0	28	12	US-10-671-242-26	Sequence
65	11	2.0	28	13	US-10-023-529-26	Sequence
66	11	2.0	28	13	US-10-023-523-26	Sequence
67	11	2.0	28	15	US-10-616-187-26	Sequence
68	11	2.0	129	14	US-10-357-322-12	Sequence
69	11	2.0	135	12	US-10-425-114-42252	Sequence
70	11	2.0	189	9	US-09-810-264-20	Sequence
71	11	2.0	334	15	US-10-108-260A-4241	Sequence
72	11	2.0	2103	14	US-10-184-644-319	Sequence
73	11	2.0	2103	14	US-10-184-634-319	Sequence
74	11	2.0	2103	14	US-10-063-685-105	Sequence
75	11	2.0	2340	14	US-10-184-644-333	Sequence
76	11	2.0	2340	14	US-10-184-634-333	Sequence
77	10	1.9	10	9	US-09-962-055-22	Sequence
78	10	1.9	10	9	US-09-962-055-28	Sequence
79	10	1.9	10	9	US-09-976-740-22	Sequence
80	10	1.9	10	9	US-09-976-740-28	Sequence
81	10	1.9	10	12	US-10-671-242-22	Sequence
82	10	1.9	10	12	US-10-671-242-28	Sequence
83	10	1.9	10	13	US-10-023-529-22	Sequence
84	10	1.9	10	13	US-10-023-529-28	Sequence
85	10	1.9	10	13	US-10-023-523-22	Sequence
86	10	1.9	10	13	US-10-023-523-28	Sequence
87	10	1.9	10	15	US-10-616-187-28	Sequence
88	10	1.9	10	15	US-10-616-187-28	Sequence

[illegible]
$$\lim_{n \rightarrow \infty} \frac{1}{n} \sum_{i=1}^n \frac{1}{i} = 0$$

RESULT 2
US-10-671-242-43
; Sequence 43, Application US/10671242
; Publication No. US20040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.

Simon W.
 na, Anibal A.
 ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ION: ATHEROSCLEROSIS
 10797-004001
 ION NUMBER: US/10/671,242
 DATE: 2003-09-24
 N NUMBER: US/09/616,289
 TE: 2000-07-14
 N NUMBER: US 09/517,849
 TE: 2000-03-02
 N NUMBER: US 08/979,608
 TE: 1997-11-26
 N NUMBER: US 60/031,930
 TE: 1996-11-27
 N NUMBER: US 60/048,547
 TE: 1997-06-03
 NOS: 53
 Q for Windows Version 4.0

sapiens
 100.0%; Score 538; DB 12; Length 538;
 100.0%; Pred. No. 0;
 0; Mismatches 0; Indels 0; Gaps 0;
 'ALPPETAATAATAAASAAASPHYQWILDTIDSLRSRKARPDLEICRMVRR 60
 'ALPPETAATAATAAASAAASPHYQWILDTIDSLRSRKARPDLEICRMVRR 60
 'PERTAELEKLIQORAVLRVSKGSI SYRNAARVQPPRRGATPPAPPAPGAPA 120
 'PERTAELEKLIQORAVLRVSKGSI SYRNAARVQPPRRGATPPAPPAPGAPA 120
 'APPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPRAQAAPLAAP 180
 'APPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPRAQAAPLAAP 180
 'APPAVAPPAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPQPPPPGAV 240
 'APPAVAPPAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPQPPPPGAV 240
 'ARVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALPRG 300
 'ARVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALPRG 300
 'APPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 'APPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDE 360
 'GERGQSAKERVKEWTGCGPHQODEGRGPAGSGTRQVFSMAANKKEGGTASVA 420
 'GERGQSAKERVKEWTGCGPHQODEGRGPAGSGTRQVFSMAANKKEGGTASVA 420
 'PSPVPLPGKALPCADGTPGCPGPKPKPKPSDPVMTVMDVVEYFTFAGFPEQA 480
 'PSPVPLPGKALPCADGTPGCPGPKPKPKPSDPVMTVMDVVEYFTFAGFPEQA 480
 'QEIDGKSILLMORTDVLTLGLSIRLGPALKIYEHHIKVLQOCHFDDEDDPDGFLG 538
 'QEIDGKSILLMORTDVLTLGLSIRLGPALKIYEHHIKVLQOCHFDDEDDPDGFLG 538

ication US/10023529
 S20020129388A1
 ON:
 Ann M.

APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/10/023,529
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 43
 LENGTH: 538
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-023-529-43

Query Match 100.0%; Score 538; DB 13; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MAGPPALPPETATAAATAAASAAASPHYQWILDTIDSLRSRKARPDLEICRI
 DB 1 MAGPPALPPETATAAATAAASAAASPHYQWILDTIDSLRSRKARPDLEICRI
 QY 61 RHGPEPERTRAELEKLIQORAVLRVSKGSI SYRNAARVQPPRRGATPPAPPAPR
 DB 61 RHGPEPERTRAELEKLIQORAVLRVSKGSI SYRNAARVQPPRRGATPPAPPAPR
 QY 121 AAAAAAPPPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPRAQAAP
 DB 121 AAAAAAPPPTTAPPPPPAPVAAAPARAPRAAAAAATAPPSPGPAQPGPRAQAAP
 QY 181 PPAPAPPAVAPPAAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPGAV
 DB 181 PPAPAPPAVAPPAAGRRAPPPAVAAAREPPLPPPPQPPPPQPPPPQPPPPGAV
 QY 241 RAGGAARPVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALAI
 DB 241 RAGGAARPVSLREVRYLGGSGGAGGLTRGRVQGLLEEEAAARGRLERLGLALAI
 QY 301 DRPGAPPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDE 360
 DB 301 DRPGAPPAASAPRSKRGGSERVLEKEEEDDEDEDEDEDEDEDEDEDEDEDE 360
 QY 361 HHQNGERGQSAKERVKEWTGCGPHQODEGRGPAGSGTRQVFSMAANKKEGGT
 DB 361 HHQNGERGQSAKERVKEWTGCGPHQODEGRGPAGSGTRQVFSMAANKKEGGT
 QY 421 TGPDSFPSVPLPGKALPCADGTPGCPGPKPKPKPSDPVMTVMDVVEYFTFAGF
 DB 421 TGPDSFPSVPLPGKALPCADGTPGCPGPKPKPKPSDPVMTVMDVVEYFTFAGF
 QY 481 TAFQOEIDGKSILLMORTDVLTLGLSIRLGPALKIYEHHIKVLQOCHFDDEDDPDGFI
 DB 481 TAFQOEIDGKSILLMORTDVLTLGLSIRLGPALKIYEHHIKVLQOCHFDDEDDPDGFI

RESULT 4
 US-10-023-529-43
 ; Sequence 43, Application US/10023529
 ; Publication No. US20020152485A1
 ; GENERAL INFORMATION:

S, Ann M.
 es, Robert S.
 w, Simon W.
 jona, Anibal A.
 TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 TION: ATHEROSCLEROSIS
 : 10797-004001
 ATION NUMBER: US/10/023,523
 DATE: 2001-12-17
 ION NUMBER: US/09/616,289
 ATE: 2000-07-14
 ION NUMBER: US 09/517,849
 ATE: 2000-03-02
 ION NUMBER: US 08/979,608
 ATE: 1997-11-26
 ION NUMBER: US 60/031,930
 ATE: 1996-11-27
 ION NUMBER: US 60/048,547
 ATE: 1997-06-03
 ID NOS: 53
 SEQ for Windows Version 4.0

> sapiens

100.0%; Score 538; DB 13; Length 538;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ?PALPPETAAATTAASSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRR 60
 ?PALPPETAAATTAASSAASPHYQEWILDTIDSLRSRKARPDLEICRMVRR 60
 ?PERTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPGAPA 120
 ?PERTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPGAPA 120
 ?AAPPPTAPPPPPAPVAAAPARAAPRAAAAAATAPPSPGPAQPGRAAPLAAP 180
 ?AAPPPTAPPPPPAPVAAAPARAAPRAAAAAATAPPSPGPAQPGRAAPLAAP 180
 ?AAPPVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPQPPPPQPPPPGAV 240
 ?AAPPVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPQPPPPQPPPPGAV 240
 ?AAPPVSLREVVRVYLGSGGAGGLTRGVQGLLEEEAAARGLETRIGALALPRG 300
 ?AAPPVSLREVVRVYLGSGGAGGLTRGVQGLLEEEAAARGLETRIGALALPRG 300
 ?APPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDRPAGAQ 360
 ?APPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDRPAGAQ 360
 ?NGERGQSAKRVKEWTPCGHQODEGRGPAQSGTRQVFSMAAMNKEGTSVA 420
 ?NGERGQSAKRVKEWTPCGHQODEGRGPAQSGTRQVFSMAAMNKEGTSVA 420
 ?SPSPVPLPPGKPALPGADGTPPGCPGKPKSDPVEWTVMDVVEYFTEAGF 480
 ?SPSPVPLPPGKPALPGADGTPPGCPGKPKSDPVEWTVMDVVEYFTEAGF 480
 ?EQEIDGKSLLMQRTDVLTLGLSIRLPALKIYEHHIKVLQOQHFEEDDDPDGFLG 538
 ?EQEIDGKSLLMQRTDVLTLGLSIRLPALKIYEHHIKVLQOQHFEEDDDPDGFLG 538

lication US/10616187
 US20040013668A1

GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/616,187
 ; CURRENT FILING DATE: 2003-07-09
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 538
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-616-187-43

Query Match 100.0%; Score 538; DB 15; Length 538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAGPALPPETAAATTAASSAASPHYQEWILDTIDSLRSRKARPDLEIC
 Db 1 MAGPALPPETAAATTAASSAASPHYQEWILDTIDSLRSRKARPDLEIC
 QY 61 RHGPPEPTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPI
 Db 61 RHGPPEPTRAELKLIQORAVLRVSYKGSISYRNAARVQPPRGATPPAPRAPI
 QY 121 AAAAAAPPTTAPPPPPAPVAAAPARAAPRAAAAAATAPPSPGPAQPGRAAAI
 Db 121 AAAAAAPPTTAPPPPPAPVAAAPARAAPRAAAAAATAPPSPGPAQPGRAAAI
 QY 181 PPAPAPVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPQPPPPQPPPP
 Db 181 PPAPAPVAPAGPRRAPPAVAAAREPPLPPPPQPPAPQPPPPQPPPPQPPPP
 QY 241 RAGGAARVSVLRVYLGSGGAGGLTRGVQGLLEEEAAARGLETRIGAL
 Db 241 RAGGAARVSVLRVYLGSGGAGGLTRGVQGLLEEEAAARGLETRIGAL
 QY 301 DRGRAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDR
 Db 301 DRGRAPPAASARPSRKSGGEERVLEKEEEDDDDEDEDDVSEGEVPSDR
 QY 361 HHQJNGERGQSAKRVKEWTPCGHQODEGRGPAQSGTRQVFSMAAMNKEGT
 Db 361 HHQJNGERGQSAKRVKEWTPCGHQODEGRGPAQSGTRQVFSMAAMNKEGT
 QY 421 TGPDSPSFVPLPPGKPALPGADGTPPGCPGKPKSDPVEWTVMDVVEYFTEAGF
 Db 421 TGPDSPSFVPLPPGKPALPGADGTPPGCPGKPKSDPVEWTVMDVVEYFTEAGF
 QY 481 TAFEQEIIDGKSLLMQRTDVLTLGLSIRLPALKIYEHHIKVLQOQHFEEDDDPDG
 Db 481 TAFEQEIIDGKSLLMQRTDVLTLGLSIRLPALKIYEHHIKVLQOQHFEEDDDPDG

RESULT 6
 US-09-962-055-7
 ; Sequence 7, Application US/09962055

20052033A1
 ACTION:
 : Lees, Ann M.
 : Lees, Robert S.
 : Law, Simon W.
 : Arjona, Anibal A.
 INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS
 SEQUENCES: 42
 DENCE ADDRESS:
 ESSEE: Fish & Richardson P.C.
 ET: 225 Franklin Street
 : Boston
 3: MA
 TRY: USA
 02110-2804
 READABLE FORM:
 JM TYPE: Diskette
 JTER: IBM Compatible
 ATING SYSTEM: DOS
 VARE: FastSEQ for Windows Version 2.0
 PPLICATION DATA:
 CATION NUMBER: US/09/962,055
 IG DATE: 24-Sep-2001
 CATION DATA:
 CATION NUMBER: 08/979,608
 IG DATE: 26-NOV-1997
 CATION NUMBER: US 60/031,930
 IG DATE: 27-NOV-1996
 GENT INFORMATION:
 Myers, Louis
 TRATION NUMBER: 35,965
 ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
 CATION INFORMATION:
 HONE: 617/542-5070
 AX: 617/542-8906
 SEQ ID NO: 7:
 CHARACTERISTICS:
 H: 217 amino acids
 amino acid
 OG: linear
 YPE: protein
 ESCRIPTION: SEQ ID NO: 7:
 40.3%; Score 217; DB 9; Length 217;
 rity 100.0%; Pred. No. 1.6e-161;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHLNGERGQSAKERVKWT 381
 EKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHLNGERGQSAKERVKWT 60
 QQDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGDPSPVPLPGKALPCA 441
 QQDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGDPSPVPLPGKALPCA 120
 GCPGRKEKSDPVWVMTVDVVEYFTAGFPEQATAFQEQIDGKSLLMORTDV 501
 GCPGRKEKSDPVWVMTVDVVEYFTAGFPEQATAFQEQIDGKSLLMORTDV 180
 IRLGPALKIYHHIKVQLQQGHFEDDDPDGFLG 538
 IRLGPALKIYHHIKVQLQQGHFEDDDPDGFLG 217
 cation US/09976740
 S20020194633A1
 ON:
 Ann M.

APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
 TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/09/976,740
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 217
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-976-740-7
 Query Match 40.3%; Score 217; DB 9; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.6e-161;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; G
 QY 322 EERVLEKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHLNGERGQSAKERV
 DB 1 EERVLEKEEEDDDDEDEDDVSEGVESVPSDRPAGAHQHLNGERGQSAKERV
 QY 382 PCGPHQCGDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGDPSPVPLPGKPA
 DB 61 PCGPHQCGDEGRGAPGSGTRQVFSMAAMNKEGGTASVATGDPSPVPLPGKPA
 QY 442 DGTFFCGCPGRKEKSDPVWVMTVDVVEYFTAGFPEQATAFQEQIDGKSLLMQ
 DB 121 DGTFFCGCPGRKEKSDPVWVMTVDVVEYFTAGFPEQATAFQEQIDGKSLLMQ
 QY 502 LTGLSIRLGPALKIYHHIKVQLQQGHFEDDDPDGFLG 538
 DB 181 LTGLSIRLGPALKIYHHIKVQLQQGHFEDDDPDGFLG 217
 RESULT 8
 US-10-671-242-7
 ; Sequence 7, Application US/10671242
 ; Publication No. US20040040049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/671,242
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSEQ for Windows Version 4.0

```
> sapiens
      40.3%; Score 217; DB 12; Length 217;
      larity 100.0%; Pred. No. 1.6e-161;
      conservative 0; Mismatches 0; Indels 0; Gaps 0;
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      LEKEEEEDDEDEDDVSEGVPSDRPAGAHQHQLNGERGQSAKERVKEWT 60
      HQQDEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPALPGA 441
      HQQDEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPALPGA 120
      FCGPPGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC 501
      FCGPPGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC 180
      SIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 538
      SIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 217
      .ication US/10023529
      US20020129388A1
      ION:
      s, Ann M.
      s, Robert S.
      , Simon W.
      ona, Anibal A.
      ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
      ION: ATHEROSCLEROSIS
      10797-004001
      TION NUMBER: US/10/023,529
      DATE: 2001-12-17
      CN NUMBER: 09/616,289
      TE: 2000-07-14
      CN NUMBER: US 09/517,849
      TE: 2000-03-02
      CN NUMBER: US 08/979,608
      TE: 1997-11-26
      CN NUMBER: US 60/031,930
      TE: 1996-11-27
      CN NUMBER: US 60/048,547
      TE: 1997-06-03
      D NOS: 53
      EQ for Windows Version 4.0
      . sapiens
      40.3%; Score 217; DB 13; Length 217;
      arity 100.0%; Pred. No. 1.6e-161;
      onservative 0; Mismatches 0; Indels 0; Gaps 0;
      LEKEEEEDDEDEDDVSEGVPSDRPAGAHQHQLNGERGQSAKERVKEWT 381
      LEKEEEEDDEDEDDVSEGVPSDRPAGAHQHQLNGERGQSAKERVKEWT 60
      HQQDEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPALPGA 441
      HQQDEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPALPGA 120
      FCGPPGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC 501
      FCGPPGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC 180
      SIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 538
      SIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 217
      .ication US/10023523
      US20020152485A1
      ION:
      s, Ann M.
      s, Robert S.
      , Simon W.
      APPLICANT: Lees, Robert S.
      APPLICANT: Law, Simon W.
      APPLICANT: Arjona, Anibal A.
      TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
      TITLE OF INVENTION: ATHEROSCLEROSIS
      FILE REFERENCE: 10797-004001
      CURRENT APPLICATION NUMBER: US/10/023,523
      CURRENT FILING DATE: 2001-12-17
      PRIOR APPLICATION NUMBER: US/09/616,289
      PRIOR FILING DATE: 2000-07-14
      PRIOR APPLICATION NUMBER: US 09/517,849
      PRIOR FILING DATE: 2000-03-02
      PRIOR APPLICATION NUMBER: US 08/979,608
      PRIOR FILING DATE: 1997-11-26
      PRIOR APPLICATION NUMBER: US 60/031,930
      PRIOR FILING DATE: 1996-11-27
      PRIOR APPLICATION NUMBER: US 60/048,547
      PRIOR FILING DATE: 1997-06-03
      NUMBER OF SEQ ID NOS: 53
      SOFTWARE: FastSeq for Windows Version 4.0
      SEQ ID NO 7
      LENGTH: 217
      TYPE: PRT
      ORGANISM: Homo sapiens
      US-10-023-523-7
      Query Match 40.3%; Score 217; DB 13; Length 217;
      Best Local Similarity 100.0%; Pred. No. 1.6e-161;
      Matches 217; Conservative 0; Mismatches 0; Indels 0;
      QY 322 EERVLEKEEEEDDEDEDDVSEGVPSDRPAGAHQHQLNGERGQSAKERV
      DB 1 EERVLEKEEEEDDEDEDDVSEGVPSDRPAGAHQHQLNGERGQSAKERV
      QY 382 PCGPHQODEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPF
      DB 61 PCGPHQODEGRGAPGSGTRQVFSMAANKEGGTASVATGDPSPVPLPGKPF
      QY 442 DGTGPGCPGGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC
      DB 121 DGTGPGCPGGRKEKPSDPVEMTMDVVEYFTAGFPEQATAFQEQEIDGKSLLLMC
      QY 502 LTGLSIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 538
      DB 181 LTGLSIRLGPALKIYEHHIKVLQOQHFEDEDDPDGFLG 217
      RESULT 11
      US-10-616-187-7
      ; Sequence 7, Application US/10616187
      ; Publication No. US20040013668A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Lees, Ann M.
      ; APPLICANT: Lees, Robert S.
      ; APPLICANT: Law, Simon W.
      ; APPLICANT: Arjona, Anibal A.
      ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
      ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
```

ON: ATHEROSCLEROSIS
 10797-004001
 ION NUMBER: US/10/616,187
 ATE: 2003-07-09
 N NUMBER: US/09/616,289
 E: 2000-07-14
 N NUMBER: US 09/517,849
 E: 2000-03-02
 N NUMBER: US 08/979,608
 E: 1997-11-26
 N NUMBER: US 60/031,930
 E: 1996-11-27
 N NUMBER: US 60/048,547
 E: 1997-06-03
 NOS: 53
 Q for Windows Version 4.0

sapiens

40.3%; Score 217; DB 15; Length 217;
 rity 100.0%; Pred. No. 1.6e-161; Indels 0; Gaps 0;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EKEEEDEDEDEDDVSEGEVPSDRPAGAHQHQLNGRGPQSAKERVKWT 381
 EKEEEDEDEDEDDVSEGEVPSDRPAGAHQHQLNGRGPQSAKERVKWT 60
 QQDEGRGPAGSGTRQVFSMAANKKEGGTASVATGPDSPVPLPGKPALPGA 441
 QQDEGRGPAGSGTRQVFSMAANKKEGGTASVATGPDSPVPLPGKPALPGA 120
 GCPGRKPKDPVETVMDVVEYFTEAGFPEQATAFQEQIDGKSLLMORTDV 501
 GCPGRKPKDPVETVMDVVEYFTEAGFPEQATAFQEQIDGKSLLMORTDV 180
 IRLGPALKIYHHIKVLQGGHFEDDDPDGFLG 538
 IRLGPALKIYHHIKVLQGGHFEDDDPDGFLG 217

lication US/10102806
 S20030054421A1
 ON:

et al.
 ON: Nucleic Acids, Proteins and Antibodies

PA103FIC1
 ION NUMBER: US/10/102,806
 ATE: 2002-03-22
 N NUMBER: 09/925,298
 E: 2001-08-10
 N NUMBER: PCT/US00/05881
 E: 2000-03-08
 N NUMBER: 60/124,270
 E: 1999-03-12
 NOS: 846
 In Ver. 2.0

sapiens

ON: Xaa equals any of the naturally occurring L-amino acids
 ON: Xaa equals any of the naturally occurring L-amino acids

Query Match 20.8%; Score 112; DB 14; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.1e-79;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; G
 QY 307 PPAASARPSRSGGERSVLEKEEEDDEDEDDVSEGEVPSDRPAGAHQH
 DB 10 PPAASARPSRSGGERSVLEKEEEDDEDEDDVSEGEVPSDRPAGAHQH
 QY 367 ERGPOSASERVKEWTPCGPHQGDGRGPAGSGTRQVFSMAANKKEGGTAS 418
 DB 70 ERGPOSASERVKEWTPCGPHQGDGRGPAGSGTRQVFSMAANKKEGGTAS 121

RESULT 13

US-09-976-740-47
 ; Sequence 47, Application US/09976740
 ; Publication No. US20020194633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/976,740
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-976-740-47

Query Match 18.4%; Score 99; DB 9; Length 550;
 Best Local Similarity 100.0%; Pred. No. 6e-69;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; G
 QY 19 AAAASSAASPHYQEWILDTIDSLRSRKARPDLERICMVRRRHGPPEPTRAELEI
 DB 20 AAAASSAASPHYQEWILDTIDSLRSRKARPDLERICMVRRRHGPPEPTRAELEI
 QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPRAPRG 117
 DB 80 QRAVLRSYKGSISYRNAARVQPPRGATPPRAPRG 118

RESULT 14

US-10-671-242-47
 ; Sequence 47, Application US/10671242
 ; Publication No. US200400040049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/671,242
 ; CURRENT FILING DATE: 2003-09-24

ION NUMBER: US/09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

ctolagus cuniculus

18.4%; Score 99; DB 12; Length 550;
arity 100.0%; Pred. No. 6e-69; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 78
|||||
ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 79
|||||

/LRVSYKGSISYRNAARVQPPRGATPPAPRPG 117
|||||
/LRVSYKGSISYRNAARVQPPRGATPPAPRPG 118
|||||

Application US/10023529
US20020129388A1
TION:

Ann M.

Robert S.

Simon W.

Arjona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/10/023,529
DATE: 2001-12-17
ION NUMBER: 09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

ctolagus cuniculus

18.4%; Score 99; DB 13; Length 550;
arity 100.0%; Pred. No. 6e-69; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 78
|||||
ASSAASPHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELEKLIQ 79
|||||

/LRVSYKGSISYRNAARVQPPRGATPPAPRPG 117

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPRPG 118
|||||

RESULT 16

US-10-023-523-47
; Sequence 47, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-47

Query Match 18.4%; Score 99; DB 13; Length 550;
Best Local Similarity 100.0%; Pred. No. 6e-69;
Matches 99; Conservative 0; Mismatches 0; Indels 0;

QY 19 AAAASSAASHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELE
|||||

Db 20 AAAASSAASHYQEWILDTLSRSKARPDLEICRMVRRHGPPEPTRAELE
|||||

QY 79 QRAVLRSYKGSISYRNAARVQPPRGATPPAPRPG 117
|||||

Db 80 QRAVLRSYKGSISYRNAARVQPPRGATPPAPRPG 118
|||||

RESULT 17

US-10-616-187-47
; Sequence 47, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27

1.33:40 2004

us-09-976-740-43.olig.rapb

Y NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

olagus cuniculus

18.4%; Score 99; DB 15; Length 550;
rity 100.0%; Pred.No. 6e-69; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

SSAASPHYQEWILDTIDSLRSRKARPDLERICRMVRRHGHGPEPTRAELEKLIQ 78
SSAASPHYQEWILDTIDSLRSRKARPDLERICRMVRRHGHGPEPTRAELEKLIQ 79

RVSYKGSISYNAARVOPPRGATPPAPRPG 117
RVSYKGSISYNAARVOPPRGATPPAPRPG 118

cation US/09962055
0052033A1
TION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSSE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston

: MA

RY: USA

02110-2804

EADABLE FORM:

M TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/962,055

G DATE: 24-Sep-2001

ICATION DATA:

CATION NUMBER: 08/979,608

G DATE: 26-NOV-1997

CATION NUMBER: US 60/031,930

G DATE: 27-NOV-1996

GENT INFORMATION:

Myers, Louis

TRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

'PHONE: 617/542-5070

'AX: 617/542-8906

: SEQ ID NO: 3:

'HARACTERISTICS:

'H: 232 amino acids

amino acid

LOGY: linear

YPE: protein

DESCRIPTION: SEQ ID NO: 3:

14.1%; Score 76; DB 9; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTVMDEVVEYFTEAGFPQATAFQOEIDGKSLLLMORTDVLTLGSLRGLPALH
DB 152 DPVEWTVMDEVVEYFTEAGFPQATAFQOEIDGKSLLLMORTDVLTLGSLRGLPALH

QY 518 HHIKVLQGGHFEDDDP 533
DB 212 HHIKVLQGGHFEDDDP 227

RESULT 19

US-09-976-740-3

; Sequence 3, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-976-740-3

Query Match

Best Local Similarity 14.1%; Score 76; DB 9; Length 232;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTVMDEVVEYFTEAGFPQATAFQOEIDGKSLLLMORTDVLTLGSLRGLPALH
DB 152 DPVEWTVMDEVVEYFTEAGFPQATAFQOEIDGKSLLLMORTDVLTLGSLRGLPALH

QY 518 HHIKVLQGGHFEDDDP 533
DB 212 HHIKVLQGGHFEDDDP 227

RESULT 20

US-10-671-242-3

; Sequence 3, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

11:33:40 2004

us-09-976-740-43.olig.rapb

ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 12; Length 232;
arity 100.0%; Pred. No. 2.8e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTVMVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTVMVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211
|||||

VLOQGHFEDDDP 533
|||||
VLOQGHFEDDDP 227

ication US/10023529
US20020129388A1
TON:

, Ann M.
, Robert S.
, Simon W.
ona, Anibal A.
TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TON: ATHEROSCLEROSIS
10797-004001

TION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 13; Length 232;
arity 100.0%; Pred. No. 2.8e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTVMVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTVMVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 211
|||||

VLOQGHFEDDDP 533
|||||
VLOQGHFEDDDP 227

RESULT 22

US-10-023-523-3
; Sequence 3, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-3

Query Match 14.1%; Score 76; DB 13; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; C

QY 458 DPVETWMDVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
|||||
Db 152 DPVETWMDVVEYFEAGPPEQATAFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
|||||
QY 518 HHKVLQGHFEDDDP 533
|||||
Db 212 HHKVLQGHFEDDDP 227

RESULT 23

US-10-616-187-3
; Sequence 3, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03

NOS: 53
Q for Windows Version 4.0

olagus cuniculus

14.1%; Score 76; DB 15; Length 232;

arity 100.0%; Pred. No. 2.8e-51;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

TMVMDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL; 517

TMVMDVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL; 211

TQQGHFEDDDP 533

TQQGHFEDDDP 227

cation US/09962055

0052033A1

ATION:

Lees, Ann M.

Lees, Robert S.

Law, Simon W.

Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

ESSEE: Fish & Richardson P.C.

ET: 225 Franklin Street

Boston

MA

RY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

ITER: IBM Compatible

ATING SYSTEM: DOS

WARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/962,055

IG DATE: 24-Sep-2001

ICATION DATA:

ICATION NUMBER: 08/979,608

IG DATE: 26-NOV-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

: Myers, Louis

INATION NUMBER: 35,965

ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

SEQ ID NO: 4

CHARACTERISTICS:

PH: 252 amino acids

: amino acid

LOGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 4:

14.1%; Score 76; DB 9; Length 252;

arity 100.0%; Pred. No. 3e-51;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL;

Db 172 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL;

QY 518 HHKVLQOQHFEEDDDP 533

Db 232 HHKVLQOQHFEEDDDP 247

RESULT 25

US-09-976-740-4

; Sequence 4, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Robert S.

; APPLICANT: Lees, Ann M.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-976-740-4

Query Match 14.1%; Score 76; DB 9; Length 252;

Best Local Similarity 100.0%; Pred. No. 3e-51;

Matches 76; Conservative 0; Mismatches 0; Indels 0; G

QY 458 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL;

Db 172 DPVEWTVMVVEYFTAGPPEQATAFQEQEIDGKSLLMQRTDVLGLSIRLGPAL;

QY 518 HHKVLQOQHFEEDDDP 533

Db 232 HHKVLQOQHFEEDDDP 247

RESULT 26

US-10-671-242-4

; Sequence 4, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/671,242

; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 12; Length 252;
arity 100.0%; Pred. No. 3e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231
VLOQGHFEDDDP 533
VLOQGHFEDDDP 247

ication US/10023529
US20020129388A1
ION:

, Ann M.
s, Robert S.
, Simon W.
ona, Anibal A.
ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001

TION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

14.1%; Score 76; DB 13; Length 252;
arity 100.0%; Pred. No. 3e-51;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
|||||
WTWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231
VLOQGHFEDDDP 533
VLOQGHFEDDDP 247

RESULT 28

US-10-023-523-4
; Sequence 4, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-4

Query Match 14.1%; Score 76; DB 13; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; C
QY 458 DPVETWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
DB 172 DPVETWMDVVEYFTEAGFPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQGHFEDDDP 533
DB 232 HHKVLQGHFEDDDP 247

RESULT 29

US-10-616-187-4
; Sequence 4, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0

plagus cuniculus

14.1%; Score 76; DB 15; Length 252;
city 100.0%; Pred. No. 3e-51;
inservative 0; Mismatches 0; Indels 0; Gaps 0;

TVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517
TVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 231
LQOQHFEEDDP 533
LQOQHFEEDDP 247

cation US/09962055
0052033A1
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA

RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA:
CATION NUMBER: US/09/962,055
G DATE: 24-Sep-2001
ICATION DATA:
CATION NUMBER: 08/979,608
G DATE: 26-NOV-1997
CATION NUMBER: US 60/031,930
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
PHONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 2:
CHARACTERISTICS:
H: 317 amino acids
amino acid
OGY: linear
YPE: protein
DESCRIPTION: SEQ ID NO: 2:
14.1%; Score 76; DB 9; Length 317;
urity 100.0%; Pred. No. 3.6e-51;
inservative 0; Mismatches 0; Indels 0; Gaps 0;

TVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKIYE 517

Db 237 DPVETVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKI
QY 518 HHKVLQOQHFEEDDP 533
Db 297 HHKVLQOQHFEEDDP 312

RESULT 31
US-09-976-740-2
; Sequence 2, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(317)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-976-740-2

Query Match 14.1%; Score 76; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVETVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKI
Db 237 DPVETVMDVVEYFTEAGPPEQATFQEQEIDGKSLLMQRTDVLTLGLSIRLGPALKI
QY 518 HHKVLQOQHFEEDDP 533
Db 297 HHKVLQOQHFEEDDP 312

RESULT 32
US-10-671-242-2
; Sequence 2, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14

IN NUMBER: US 09/517,849
TE: 2000-03-02
IN NUMBER: US 08/979,608
TE: 1997-11-26
IN NUMBER: US 60/031,930
TE: 1996-11-27
IN NUMBER: US 60/048,547
TE: 1997-06-03
J NOS: 53
SEQ for Windows Version 4.0

tolagus cuniculus

ANT
..(317)
ION: Xaa = Any Amino Acid

14.1%; Score 76; DB 12; Length 317;
arity 100.0%; Pred. No. 3.6e-51;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

WTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
WTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
WTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL

VLOQGHFEDDDP 533
VLOQGHFEDDDP 312

ication US/10023529
US20020129388A1
ION:

.. Ann M.
.. Robert S.
.. Simon W.
ona, Anibal A.
ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001

ION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

tolagus cuniculus

IANT
...(317)
ION: Xaa = Any Amino Acid

14.1%; Score 76; DB 13; Length 317;
larity 100.0%; Pred. No. 3.6e-51;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQOQHFEEDDDP 533
Db 297 HHKVLQOQHFEEDDDP 312

RESULT 34

US-10-023-523-2
; Sequence 2, Application US/10023523
; Publication NO. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(317)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-023-523-2

Query Match 14.1%; Score 76; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 76; Conservative 0; Mismatches 0; Indels 0;

QY 458 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
Db 237 DPVEWTMDVVEYFTEAGFPQATAFQOEIDGKSLLMQRTDVLTLGLSIRLGPAL
QY 518 HHKVLQOQHFEEDDDP 533
Db 297 HHKVLQOQHFEEDDDP 312

RESULT 35

US-10-616-187-2
; Sequence 2, Application US/10616187
; Publication NO. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREA
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001

1:33:40 2004

us-09-976-740-43.olog.rapb

P:

ON NUMBER: US/10/616,187
TE: 2003-07-09
I NUMBER: US/09/616,289
I: 2000-07-14
I NUMBER: US 09/517,849
I: 2000-03-02
I NUMBER: US 08/979,608
I: 1997-11-26
I NUMBER: US 60/031,930
I: 1996-11-27
I NUMBER: US 60/048,547
I: 1997-06-03
NOS: 53
for Windows Version 4.0

lagus cuniculus

VT
(317)

DN: Xaa = Any Amino Acid

14.1%; Score 76; DB 15; Length 317;
rity 100.0%; Pred. No. 3.6e-51;
servative 0; Mismatches 0; Indels 0; Gaps 0;

IVMDVVEYFTAGPPEQATFQEQEIDGKLLMORTDVLTLGSLRGLPKIYE 517
IVMDVVEYFTAGPPEQATFQEQEIDGKLLMORTDVLTLGSLRGLPKIYE 296

LOQHFPEDDP 533
LOQHFPEDDP 312

ication US/09962055
052033A1
TION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.

Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSES: Fish & Richardson P.C.

T: 225 Franklin Street

Boston

: MA

RY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/962,055

IG DATE: 24-Sep-2001

ICATION DATA:

ICATION NUMBER: 08/979,608

IG DATE: 26-NOV-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

: Myers, Louis

STRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981:
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-962-055-20

Query Match

Best Local Similarity 4.8%; Score 26; DB 9; Length 26;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 329 EEEEDDEDEDEDDVSGSEVPESD 354

Db 1 EEEEDDEDEDEDDVSGSEVPESD 26

RESULT 37

US-09-976-740-20

; Sequence 20, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATI

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/976,740

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 26

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-976-740-20

Query Match 4.8%; Score 26; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.6e-13; Indels 0; Gaps

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 329 EEEEDDEDEDEDDVSGSEVPESD 354

Db 1 EEEEDDEDEDEDDVSGSEVPESD 26

RESULT 38

US-10-671-242-20

; Sequence 20, Application US/10671242

; Publication No. US20040040049A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATI

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATI

ION: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/10/671,242
DATE: 2003-09-24
ON NUMBER: US/09/616,289
TE: 2000-07-14
ON NUMBER: US 09/517,849
TE: 2000-03-02
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

> sapiens

4.8%; Score 26; DB 12; Length 26;
arity 100.0%; Pred. No. 5.6e-13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3DDDEDEDDVSGSEVPESD 354
|||||
3DDDEDEDDVSGSEVPESD 26

Application US/10023529
US20020129388A1
TION:
s, Ann M.
as, Robert S.
ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
: 10797-004001
TION NUMBER: US/10/023,529
DATE: 2001-12-17
ION NUMBER: 09/616,289
ATE: 2000-07-14
ION NUMBER: US 09/517,849
ATE: 2000-03-02
ION NUMBER: US 08/979,608
ATE: 1997-11-26
ION NUMBER: US 60/031,930
ATE: 1996-11-27
ION NUMBER: US 60/048,547
ATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

> sapiens

4.8%; Score 26; DB 13; Length 26;
arity 100.0%; Pred. No. 5.6e-13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3DDDEDEDDVSGSEVPESD 354
|||||
3DDDEDEDDVSGSEVPESD 26

RESULT 40

US-10-023-523-20
; Sequence 20, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-523-20

Query Match 4.8%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 329 EEEEDDEDEDDVSGSEVPESD 354
|||||
DB 1 EEEEDDEDEDDVSGSEVPESD 26

RESULT 41

US-10-616-187-20
; Sequence 20, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens

4.8%; Score 26; DB 15; Length 26;
rity 100.0%; Pred. No. 5.6e-13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDDYSEGESEVPESD 354
|||||
DDEDEDDYSEGESEVPESD 26

ication US/09962055
0052033A1
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
SEQUENCES: 42
ENCE ADDRESS:
SSEER: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
: MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible
TING SYSTEM: DOS
ARE: FastSeq for Windows Version 2.0
PLICATION DATA: US/09/962,055
G DATE: 24-Sep-2001
ICATION DATA:
CATION NUMBER: 08/979,608
G DATE: 26-NOV-1997
CATION NUMBER: US 60/031,930
G DATE: 27-NOV-1996
GENT INFORMATION:
Myers, Louis
TRATION NUMBER: 35,965
ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
ICATION INFORMATION:
HONE: 617/542-5070
AX: 617/542-8906
SEQ ID NO: 19;
HARACTERISTICS:
H: 15 amino acids
amino acid
OGY: linear
YPE: protein
ESCRPTION: SEQ ID NO: 19;

2.8%; Score 15; DB 9; Length 15;
rity 100.0%; Pred. No. 0.00014;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DDEDEDEDD 343
|||||
DDEDEDEDD 15

ication US/09976740
S20020194633A1

GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-740-19

Query Match 2.8%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 329 EEEEDDEDEDD 343
DB 1 EEEEDDEDEDD 15

RESULT 44
US-10-671-242-19
; Sequence 19, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-242-19

Query Match 2.8%; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

DDDEDEDD 343
|||||
DDDEDEDD 15

lication US/10023529

US20020129389A1

ION:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,529

DATE: 2001-12-17

ON NUMBER: 09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

EQ for Windows Version 4.0

sapiens

2.8%; Score 15; DB 13; Length 15;
arity 100.0%; Pred. No. 0.00014;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

DDDEDEDD 343

|||||

DDDEDEDD 15

lication US/10023523

US20020152485A1

ION:

, Ann M.

s, Robert S.

, Simon W.

ona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,523

DATE: 2001-12-17

ON NUMBER: US/09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-023-523-19

Query Match

2.8%; Score 15; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDEDEDD 343

|||||

Db 1 EEEEDDEDEDD 15

RESULT 47

US-10-616-187-19

; Sequence 19, Application US/10616187

; Publication No. US20040013668A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/10/616,187

; CURRENT FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: US/09/616,289

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-616-187-19

Query Match

2.8%; Score 15; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; G

Qy 329 EEEEDDEDEDD 343

|||||

Db 1 EEEEDDEDEDD 15

RESULT 48

US-10-221-625-66

; Sequence 66, Application US/10221625

; Publication No. US20040033942A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: HILLMAN, Jennifer L.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: PATTERSON, Chandra

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: BANDMAN, Olga

; APPLICANT: TANG, Y. Tom

UR, Preete
Y, Purvi

OUNG, Janice

Y, Roopa

ON: TRANSCRIPTION FACTORS

PF-0761 PCT

ION NUMBER: US/10/221,625

ATE: 2001-03-13

NOS: 214

rogram

sapiens

feature

ION: Incyte ID No. US20040033942A1 2672566CD1

urity 2.8%; Score 15; DB 12; Length 102;

nservative 100.0%; Pred.No. 0.00069;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EDGKSLILM 496

|||||

EDGKSLILM 65

pplication US/10094749

IS20030219741A1

ION:

AI, TAKAO

YAMA, TOMOYASU

IKI, TETSUJI

AMATSU, AI

), HIROYUKI

LI, SHIZUKO

AMOTO, JUN-ICHI

MO, YUUKO

YURI

YKA, KAORU

AI, KEIICHI

RYOTARO

CHIKA, ICHIRO

NAOHIKO

IKAWA, TSUTOMU

IKAWA, MOTOFUKI

AHARI, KENJI

HO, YASUHIKO

ION: NOVEL FULL-LENGTH CDNA

084335/0160

ION NUMBER: US/10/094,749

DATE: 2002-03-12

ION NUMBER: 60/350,435

TE: 2002-01-24

ION NUMBER: JP 2001-328381

TE: 2001-09-14

NOS: 3381

In Ver. 2.1

sapiens

urity 2.8%; Score 15; DB 15; Length 116;

nservative 100.0%; Pred.No. 0.00077;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

EDGKSLILM 496

|||||

Db 65 AFOEQEIDGKSLILM 79

RESULT 50

US-09-962-055-21

; Sequence 21, Application US/09962055

; Patent No. US20020052033A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNO
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/962,055

; FILING DATE: 24-Sep-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608

; FILING DATE: 26-NOV-1997

; APPLICATION NUMBER: US 60/031,930

; FILING DATE: 27-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-962-055-21

Query Match 2.0%; Score 11; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; G

Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 344 VSEGEVPEPSD 354

|||||

Db 1 VSEGEVPEPSD 11

RESULT 51

US-09-976-740-21

; Sequence 21, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT

; TITLE OF INVENTION: ATHEROSCLEROSIS

11:33:40 2004

us-09-976-740-43.olig.rapb

10797-004001
Publication No. US/09/976,740
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
PRIORITY FILING DATE: 2001-12-17
PRIORITY APPLICATION NUMBER: 09/616,289
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/517,849
PRIORITY FILING DATE: 2000-03-02
PRIORITY APPLICATION NUMBER: US 08/979,608
PRIORITY FILING DATE: 1997-11-26
PRIORITY APPLICATION NUMBER: US 60/031,930
PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens

sapiens

2.0%; Score 11; DB 9; Length 11;
Identity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 11

Publication US/10671242
US2004004049A1
TITLE: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
PRIORITY FILING DATE: 2003-09-24
PRIORITY APPLICATION NUMBER: US/09/616,289
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/517,849
PRIORITY FILING DATE: 2000-03-02
PRIORITY APPLICATION NUMBER: US 08/979,608
PRIORITY FILING DATE: 1997-11-26
PRIORITY APPLICATION NUMBER: US 60/031,930
PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens

sapiens

2.0%; Score 11; DB 12; Length 11;
Identity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 11

Publication US/10023529

Publication No. US20020129389A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
PRIORITY FILING DATE: 2001-12-17
PRIORITY APPLICATION NUMBER: 09/616,289
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/517,849
PRIORITY FILING DATE: 2000-03-02
PRIORITY APPLICATION NUMBER: US 08/979,608
PRIORITY FILING DATE: 1997-11-26
PRIORITY APPLICATION NUMBER: US 60/031,930
PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-529-21

Query Match 2.0%; Score 11; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 344 VSEGEVPESD 354
|||||||
DB 1 VSEGEVPESD 11

RESULT 54
US-10-023-523-21
Sequence 21, Application US/10023523
Publication No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
PRIORITY FILING DATE: 2001-12-17
PRIORITY APPLICATION NUMBER: US/09/616,289
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 09/517,849
PRIORITY FILING DATE: 2000-03-02
PRIORITY APPLICATION NUMBER: US 08/979,608
PRIORITY FILING DATE: 1997-11-26
PRIORITY APPLICATION NUMBER: US 60/031,930
PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-523-21

Query Match 2.0%; Score 11; DB 13; Length 11;

ity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EVPSD 354
|||||
EVPSD 11

ication US/10616187
S20040013668A1
ON:
Ann M.
, Robert S.
, Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS
10797-004001
ION NUMBER: US/10/616,187
ATE: 2003-07-09
N NUMBER: US/09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

sapiens

2.0%; Score 11; DB 15; Length 11;
ity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
EVPSD 354
|||||
EVPSD 11

ication US/09962055
0052033A1
TION:
Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
NVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42
ENCE ADDRESS:
SSEE: Fish & Richardson P.C.
T: 225 Franklin Street
Boston
MA
RY: USA
02110-2804
EADABLE FORM:
M TYPE: Diskette
TER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-962-055-27

Query Match 2.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 VSEGEVPSD 354
Db 2 VSEGEVPSD 12

RESULT 57
US-09-976-740-27
Sequence 27, Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 12
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-976-740-27

Query Match 2.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 344 VSEGEVPSD 354
Db 2 VSEGEVPSD 12

```
Publication US/10671242
US20040040049A1
ION:
, Ann M.
s, Robert S.
, Simon W.
ona, Anibal A.
ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/10/671,242
DATE: 2003-09-24
ON NUMBER: US/09/616,289
TE: 2000-07-14
ON NUMBER: US/09/517,849
TE: 2000-03-02
ON NUMBER: US/08/979,608
TE: 1997-11-26
ON NUMBER: US/60/031,930
TE: 1996-11-27
ON NUMBER: US/60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

2.0%; Score 11; DB 12; Length 12;
arity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
SEVPESD 354
|||||
SEVPESD 12

lication US/10023529
US20020129388A1
ION:
, Ann M.
s, Robert S.
, Simon W.
ona, Anibal A.
ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ION: ATHEROSCLEROSIS
10797-004001
TION NUMBER: US/10/023,529
DATE: 2001-12-17
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US/09/517,849
TE: 2000-03-02
ON NUMBER: US/08/979,608
TE: 1997-11-26
ON NUMBER: US/60/031,930
TE: 1996-11-27
ON NUMBER: US/60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0
```

```
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-27

Query Match 2.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; C

QY 344 VSEGEVPESED 354
|||||
Db 2 VSEGEVPESED 12

RESULT 60
US-10-023-523-27
; Sequence 27, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-27

Query Match 2.0%; Score 11; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; C

QY 344 VSEGEVPESED 354
|||||
Db 2 VSEGEVPESED 12

RESULT 61
US-10-616-187-27
; Sequence 27, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
```

E: 2000-03-02
 IN NUMBER: US 08/979,608
 E: 1997-11-26
 IN NUMBER: US 60/031,930
 E: 1996-11-27
 IN NUMBER: US 60/048,547
 E: 1997-06-03
 NOS: 53
 Q for Windows Version 4.0

olagus cuniculus

2.0%; Score 11; DB 15; Length 12;
 rity 100.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

EVPSD 354
 |||||
 EVPSD 12

ication US/09962055
 0052033A1

ATION:
 Lees, Ann M.
 Lees, Robert S.
 Law, Simon W.

Arjona, Anibal A.

VENTION: NOVEL LOW DENSITY LIPOPROTEIN
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 TREATING ATHEROSCLEROSIS

SEQUENCES: 42

ENCE ADDRESS:

SSER: Fish & Richardson P.C.

T: 225 Franklin Street

Boston

MA

RY: USA

02110-2804

EADABLE FORM:

M TYPE: Diskette

TER: IBM Compatible

TING SYSTEM: DOS

ARE: FastSeq for Windows Version 2.0

PLICATION DATA:

CATION NUMBER: US/09/962,055

G DATE: 24-Sep-2001

ICATION DATA:

CATION NUMBER: 08/979,608

G DATE: 26-NOV-1997

CATION NUMBER: US 60/031,930

G DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

TRATION NUMBER: 35,965

ENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

AX: 617/542-8906

SEQ ID NO: 26;

CHARACTERISTICS:

H: 28 amino acids

amino acid

OGY: linear

YPE: protein

SCRIPTION: SEQ ID NO: 26;

Query Match 2.0%; Score 11; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; G;

QY 344 VSEGSEVPESD 354
 |||||
 Db 18 VSEGSEVPESD 28

RESULT 63

US-09-976-740-26
 ; Sequence 26, Application US/09976740
 ; Publication No. US20020194633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREAT-
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT-
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/976,740
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-976-740-26

Query Match 2.0%; Score 11; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.31;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; G;

QY 344 VSEGSEVPESD 354
 |||||
 Db 18 VSEGSEVPESD 28

RESULT 64

US-10-671-242-26
 ; Sequence 26, Application US/10671242
 ; Publication No. US20040040049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT-
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/10/671,242
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: US/09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547

TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

US

tolagus cuniculus

2.0%; Score 11; DB 12; Length 28;
arity 100.0%; Pred. No. 0.31;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 28

lication US/10023529
US20020129388A1

TON:

s, Robert S.

, Ann M.

, Simon W.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

TION NUMBER: US/10/023,529

DATE: 2001-12-17

ON NUMBER: 09/616,289

TE: 2000-07-14

ON NUMBER: US 09/517,849

TE: 2000-03-02

ON NUMBER: US 08/979,608

TE: 1997-11-26

ON NUMBER: US 60/031,930

TE: 1996-11-27

ON NUMBER: US 60/048,547

TE: 1997-06-03

D NOS: 53

EQ for Windows Version 4.0

tolagus cuniculus

2.0%; Score 11; DB 13; Length 28;
arity 100.0%; Pred. No. 0.31;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

SEVPESD 354
|||||||
SEVPESD 28

lication US/10023523
US20020152485A1

TON:

s, Robert S.

, Ann M.

, Simon W.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

10797-004001

; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-26

Query Match 2.0%; Score 11; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; C

QY 344 VSEGSEVPESD 354

|||||||

DB 18 VSEGSEVPESD 28

RESULT 67

US-10-616-187-26
; Sequence 26, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREAT
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-616-187-26

Query Match 2.0%; Score 11; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 344 VSEGSEVPESD 354

|||||||

DB 18 VSEGSEVPESD 28

RESULT 68

US-10-357-322-12

```
ication US/10357322
IS20030180769A1
ION:
a et al.
ION: SCAY GENE AND METHODS OF USE
Regents of the University of Minnesota
TION NUMBER: US/10/357,322
DATE: 2003-02-03
ON NUMBER: US/09/684,843
CE: 2000-10-06
ON NUMBER: 60/056,170
CE: 1997-08-19
ON NUMBER: 09/135,994
CE: 1998-08-18
ONOS: 14
In Ver. 2.0

sapiens
2.0%; Score 11; DB 14; Length 129;
arity 100.0%; Pred. No. 1.1;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

pppppq 232
|||||
pppppq 44

Application US/10425114
IS20040034889A1
ION:
Jingdong
Yihua
lic, David K.
en, Steven E
ska, Jack E
Yongwei
ION: Nucleic Acid Molecules and Other Molecules Associated with
ION: Plants and Uses Thereof for Plant Improvement
38-21(53313)B
TION NUMBER: US/10/425,114
DATE: 2003-04-28
NOS: 73128

re max

ON: Clone ID: JC-GMLE01810087E09_FLI.pep
2.0%; Score 11; DB 12; Length 135;
arity 100.0%; Pred. No. 1.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
TTAAAA 22
|||||
TTAAAA 101

ication US/09810264
0076775A1
ION:
du, Virginia C.
du, Omolayo O.
Xu
```

```
APPLICANT: Lu, Guihua
APPLICANT: Zhang, Lingyu
TITLE OF INVENTION: WRKY Transcription Factors and Methods
FILE REFERENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 189
TYPE: PRT
ORGANISM: Oryza sativa
US-09-810-264-20

Query Match 2.0%; Score 11; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 133 PPPPPAPVAAA 143
Db 104 PPPPPAPVAAA 114

RESULT 71
US-10-108-260A-4241
Sequence 4241, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4241
LENGTH: 334
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-4241

Query Match 2.0%; Score 11; DB 15; Length 334;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 225 QPPPPQPPPP 235
Db 230 QPPPPQPPPP 240

RESULT 72
US-10-184-644-319
Sequence 319, Application US/10184644
Publication No. US2003004930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCI
FILE REFERENCE: P3430RIC227
CURRENT APPLICATION NUMBER: US/10/184,644
```

11:33:40 2004

us-09-976-740-43.olig.rapb

DATE: 2002-06-28
on removed - See File Wrapper or Palm
ID NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2103;
arity 100.0%; Pred. No. 11;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||||
ATTAAAA 521

Application US/10184634
US20030068684A1

ION:

Kevin P.

an, Jian

noyers, Luc

Idard, Audrey

owski, Paul J.

ney, Austin L.

James

th, Victoria

anabe, Colin K.

od, William I.

ing, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

3430R1C217

ATION NUMBER: US/10/184,634

DATE: 2002-06-28

on removed - See File Wrapper or Palm

ID NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2103;
arity 100.0%; Pred. No. 11;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||||
ATTAAAA 521

Application US/10063685
US20030180909A1

ION:

an, Dan L.

lvoroff, Ellen

rittsen, Mary E.

Idard, Audrey

dowski, Paul J.

imaldi, Christopher J.

ney, Austin L.

tanabe, Colin K.

od, William I.

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

3430R1C1

CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 105

LENGTH: 2103

TYPE: DNA

ORGANISM: Homo Sapien

US-10-063-685-105

Query Match 2.0%; Score 11; DB 14; Length 2103;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 12 TAAATTTAAAA 22
|||||||
DB 511 TAAATTTAAAA 521

RESULT 75

US-10-184-644-333

Sequence 333, Application US/10184644

Publication No. US2003004930A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C227

CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 333

LENGTH: 2340

TYPE: DNA

ORGANISM: Homo Sapien

US-10-184-644-333

Query Match 2.0%; Score 11; DB 14; Length 2340;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 12 TAAATTTAAAA 22
|||||||
DB 2329 TAAATTTAAAA 2339

RESULT 76

US-10-184-634-333

Sequence 333, Application US/10184634

Publication No. US20030068684A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

11:33:40 2004

us-09-976-740-43.olig.rapb

I

ON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ON: ACIDS ENCODING THE SAME
P3430R1C217
ION NUMBER: US/10/184,634
ATE: 2002-06-28
n removed - See File Wrapper or Palm
NOS: 612

Sapien

2.0%; Score 11; DB 14; Length 2340;
urity 100.0%; Pred.No.13;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

WTAAAA 22
|||||
WTAAAA 2339

ication US/09962055
0052033A1
ATION:

Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.

INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS

SEQUENCES: 42

DENCE ADDRESS:

ESSEE: Fish & Richardson P.C.
ET: 225 Franklin Street
Boston
MA

RY: USA

02110-2804

READABLE FORM:

IM TYPE: Diskette

ITER: IBM Compatible

ATING SYSTEM: DOS

ARE: FastSEQ for Windows Version 2.0

PLICATION DATA:

ICATION NUMBER: US/09/962,055

IG DATE: 24-Sep-2001

ICATION DATA:

ICATION NUMBER: 08/979,608

IG DATE: 26-NOV-1997

ICATION NUMBER: US 60/031,930

IG DATE: 27-NOV-1996

AGENT INFORMATION:

Myers, Louis

ISTRATION NUMBER: 35,965

ERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

ICATION INFORMATION:

PHONE: 617/542-5070

FAX: 617/542-8906

SEQ ID NO: 22:

CHARACTERISTICS:

CH: 10 amino acids

: amino acid

OGY: linear

TYPE: protein

DESCRIPTION: SEQ ID NO: 22:

urity 1.9%; Score 10; DB 9; Length 10;
urity 100.0%; Pred.No. 0.81;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G:
QY 529 EDDDPDGFGLG 538
Db |||||
1 EDDDPDGFGLG 10

RESULT 78

US-09-962-055-28

; Sequence 28, Application US/09962055

; Patent No. US20020052033A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; Lees, Robert S.

; Law, Simon W.

; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNO
TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/962,055

; FILING DATE: 24-Sep-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/979,608

; FILING DATE: 26-NOV-1997

; APPLICATION NUMBER: US 60/031,930

; FILING DATE: 27-NOV-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Myers, Louis

; REGISTRATION NUMBER: 35,965

; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/598

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-962-055-28

Query Match

Best Local Similarity 1.9%; Score 10; DB 9; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G:

QY 432 PPGKPALPGA 441

Db |||||

1 PPGKPALPGA 10

RESULT 79

US-09-976-740-22

; Sequence 22, Application US/09976740

; Publication No. US20020194633A1

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/09/976,740
DATE: 2001-10-12
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 08/979,608
TE: 1997-11-26
TE: 1996-11-27
ON NUMBER: US 60/031,930
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

, sapiens

1.9%; Score 10; DB 9; Length 10;
arity 100.0%; Pred.No. 0.81; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PDGFLG 538
||||||
PDGFLG 10

lication US/09976740
US20020194633A1
TION:

, Ann M.
s, Robert S.
, Simon W.

ona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/09/976,740
DATE: 2001-10-12
ON NUMBER: 09/616,289
TE: 2000-07-14
ON NUMBER: US 08/979,608
TE: 1997-11-26
ON NUMBER: US 60/031,930
TE: 1996-11-27
ON NUMBER: US 60/048,547
TE: 1997-06-03
D NOS: 53
EQ for Windows Version 4.0

tolagus cuniculus

1.9%; Score 10; DB 9; Length 10;
arity 100.0%; Pred.No. 0.81; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441
||||||
PALPGA 10

US-10-671-242-22
; Sequence 22, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-242-22

Query Match 1.9%; Score 10; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 529 EDDPDGFLG 538
DB 1 EDDPDGFLG 10
|||||||
|

RESULT 82
US-10-671-242-28
; Sequence 28, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-671-242-28

1.9%; Score 10; DB 12; Length 10;
rity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

ALPGA 441
|||||
ALPGA 10

ication US/10023529
S20020129388A1

ON:
Ann M.
, Robert S.
, Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS

10797-004001
ION NUMBER: US/10/023,529
ATE: 2001-12-17
N NUMBER: 09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26
N NUMBER: US 60/031,930
E: 1996-11-27
N NUMBER: US 60/048,547
E: 1997-06-03
NOS: 53
Q for Windows Version 4.0

sapiens

1.9%; Score 10; DB 13; Length 10;
rity 100.0%; Pred. No. 0.81; 0; Indels 0; Gaps 0;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DGFLG 538
|||||
DGFLG 10

ication US/10023529
S20020129388A1

ON:
Ann M.
, Robert S.
, Simon W.
na, Anibal A.
ON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
ON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
ON: ATHEROSCLEROSIS

10797-004001
ION NUMBER: US/10/023,529
ATE: 2001-12-17
N NUMBER: 09/616,289
E: 2000-07-14
N NUMBER: US 09/517,849
E: 2000-03-02
N NUMBER: US 08/979,608
E: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-28

Query Match 1.9%; Score 10; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 PPGKALPGA 441
Db 1 PPGKALPGA 10

RESULT 85

US-10-023-523-22
; Sequence 22, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-523-22

Query Match 1.9%; Score 10; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 EDDPDGFLG 538
Db 1 EDDPDGFLG 10

RESULT 86

US-10-023-523-28
; Sequence 28, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TON: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/10/023,523
DATE: 2001-12-17
ON NUMBER: US/09/616,289
TE: 2000-07-14
ON NUMBER: US/09/517,849
TE: 2000-03-02
ON NUMBER: US/08/979,608
TE: 1997-11-26
ON NUMBER: US/60/031,930
TE: 1996-11-27
ON NUMBER: US/60/048,547
TE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

ctolagus cuniculus

1.9%; Score 10; DB 13; Length 10;
arity 100.0%; Pred.No. 0.81; 0; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PALPGA 441
|||||
PALPGA 10

lication US/10616187
US20040013668A1

TON:

is, Ann M.

is, Robert S.

ona, Anibal A.

TON: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TON: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TON: ATHEROSCLEROSIS

10797-004001
TION NUMBER: US/10/616,187
DATE: 2003-07-09
ON NUMBER: US/09/616,289
TE: 2000-07-14
ON NUMBER: US/09/517,849
TE: 2000-03-02
ON NUMBER: US/08/979,608
TE: 1997-11-26
ON NUMBER: US/60/031,930
TE: 1996-11-27
ON NUMBER: US/60/048,547
TE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

sapiens

1.9%; Score 10; DB 15; Length 10;
arity 100.0%; Pred.No. 0.81; 0; Indels 0; Gaps 0;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PDGFLG 538
|||||
PDGFLG 10

RESULT 88

US-10-616-187-28
; Sequence 28, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US/09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US/08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US/60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US/60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-616-187-28

Query Match 1.9%; Score 10; DB 15; Length 10;
Best Local Similarity 100.0%; Pred.No. 0.81;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QY 432 PPGKPALPGA 441

|||||

Db 1 PPGKPALPGA 10

RESULT 89

US-10-424-599-175120
; Sequence 175120, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 175120
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(142)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129151C.1.pep
US-10-424-599-175120

Query Match 1.9%; Score 10; DB 12; Length 142;
Best Local Similarity 100.0%; Pred.No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

TAPPS 161
|||||
TAPPS 62

Application US/10425114
US20040034888A1

ON:

Jingdong

Yihua

Li, David K.

en, Steven E.

uska, Jack E

Yongwei

ON: Nucleic Acid Molecules and Other Molecules Associated With
ON: Plants and Uses Thereof for Plant Improvement

38-21(53223)B

ION NUMBER: US/10/425,114

ATE: 2003-04-28

NOS: 73128

ays

ON: Clone ID: LIB3356-019-E1_FLI.pep

1.9%; Score 10; DB 12; Length 154;
rity 100.0%; Pred. No. 7.9;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 127

|||||

AAAA 152

8

Application US/10424599

US20040031072A1

ON:

La Rosa Thomas J

lic David K

Yihua

Yongwei

ON: Soy Nucleic Acid Molecules and Other Molecules Associated With
ON: Plants and Uses Thereof for Plant Improvement

38-21(53223)B

ION NUMBER: US/10/424,599

ATE: 2003-04-28

NOS: 285684

ne max

ON: Clone ID: PAT_MRT3847_97045C.1.pep

8

1.9%; Score 10; DB 12; Length 181;

rity 100.0%; Pred. No. 9;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 127

|||||

AAAA 170

US-10-424-599-188876
; Sequence 188876, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 188876

; LENGTH: 187

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_14156C.1.pep

US-10-424-599-188876

Query Match 1.9%; Score 10; DB 12; Length 187;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEED 342

|||||

Db 96 DDEDEDEED 105

RESULT 93

US-10-424-599-224491

; Sequence 224491, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 224491

; LENGTH: 188

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_44746C.1.pep

US-10-424-599-224491

Query Match 1.9%; Score 10; DB 12; Length 188;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEED 342

|||||

Db 98 DDEDEDEED 107

RESULT 94

US-10-282-122A-45132

; Sequence 45132, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlser, Karl

11:33:40 2004

us-09-976-740-43.olog.rabb

kind, Judith
l, Daniel
wick, John
r, Grant
amoto, Robert
syth, R.
H.

TON: Identification of Essential Genes in Microorganisms

ELITRA.034A

ATION NUMBER: US/10/282,122A

DATE: 2003-02-20

ON NUMBER: 60/191,078

TE: 2000-03-21

ON NUMBER: 60/206,848

TE: 2000-05-23

ON NUMBER: 60/207,727

TE: 2000-05-26

ON NUMBER: 60/230,335

TE: 2000-09-06

ON NUMBER: 60/230,347

TE: 2000-09-09

ON NUMBER: 60/242,578

TE: 2000-10-23

ON NUMBER: 60/253,625

TE: 2000-11-27

ON NUMBER: 60/257,931

TE: 2000-12-22

ON NUMBER: 60/267,636

TE: 2001-02-09

ON NUMBER: 60/269,308

TE: 2001-02-16

Application data removed - See File Wrapper or PALM.

ID NOS: 78614

itIn version 3.1

etobacter baumannii

.32

arity 1.9%; Score 10; DB 12; Length 238;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

'AAAPPA 146

|||||

'AAAPPA 141

14 Application US/10425114

US2004003488A1

ATION:

Jingdong

u, Yihua

alic, David K.

reen, Steven E

aska, Jack E

), Yongwei

ATION: Nucleic Acid Molecules and Other Molecules Associated With

ATION: Plants and Uses Thereof for Plant Improvement

: 38-21(5313)B

ATION NUMBER: US/10/425,114

DATE: 2003-04-28

ID NOS: 73128

mays

ATION: Clone ID: UC-ZMELMO17014A11_FLI pep

04

Query Match 1.9%; Score 10; DB 12; Length 253;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QY 118 APAAAAAAP 127

|||||

Db 244 APAAAAAAP 253

RESULT 96

US-10-425-114-50072

; Sequence 50072, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assc

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 50072

; LENGTH: 307

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3594-013-A4_FLI pep

US-10-425-114-50072

Query Match

Best Local Similarity 1.9%; Score 10; DB 12; Length 307;

Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QY 120 AAAAAAAPPP 129

|||||

Db 239 AAAAAAAPPP 248

RESULT 97

US-10-425-114-64408

; Sequence 64408, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assc

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 64408

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3732-052-H7_FLI pep

US-10-425-114-64408

Query Match

Best Local Similarity 1.9%; Score 10; DB 12; Length 361;

Matches 10; Conservative 0; Mismatches 0; Indels 0; C

SSSAA 27
|||||
SSSAA 88

9 Application US/10424599
US20040031072A1

ON:

isa Thomas J

ilic David K

Yihua

Yongwei

ON: Soy Nucleic Acid Molecules and Other Molecules Associated With

ON: Plants and Uses Thereof for Plant Improvement

38-21(53223)B

ION NUMBER: US/10/424,599

ATE: 2003-04-28

NOS: 285684

ne max

ON: Clone ID: PAT_MRT3847_74372C.1.pap

9

1.9%; Score 10; DB 12; Length 368;

ity 100.0%; Pred. No. 16;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

ATAPP 160

|||||

ATAPP 37

Application US/10369493

US20030233675A1

ON:

Yongwei

ile, Gregory J.

er, Steven C.

man, Barry S.

Li, Xianfeng

ON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

ON: PLANTS WITH IMPROVED PROPERTIES

38-10(52052)B

ION NUMBER: US/10/369,493

ATE: 2003-02-28

ION NUMBER: US 60/360,039

E: 2002-02-21

NOS: 47374

ionomas campestris

1.9%; Score 10; DB 15; Length 401;

ity 100.0%; Pred. No. 17;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127

|||||

AAAAA 112

.ication US/10229345

; Publication No. US20040038220A1
; GENERAL INFORMATION:
; APPLICANT: MARKOWITZ, Sanford D.
; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
; FILE REFERENCE: CWRU-P01-003
; CURRENT APPLICATION NUMBER: US/10/229,345
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-229-345-18

Query Match 1.9%; Score 10; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 178 AAPPAPAAP 187

|||||

DB 236 AAPPAPAAP 245

RESULT 101

US-10-274-177-18

; Sequence 18, Application US/10274177

; Publication No. US20040038225A1

; GENERAL INFORMATION:

; APPLICANT: MARKOWITZ, Sanford D.

; TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS

; FILE REFERENCE: CWRU-P01-003

; CURRENT APPLICATION NUMBER: US/10/274,177

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/10/229,345

; PRIOR FILING DATE: 2002-08-26

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 402

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-274-177-18

Query Match 1.9%; Score 10; DB 12; Length 402;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 178 AAPPAPAAP 187

|||||

DB 236 AAPPAPAAP 245

RESULT 102

US-10-087-080-32

; Sequence 32, Application US/10087080

; Publication No. US20030235820A1

; GENERAL INFORMATION:

; APPLICANT: Mack, David H.

; APPLICANT: Markowitz, Sanford David

; APPLICANT: Eos Biotechnology, Inc.

; APPLICANT: Case Western Reserve University

; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Me

; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening i

; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

; FILE REFERENCE: 018501-0008400S

; CURRENT APPLICATION NUMBER: US/10/087,080

; CURRENT FILING DATE: 2002-10-25

; PRIOR APPLICATION NUMBER: US 60/272,206

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 60/281,149

; PRIOR FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: US 60/284,555

TE: 2001-04-17
D NOS: 41
tIn Ver. 2.1

sapiens

TON: winged helix/forkhead transcription factor (HFX1)

1.9%; Score 10; DB 15; Length 402;
arity 100.0%; Pred. No. 17;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

PAPAAP 187

|||||

PAPAAP 245

Application US/10369493
US20030233675A1

TON:

Yongwei
Kle, Gregory J.
ter, Steven C.
dman, Barry S.

et, Xianfeng

TON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TON: PLANTS WITH IMPROVED PROPERTIES

38-10(52052)B

ATION NUMBER: US/10/369,493

DATE: 2003-02-28

ION NUMBER: US 60/360,039

ATE: 2002-02-21

ID NOS: 47374

thomonas campestris

1.9%; Score 10; DB 15; Length 404;
arity 100.0%; Pred. No. 18;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 127

|||||

AAAAAP 115

Application US/10369493
US20030233675A1

TON:

Yongwei
Kle, Gregory J.
ter, Steven C.
ldman, Barry S.

an, Xianfeng

TON: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TON: PLANTS WITH IMPROVED PROPERTIES

38-10(52052)B

ATION NUMBER: US/10/369,493

DATE: 2003-02-28

ION NUMBER: US 60/360,039

ATE: 2002-02-21

ID NOS: 47374

TYPE: PRT
ORGANISM: Xanthomonas campestris
US-10-369-493-16231

Query Match 1.9%; Score 10; DB 15; Length 404;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 118 APAAAAAAP 127

|||||

DB 106 APAAAAAAP 115

RESULT 105

US-10-282-122A-50659

Sequence 50659, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganism

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PAL

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50659

LENGTH: 588

TYPE: PRT

ORGANISM: Burkholderia mallei

US-10-282-122A-50659

Query Match 1.9%; Score 10; DB 12; Length 588;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 118 APAAAAAAP 127

|||||

DB 476 APAAAAAAP 485

RESULT 106

```
13 Application US/10282122A
IS20040029129A1
CON:
  Liangsu
  idio, Carlos
  me, Cheryl
  ilbeck, Robert
  sen, Kari
  kind, Judith
  l, Daniel
  vick, John
  r, Grant
  amoto, Robert
  syth, R.
  H.
[ON: Identification of Essential Genes in Microorganisms
ELITRA.034A
TION NUMBER: US/10/282,122A
)ATE: 2003-02-20
N NUMBER: 60/191,078
TE: 2000-03-21
N NUMBER: 60/206,848
TE: 2000-05-23
N NUMBER: 60/207,727
TE: 2000-05-26
N NUMBER: 60/230,335
TE: 2000-09-06
N NUMBER: 60/230,347
TE: 2000-09-09
N NUMBER: 60/242,578
TE: 2000-10-23
N NUMBER: 60/253,625
TE: 2000-11-27
N NUMBER: 60/257,931
TE: 2000-12-22
N NUMBER: 60/267,636
TE: 2001-02-09
N NUMBER: 60/269,308
TE: 2001-02-16
Application data removed - See File Wrapper or PALM.
NOS: 78614
in version 3.1
```

```
erichia coli
33
```

```
arity 1.9%; Score 10; DB 12; Length 613;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDEED 342
|||||
DEDEED 200
```

```
39 Application US/10282122A
JS20040029129A1
CON:
  Liangsu
  idio, Carlos
  one, Cheryl
  elbeck, Robert
  sen, Kari
  kind, Judith
  l, Daniel
  wick, John
  r, Grant
  amoto, Robert
```

```
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorgan
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74989
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74989
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Query Match 1.9%; Score 10; DB 12; Length 660;
Best Local Similarity 100.0%; Pred. NO. 26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
QY 333 DDEDEDEED 342
|||||
Db 238 DDEDEDEED 247
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RESULT 108
US-10-282-122A-75492
; Sequence 75492, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorgan
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
```

ION NUMBER: 60/230,347
ATE: 2000-09-09
ION NUMBER: 60/242,578
ATE: 2000-10-23
ION NUMBER: 60/253,625
ATE: 2000-11-27
ION NUMBER: 60/257,931
ATE: 2000-12-22
ION NUMBER: 60/267,636
ATE: 2001-02-09
ION NUMBER: 60/269,308
ATE: 2001-02-16
r Application data removed - See File Wrapper or PALM.
ID NOS: 78614
ntin version 3.1

monella typhi
492

1.9%, Score 10; DB 12; Length 660;
larity 100.0%; Pred. No. 26;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EDDEED 342
|||||||
EDEDEED 247

plication US/10627476
US20040030116A1

IIION:

pejus, Mark
gger, Burkhard
oder, Hartwig
lger, Oskar

berhauer, Gregor
TION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

IIION: TRANSPORT

: BGI-125CPCN
TION NUMBER: US/10/627,476
DATE: 2003-07-25

ION NUMBER: 09/602,787

ATE: 2000-06-23

ION NUMBER: USSN 60/141031

ATE: 1999-06-25

ION NUMBER: DE 19931454.3

ATE: 1999-07-08

ION NUMBER: DE 19931478.0

ATE: 1999-07-08

ION NUMBER: DE 19931563.9

ATE: 1999-07-08

ION NUMBER: DE 19932122.1

ATE: 1999-07-09

ION NUMBER: DE 19932124.8

ATE: 1999-07-09

ION NUMBER: DE 19932125.6

ATE: 1999-07-09

ION NUMBER: DE 19932128.0

ATE: 1999-07-09

ION NUMBER: DE 19932180.9

ATE: 1999-07-09

r Application data removed - See File Wrapper or PALM.
ID NOS: 678

ynebacterium glutamicum

Query Match 1.9%; Score 10; DB 12; Length 1277;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAFVAAAAPA 146

Db 984 PAFVAAAAPA 993

RESULT 110

US-10-092-900A-224

; Sequence 224, Application US/10092900A

; Publication No. US20040043382A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Taupier Jr., Raymond J.

; APPLICANT: Pena, Carol E.A.

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: Gorman, Linda

; APPLICANT: Miller, Charles E.

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gangolli, Baha A.

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Guo, Xiaojia Sasha

; APPLICANT: Tchernev, Velizar T.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Liu, Yi

; APPLICANT: Anderson, David W.

; APPLICANT: Spaderna, Steven K.

; APPLICANT: Catterton, Elina

; APPLICANT: Leite, Mario W.

; APPLICANT: Zhong, Hailong

; APPLICANT: Alsobrook, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Aci

; FILE REFERENCE: 21402-290C

; CURRENT APPLICATION NUMBER: US/10/092,900A

; PRIOR FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: USSN 60/274,322

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/283,675

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: USSN 60/338,092

; PRIOR FILING DATE: 2001-12-03

; PRIOR APPLICATION NUMBER: USSN 60/274,281

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/274,191

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/325,681

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: USSN 60/304,354

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: USSN 60/279,995

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: USSN 60/294,899

; PRIOR FILING DATE: 2001-05-31

; PRIOR APPLICATION NUMBER: USSN 60/287,424

; PRIOR FILING DATE: 2001-04-30

; Remaining Prior Application data removed - See File Wrapper or PALM

; NUMBER OF SEQ ID NOS: 768

; SEQ ID NO 224

sapiens

1.9%; Score 10; DB 12; Length 1390;
arity 100.0%; Pred. No. 49;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
PQPPP 235
|||||
PQPPP 986
Application US/10032585
IS20030180953A1
[ON: Roemer D.
Jiang
les, Boone
ird, Bussey
[ON: Gene Disruption Methodologies for Drug Target Discovery
10182-005-999
[ION NUMBER: US/10/032,585
[ATE: 2001-12-20
[NOS: 8000
[In version 3.1

da albicans

1.9%; Score 10; DB 14; Length 1461;
arity 100.0%; Pred. No. 51;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DEEDD 343
|||||
DEEDD 1445

ication US/10073912
IS2003007703A1
[ON:

et al.
[ON: Nucleic Acids, Proteins, and Antibodies
PTZ34C1
[ION NUMBER: US/10/073,912
[ATE: 2002-02-14
[n removed - See file Wrapper or Palm
[NOS: 18
[In Ver. 2.0

sapiens

feature

[ON: n equals a,t,g, or c

1.9%; Score 10; DB 14; Length 1591;
arity 100.0%; Pred. No. 55;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
TAAAA 22
|||||

Db 795 AAAATTAAAA 804

RESULT 113

US-10-142-426-309
; Sequence 309, Application US/10142426
; Publication No. US20040048333A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3330R1C224
; CURRENT APPLICATION NUMBER: US/10/142,426
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 309
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1837
; OTHER INFORMATION: unknown base
US-10-142-426-309

Query Match 1.9%; Score 10; DB 12; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

Db 1826 AAAATTAAAA 1835

RESULT 114

US-10-123-155-309
; Sequence 309, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

11:33:40 2004

us-09-976-740-43. olig.rapb

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
P3330RIC30
TION NUMBER: US/10/123,155
DATE: 2002-04-15
n removed - See Palm or File Wrapper
ID NOS: 550

Sapien

ure

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

TTTTTT

TTAAAA 1835

Application US/10146731
US20030129692A1

ION:

er, Kevin P.
resini, Maureen
orge, Laura
noyers, Luc
lvaroff, Ellen
Wei-Qiang
ritsen, Mary E.
dard, Audrey
lowski, Paul J.
ney, Austin L.
erwood, Steven
ith, Victoria
ewart, Timothy A.
as, Daniel
anabe, Colin K
d, William
ang, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

P3330RIC323

ATION NUMBER: US/10/146,731

DATE: 2002-05-15

ion removed - See File Wrapper or Palm

ID NOS: 550

Sapien

ure

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

TTTTTT

TTAAAA 1835

RESULT 116

US-10-140-472-309

; Sequence 309, Application US/10140472

; Publication No. US2003013888A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; FILE REFERENCE: P3330RIC168

; CURRENT APPLICATION NUMBER: US/10/140,472

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-140-472-309

Query Match

1.9%; Score 10; DB 14; Length 1843;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1826 AAAATTAAAA 1835

RESULT 117

US-10-141-761-309

; Sequence 309, Application US/10141761

; Publication No. US20030148432A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; FILE REFERENCE: P3330RIC168

; CURRENT APPLICATION NUMBER: US/10/140,472

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-140-472-309

P3330R1C198
ION NUMBER: US/10/141,761
DATE: 2002-05-08
on removed - See Palm or File Wrapper
D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

plication US/10142885
JS20030157604A1

ION:

r, Kevin P.

esini, Maureen

orge, Laura

oyers, Luc

varoff, Ellen

Wei-Qiang

ritsen, Mary E.

ard, Audrey

owski, Paul J.

ney, Austin L.

rwood, Steven

th, Victoria

art, Timothy A.

as, Daniel

anabe, Colin K

d, William

ag, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

P3330R1C248

ION NUMBER: US/10/142,885

DATE: 2002-05-10

ion removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 14; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

US-10-158-790-309
; Sequence 309, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C448

; CURRENT APPLICATION NUMBER: US/10/158,790

; CURRENT FILING DATE: 2002-05-30

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 309

; LENGTH: 1843

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1837

; OTHER INFORMATION: unknown base

US-10-158-790-309

Query Match 1.9%; Score 10; DB 14; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

|||||

Db 1826 AAAATTAAAA 1835

RESULT 120

US-10-137-871-309

; Sequence 309, Application US/10137871

; Publication No. US20030207350A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C153

; CURRENT APPLICATION NUMBER: US/10/137,871

DATE: 2002-05-03
on removed - See Palm or File Wrapper
D NOS: 550

Sapien

re

TION: unknown base

1.9%; Score 10; DB 15; Length 1843;
arity 100.0%; Pred. No. 62;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1835

pplication US/10140923
US20030207355A1

TION:

r, Kevin P.

esini, Maureen

orge, Laura

moyers, Luc

.varoff, Ellen

, Wei-Qiang

ritsen, Mary E.

ldard, Audrey

owski, Paul J.

ney, Austin L.

erwood, Steven

.th, Victoria

wart, Timothy A.

as, Daniel

anabe, Colin K

xd, William

ng, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

P3330R1C188

ATION NUMBER: US/10/140,923

DATE: 2002-05-07

on removed - See Palm or File Wrapper

D NOS: 550

Sapien

re

7

TION: unknown base

1.9%; Score 10; DB 15; Length 1843;
arity 100.0%; Pred. No. 62;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATAAAA 22

|||||

ATAAAA 1835

pplication US/10141756

Publication No. US20030207359A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
FILE REFERENCE: P3330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 309
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 1837
OTHER INFORMATION: unknown base
US-10-141-756-309

Query Match 1.9%; Score 10; DB 15; Length 1843;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

Db 1826 AAAATTAAAA 1835

RESULT 123

US-10-141-759-309

Sequence 309, Application US/10141759

Publication No. US20030207361A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

FILE REFERENCE: P3330R1C197

CURRENT APPLICATION NUMBER: US/10/141,759

Prior Application removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
 arity 100.0%; Pred. No. 62; Gaps 0;
 conservative 0; Mismatches 0; Indels 0;

TAAAAA 22

TAAAAA 1835

plication US/10140805
 US20030207419A1

ION:

r, Kevin P.

esini, Maureen

orge, Laura

noyers, Luc

varoff, Ellen

Wei-Qiang

ritsen, Mary E.

dard, Audrey

owski, Paul J.

ney, Austin L.

rwood, Steven

th, Victoria

wart, Timothy A.

as, Daniel

anabe, Colin K

d, William

ng, Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ACIDS ENCODING THE SAME

P3330R1C176

TION NUMBER: US/10/140,805

DATE: 2002-05-07

ion removed - See File Wrapper or Palm

D NOS: 550

Sapien

re

ION: unknown base

1.9%; Score 10; DB 15; Length 1843;
 arity 100.0%; Pred. No. 62; Gaps 0;
 conservative 0; Mismatches 0; Indels 0;

TAAAAA 22

TAAAAA 1835

plication US/10140864
 US20030207419A1

ION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Deanoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
 FILE REFERENCE: P3330R1C184
 CURRENT APPLICATION NUMBER: US/10/140,864
 CURRENT FILING DATE: 2002-05-07
 Prior Application removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 309
 LENGTH: 1843
 TYPE: DNA
 ORGANISM: Homo Sapien
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 1837
 OTHER INFORMATION: unknown base
 US-10-140-864-309

Query Match 1.9%; Score 10; DB 15; Length 1843;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

|||||

Db 1826 AAAATTAAAA 1835

RESULT 126

US-10-369-493-22455

Sequence 22455, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR

PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 39-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 22455

LENGTH: 1887

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-10-369-493-22455

Query Match 1.9%; Score 10; DB 15; Length 1887;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 137 PAPVAAAA 146

|||||

VAAAAA 134

plication US/10206915
US20040029221A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME

: P3430R1C513

ACTION NUMBER: US/10/206,915

DATE: 2002-07-26

ION NUMBER: 10/052586

ATE: 2002-01-15

ION NUMBER: 60/059263

ATE: 1997-09-18

ION NUMBER: 60/059266

ATE: 1997-09-18

ION NUMBER: 60/062250

ATE: 1997-10-17

ION NUMBER: 60/063120

ATE: 1997-10-24

ION NUMBER: 60/063121

ATE: 1997-10-24

ION NUMBER: 60/063486

ATE: 1997-10-21

ION NUMBER: 60/063540

ATE: 1997-10-28

ION NUMBER: 60/063541

ATE: 1997-10-28

ION NUMBER: 60/063544

ATE: 1997-10-28

ID NOS: 612

ion data removed - See File Wrapper or PALM.

o Sapien

larity 1.9%; Score 10; DB 12; Length 1894;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22

|||||

ATTAAAA 1060

plication US/10199670

US20040033560A1

TION:

er, Kevin P.

en, Jian

snoyers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C401

; CURRENT APPLICATION NUMBER: US/10/199,670

; CURRENT FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-199-670-97

Query Match

Best Local Similarity 1.9%; Score 10; DB 12; Length 1894;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

Db 1051 AAAATTAAAA 1060

RESULT 129

US-10-201-858-97

; Sequence 97, Application US/10201858

; Publication No. US20040038337A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C464

; CURRENT APPLICATION NUMBER: US/10/201,858

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

11:33:40 2004

us-09-976-740-43.olig.rapb

ON NUMBER: 60/062250
TE: 1997-10-17
ON NUMBER: 60/063120
TE: 1997-10-24
ON NUMBER: 60/063121
TE: 1997-10-24
ON NUMBER: 60/063486
TE: 1997-10-21
ON NUMBER: 60/063540
TE: 1997-10-28
ON NUMBER: 60/063541
TE: 1997-10-28
ON NUMBER: 60/063544
TE: 1997-10-28
on data removed - See File Wrapper or PALM.
D NOS: 612

Sapien

1.9%; Score 10; DB 12; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
|||||
TTAAAA 1060

lication US/10205890
US20040048334A1
ION:
r, Kevin P.
a, Jian
noyers, Luc
jard, Audrey
owski, Paul J.
ey, Austin L.
James
th, Victoria
anabe, Colin K.
d, William I.
ag, Zemin
ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
P3430R1C519
TION NUMBER: US/10/205,890
DATE: 2002-07-26
ON NUMBER: 10/052586
TE: 2002-01-15
ON NUMBER: 60/059263
TE: 1997-09-18
ON NUMBER: 60/059266
TE: 1997-09-18
ON NUMBER: 60/062250
TE: 1997-10-17
ON NUMBER: 60/063120
TE: 1997-10-24
ON NUMBER: 60/063121
TE: 1997-10-24
ON NUMBER: 60/063486
TE: 1997-10-21
ON NUMBER: 60/063540
TE: 1997-10-28
ON NUMBER: 60/063541
TE: 1997-10-28
ON NUMBER: 60/063544
TE: 1997-10-28
on data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-97

Query Match 1.9%; Score 10; DB 12; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

Qy 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

RESULT 131
US-10-208-024-97
; Sequence 97, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-208-024-97

Query Match 1.9%; Score 10; DB 12; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

IN NUMBER: 60/081070
TE: 1998-04-08
IN NUMBER: 60/081195
TE: 1998-04-09
IN NUMBER: 60/081838
TE: 1998-04-15
IN NUMBER: 60/082568
TE: 1998-04-21
IN NUMBER: 60/082569
TE: 1998-04-21
IN NUMBER: 60/082704
TE: 1998-04-22
IN NUMBER: 60/082797
TE: 1998-04-22
IN NUMBER: 60/083322
TE: 1998-04-28
IN NUMBER: 60/083495
TE: 1998-04-29
IN NUMBER: 60/083496
TE: 1998-04-29
IN NUMBER: 60/083499
TE: 1998-04-29
IN NUMBER: 60/083559
TE: 1998-04-29
IN NUMBER: 60/084366
TE: 1998-05-05
IN NUMBER: 60/084414
TE: 1998-05-06
IN NUMBER: 60/084639
TE: 1998-05-07
IN NUMBER: 60/084640
TE: 1998-05-07
IN NUMBER: 60/084643
TE: 1998-05-07
IN NUMBER: 60/085573
TE: 1998-05-15
IN NUMBER: 60/085579
TE: 1998-05-15
IN NUMBER: 60/085580
TE: 1998-05-15
IN NUMBER: 60/085582
TE: 1998-05-15
IN NUMBER: 60/085700
TE: 1998-05-15
IN NUMBER: 60/086023
TE: 1998-05-18
IN NUMBER: 60/086392
TE: 1998-05-22
IN NUMBER: 60/086486
TE: 1998-05-22
IN NUMBER: 60/087098
TE: 1998-05-28
IN NUMBER: 60/087208
TE: 1998-05-28
IN NUMBER: 60/087609
TE: 1998-06-02
IN NUMBER: 60/087759
TE: 1998-06-02
IN NUMBER: 60/087827
TE: 1998-06-03
IN NUMBER: 60/088025
TE: 1998-06-04
IN NUMBER: 60/088028
TE: 1998-06-04
IN NUMBER: 60/088029
TE: 1998-06-04
IN NUMBER: 60/088033
TE: 1998-06-04
IN NUMBER: 60/088167
TE: 1998-06-05
IN NUMBER: 60/088202
TE: 1998-06-05
IN NUMBER: 60/088212

IN PRIOR FILING DATE: 1998-06-05
IN PRIOR APPLICATION NUMBER: 60/088217
IN PRIOR FILING DATE: 1998-06-05
IN PRIOR APPLICATION NUMBER: 60/088326
IN PRIOR FILING DATE: 1998-06-04
IN PRIOR APPLICATION NUMBER: 60/088655
IN PRIOR FILING DATE: 1998-06-09
IN PRIOR APPLICATION NUMBER: 60/088722
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088738
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088740
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088811
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088824
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088825
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088826
IN PRIOR FILING DATE: 1998-06-10
IN PRIOR APPLICATION NUMBER: 60/088861
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/088863
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/088876
IN PRIOR FILING DATE: 1998-06-11
IN PRIOR APPLICATION NUMBER: 60/089090
IN PRIOR FILING DATE: 1998-06-12
IN PRIOR APPLICATION NUMBER: 60/089105
IN PRIOR FILING DATE: 1998-06-12
IN PRIOR APPLICATION NUMBER: 60/089512
IN PRIOR FILING DATE: 1998-06-16
IN PRIOR APPLICATION NUMBER: 60/089514
IN PRIOR FILING DATE: 1998-06-16
IN PRIOR APPLICATION NUMBER: 60/089538
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089598
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089653
IN PRIOR FILING DATE: 1998-06-17
IN PRIOR APPLICATION NUMBER: 60/089908

Query Match 1.9%; Score 10; DB 13; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 13 AAAATTTAAA 22
|||||
Db 1051 AAAATTTAAA 1060

RESULT 134
US-10-174-590-97
; Sequence 97, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18

ion removed - See File Wrapper or Palm
ID NOS: 612

> Sapien

1.9%; Score 10; DB 14; Length 1894;

larity 100.0%; Pred. No. 64; Mismatches 0; Indels 0; Gaps 0;

ATTAATA 22

|||||

ATTAATA 1060

plication US/10176758
US2003008353A1

TION:

er, Kevin P.

en, Jian

snayers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ATION: ACIDS ENCODING THE SAME

: P3430R1C104

ATION NUMBER: US/10176,758

DATE: 2002-06-21

ion removed - See File Wrapper or Palm

ID NOS: 612

> Sapien

1.9%; Score 10; DB 14; Length 1894;

larity 100.0%; Pred. No. 64; Mismatches 0; Indels 0; Gaps 0;

ATTAATA 22

|||||

ATTAATA 1060

plication US/10175737
US20030013153A1

TION:

er, Kevin P.

en, Jian

snayers, Luc

ddard, Audrey

dowski, Paul J.

rney, Austin L.

n, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ATION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 137

US-10-173-706-97

; Sequence 97, Application US/10173706

; Publication No. US2003002293A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C7

; CURRENT APPLICATION NUMBER: US/10/173,706

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 97

; LENGTH: 1894

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-706-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 138

US-10-175-738-97

; Sequence 97, Application US/10175738

; Publication No. US2003002294A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

g,Zemin
ION: ACIDS ENCODING THE SAME
P3430R1C45
TION NUMBER: US/10/175,738
DATE: 2002-06-19
on removed - See File Wrapper or Palm
D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1060

lication US/10175752
US20030022295A1

ION:

r, Kevin P.

a, Jian

oyers, Luc

dard, Audrey

owski, Paul J.

ney, Austin L.

, James

th, Victoria

anabe, Colin K.

d, William I.

g,Zemin

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

ION: ACIDS ENCODING THE SAME

P3430R1C60

TION NUMBER: US/10/175,752

DATE: 2002-06-19

on removed - See File Wrapper or Palm

D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22

|||||

TTAAAA 1060

lication US/10176482
US20030022296A1

ION:

r, Kevin P.

a, Jian

oyers, Luc

dard, Audrey

owski, Paul J.

ney, Austin L.

, James

APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
FILE REFERENCE: P3430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-482-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 141

US-10-176-757-97

Sequence 97, Application US/10176757

Publication No. US20030022297A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC

FILE REFERENCE: P3430R1C86

CURRENT APPLICATION NUMBER: US/10/176,757

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 97

LENGTH: 1894

TYPE: PRT

ORGANISM: Homo Sapien

US-10-176-757-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 13 AAAATTAAAA 22

|||||

Db 1051 AAAATTAAAA 1060

RESULT 142

US-10-176-913-97

Sequence 97, Application US/10176913

Publication No. US20030022298A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

owski, Paul J.
ney, Austin L.
i, James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
: P3430R1C66
ATION NUMBER: US/10/176,913
DATE: 2002-06-20
on removed - See file Wrapper or Palm
ID NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||
ATTAAAA 1060

lication US/10180552
US20030022300A1
TION:

r, Kevin P.
an, Jian
noyers, Luc
dard, Audrey
owski, Paul J.
ney, Austin L.
i, James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
: P3430R1C153
ATION NUMBER: US/10/180,552
on removed - See file Wrapper or Palm
ID NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22
|||||
ATTAAAA 1060

lication US/10180557
US20030022301A1
TION:

r, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-180-557-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

RESULT 145

US-10-173-700-97
Sequence 97, Application US/10173700
Publication No. US20030027262A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 97
LENGTH: 1894
TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-700-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

RESULT 146

US-10-174-572-97
Sequence 97, Application US/10174572

US20030027263A1
ION: r, Kevin P.
n, Jian
noyers, Luc
dard, Audrey
owski, Paul J.
ney, Austin L.
ey, James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
P3430R1C40
TION NUMBER: US/10/174,572
DATE: 2002-06-18
ation removed - See File Wrapper or Palm
D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
|||||
TTAAAA 1060

lication US/10174579
US20030027264A1
ION: r, Kevin P.
n, Jian
noyers, Luc
dard, Audrey
owski, Paul J.
ney, Austin L.
ey, James
th, Victoria
anabe, Colin K.
d, William I.
ng, Zemin
ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
P3430R1C31
TION NUMBER: US/10/174,579
DATE: 2002-06-18
on removed - See File Wrapper or Palm
D NOS: 612

Sapien

1.9%; Score 10; DB 14; Length 1894;
arity 100.0%; Pred. No. 64;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TTAAAA 22
|||||
TTAAAA 1060

RESULT 148

US-10-174-582-97
; Sequence 97, Application US/10174582
; Publication No. US20030027265A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C36
; CURRENT APPLICATION NUMBER: US/10/174,582
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-582-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 13 AAAATTAAAA 22
|||||
Db 1051 AAAATTAAAA 1060

RESULT 149

US-10-174-588-97
; Sequence 97, Application US/10174588
; Publication No. US20030027266A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C28
; CURRENT APPLICATION NUMBER: US/10/174,588
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-588-97

Query Match 1.9%; Score 10; DB 14; Length 1894;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 13 AAAATTAAAA 22
|||||

11:33:40 2004

us-09-976-740-43.olig.rapb

ATTAAAA 1060

plication US/10175739

US20030027267A1

TION:

er, Kevin P.

en, Jian

snovers, Luc

Idard, Audrey

owski, Paul J.

ney, Austin L.

a, James

ith, Victoria

tanabe, Colin K.

od, William I.

ang, Zemin

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TION: ACIDS ENCODING THE SAME

: P3430R1C46

ATION NUMBER: US/10/175,739

DATE: 2002-06-19

ion removed - See File Wrapper or Palm

ID NOS: 612

o Sapien

1.9%; Score 10; DB 14; Length 1894;

larity 100.0%; Pred. No. 64;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAAAA 22

|||||

ATTAAAA 1060

March 30, 2004, 15:05:55

3

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

in search, using sw model

rch 30, 2004, 14:58:06 ; Search time 45 Seconds
(without alignments)
3772.195 Million cell updates/sec

-09-976-740-43

8

YAGPPALPPETAAATAA.....HIKVLQGHFDDDDPDGFLG 538

IGO

pop 60.0 , Gapext 60.0

17041 seqs, 315518202 residues

ts satisfying chosen parameters: 1017041

yth: 0

yth: 2000000000

isting first 150 summaries

PTREMBL 25:*

sp_arChae:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mhc:*

sp_organelle:*

sp_phase:*

: sp_plant:*

: sp_rodent:*

: sp_virus:*

: sp_vertebrate:*

: sp_unclassified:*

: sp_rvirus:*

: sp_bacteriap:*

: sp_arChaeap:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ad by analysis of the total score distribution.

SUMMARIES

ary	ch	Length	DB	ID	Description
1.1	239	4	Q96IM4		Q96IM4 homo sapien
2.2	361	5	Q9VBI3		Q9VBI3 drosophila
2.2	1928	5	Q8T9H1		Q8T9H1 drosophila
1.2	2280	5	Q9V8E6		Q9V8E6 drosophila
2.2	2302	5	Q9N693		Q9N693 drosophila
2.2	2310	5	Q9GRA9		Q9GRA9 drosophila
2.0	129	4	Q43180		Q43180 homo sapien
2.0	309	10	Q7XNY2		Q7XNY2 oryza sativ
2.0	317	12	Q64812		Q64812 autographa
2.0	422	10	Q8LP98		Q8LP98 oryza sativ
2.0	438	5	Q8WSL0		Q8WSL0 plasmodium
2.0	442	5	Q8WSL3		Q8WSL3 plasmodium
2.0	445	12	Q98174		Q98174 molluscum c
2.0	464	5	Q8WSL4		Q8WSL4 plasmodium
2.0	468	16	Q9LOP9		Q9LOP9 streptomyce
2.0	556	4	Q15411		Q15411 homo sapien

Q9R101 spe
Q8B916 rac
Q961K7 homc
Q96191 homc
Q9VTD0 dros
Q8RZ96 ory
Q8W2X4 ory
Q9AYL5 ory
Q7XBY6 ory
Q52494 rale
Q8XTH8 ral
Q39491 bov
Q7X9M6 zea
Q7WEQ2 box
Q8BHG7 mus
Q7W3D2 box
Q8PFD1 xar
Q9R528 spli
Q8FDG3 esc
Q8PAJ7 xar
Q9HH51 meth
Q7WDB0 box
Q65215 zea
Q8ML75 dros
Q86XT7 homc
Q7XRW4 ory
Q9FGF3 ara
Q9LWQ9 ory
Q89392 par
Q8S7N6 ory
Q9LWJ7 ory
Q8H616 zea
Q7UBI5 shi
Q8XAN5 esc
Q8341 shi
Q96151 plas
Q8DC21 vib
Q9VNR3 dros
Q9U0N1 plas
Q8LTK1 ory
Q8HXV1 oryc
Q9AB02 cau
Q9VCS3 dros
Q96210 dros
Q8LIF6 ory
Q8BK12 mus
Q9P4C6 pich
Q97496 mus
Q9VY88 dros
Q02434 dros
Q28224 cerc
Q961R2 dros
Q9ESU6 mus
Q8VHF8 mus
Q74297 neur
Q9BHL1 caen
Q8IAK3 plas
Q8NMS0 cor
Q9BMP6 culi
Q9SMS7 ara
Q7XNS7 ory
Q8LN81 ory
Q8L874 ara
Q9MAM5 ara
Q8LCW9 ara
Q8LEQ0 ara
Q9FIK9 ara
Q852J2 ory
Q9IA73 par
Q94190 atr
Q92KS8 rhi
Q9H4X1 homo
Q96AT3 homo

rielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 g F., Gorrill J.H., Gu Z., Guan P., Harris M.,
 arvey D., Heinan T.J., Hernandez J.R., Houck J.,
 ston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 ush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 odira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 B., McIntosh T.C., McLeod M.P., McPherson D.,
 alshina N.V., Mobarri C., Morris J., Moshrefi A.,
 y M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 elson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Pittman K.S., Pan S., Pollard J., Puri V., Reese M.G.,
 mington K., Saunders R.D.C., Scheeler F., Shen H.,
 en-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 dling A.C., Stapleton M., Strong R., Sun E.,
 ector C., Turner R., Venter E., Wang A.H., Wang X.,
 ssauman D.A., Weinstein G.M., Weissenbach J.,
 Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 ong F.N., Zhong W., Zhou X., Zhu S., Zhao Q., Zheng L.,
 ers E.W., Rubin G.M., Venter J.C.;
 quence of *Drosophila melanogaster*.";
 85-2195(2000).

N.A.

Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 cayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A.,
 Center A., Champe M., Davenport L.B., Dietz S.M.,
 sett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 rise E., Galle R.F., Garg N.S., George R.A.,
 ouck J., Hoskins R.A., Hostin D., Howland T.J.,
 lali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 agas V., Park S., Patel S., Pfeiffer B.,
 S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Strong R., Svirskas R., Tector C., Tyler D.,
 Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Drosophila melanogaster genome.";
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

by M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 uang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 gman C., Berman B., Carlson J.W., Celniker S.E.,
 dale R., Emmert D., Frise E., de Grey A., Harris N.,
 Marshall B., Millburn G., Richter J., Russo S.,
 Smith E., Shu S., Smutniak F., Whitfield E.,
 Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Drosophila melanogaster genome.";
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

lniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 -2000) to the EMBL/GenBank/DBJ databases.

N.A.

-2002) to the EMBL/GenBank/DBJ databases.

N.A.

84; PubMed11578871;
 rtini M.E.;
 n and characterization of the *Drosophila* tau homolog.";
 :171-178(2001).

N.A.

y;
 Brokstein P., Hong L., Agbayani A., Carlson J.,
 vez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 zalez M., Guarini H., Kronmiller B., Li P., Liao G.,
 ngall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 ananavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR003761; AAF56732.2; -;
 DR EMBL; AY032977; AAK54456.1; -;
 DR EMBL; AY102697; ARM27526.1; -;
 DR FlyBase; FBgn0051057; tau.
 DR GO; GO:0007017; P: microtubule-based process; IEA.
 DR InterPro; IPR001084; Tubulin Tau.
 DR Pfam; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU MAP; 3.
 SQ SEQUENCE 361 AA; 38538 MW; B3DC50701DCF968A CRC64;

Query Match 2.2%; Score 12; DB 5; Length 361;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gc

QY 217 PPAPPOQQQPPPP 228

Db 43 PPAPPOQQQPPPP 54

RESULT 3

Q8T9H1

ID Q8T9H1 PRELIMINARY; PRT; 1928 AA.

AC Q8T9H1;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE SD01229P.

GN SBB OR CG5580.

OS *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]_

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY069769; AAL39914.1; -;

DR FlyBase; FBgn0010575; sbb.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0007411; P:axon guidance; IMP.

DR GO; GO:0007412; P:axon target recognition; IMP.

DR GO; GO:0008346; P:larval walking behavior; IMP.

DR InterPro; IPR006162; Ppantne S.

DR InterPro; IPR007087; Znf C2H2.

DR Pfam; PF00096; zf-C2H2; 1.

DR SMART; SM00355; Znf C2H2; 1.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 1928 AA; 193764 MW; 7EE7D606C0D59C9B CRC64;

Query Match 2.2%; Score 12; DB 5; Length 1928;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gc

QY 221 PQQQQPPPPPPQ 232

Db 1432 PQQQQPPPPPPQ 1443

RESULT 4

Q9V8E6

ID Q9V8E6 PRELIMINARY; PRT; 2280 AA.

AC Q9V8E6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

(Tremblrel. 13, Last sequence update)
 in. (Tremblrel. 25, Last annotation update)
 0.
 elanogaster (Fruit fly).
 etazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 epterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 227;
 M N.A.

levy;
 606; PubMed=107311132;
 Geniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 oup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferrier A.S., Fleischmann W.,
 abrialian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 ei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 ooy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 iden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 radling A.C., Stapleton M., Strong R., Sun E.,
 Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 asakman D.A., Weinstein G.M., Weissbach J.,
 ., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 -F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Myers E.W., Rubin G.M., Venter J.C.;
 sequence of Drosophila melanogaster.";
 2185-2195(2000).
 00; AAF57721.1; -.
 10010575; sbb.
 34; C:nucleus; IDA.
 11; P:axon guidance; IMP.
 12; P:axon target recognition; IMP.
 16; P:larval walking behavior; IMP.
 3006162; Ppantne S.
 3007087; Znf_C2H2.
 5; zf-C2H2; 1.
 55; Znf_C2H2; 1.
 0012; PHOSPHOPANTHETINE; 1.
 0028; ZINC_FINGER_C2H2_1; 1.
 0157; ZINC_FINGER_C2H2_2; 1.
 3; Zinc; Zinc-finger.
 280 AA; 228107 MW; 1C2CDA27DC77B00B CRC64;

2.2%; Score 12; DB 5; Length 2280;
 larity 100.0%; Pred. No. 0.28;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPPOQP 232

|||||

Db 1784 PQQQPPPPPOQP 1795

RESULT 5

Q9N693
 ID Q9N693 PRELIMINARY; PRT; 2302 AA.
 AC Q9N693;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE brakeless-B (Scribbler long isoform).
 GN SBB OR BKS OR CG5580.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=20265906; PubMed=10804172;
 RX Senti K., Keleman K., Eisenhaber F., Dickson B.J.;
 RA "brakeless is required for lamina targeting of R1-R6 axons in th
 RT drosophila visual system.";
 RL Development 127:2291-2301(2000).
 RN [2]
 SEQUENCE FROM N.A.
 RP MEDLINE=20341319; PubMed=10880478;
 RX Yang P., Shaver S.A., Hilliker A.J., Sokolowski M.B.;
 RA "Abnormal turning behavior in Drosophila larvae: identification
 RT molecular analysis of scribbler (sbb).";
 RL Genetics 155:1161-1174(2000).
 DR EMBL; AF242194; AAF76322.1; -.
 DR EMBL; AF247562; AAF70256.1; -.
 DR FLYBase; FBgn0010575; sbb.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR GO; GO:0007412; P:axon target recognition; IMP.
 DR GO; GO:0008346; P:larval walking behavior; IMP.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 1.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 2302 AA; 230013 MW; B35F759AE2C21729 CRC64;

Query Match 2.2%; Score 12; DB 5; Length 2302;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQPPPPPOQP 232

Db 1806 PQQQPPPPPOQP 1817

RESULT 6

Q9GRA9
 ID Q9GRA9 PRELIMINARY; PRT; 2310 AA.
 AC Q9GRA9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Master of thick veins.
 GN SBB OR MTV OR CG5580.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 SEQUENCE FROM N.A.

discs;
 Minami M., Tabata T.;
 Gene that shapes the activity gradient of the Dpp
 ough regulation of thick veins.";
 N-2000) to the EMBL/GenBank/DBJ databases.
 3: BAB20792.1; -;
 0010575; sbd.
 4: C:nucleus; IDA.
 1: P:axon guidance; IMP.
 2: P:axon target recognition; IMP.
 6: P:larval walking behavior; IMP.
 006162; Ppantae.S.
 007087; Znf_C2H2.
 ; Zf_C2H2; 1.
 5; Znf_C2H2; 1.
 012; PHOSPHOPANTETHEINE; 1.
 028; ZINC_FINGER_C2H2_1; 1.
 157; ZINC_FINGER_C2H2_2; 1.
 ; Zinc; Zinc-finger.
 10 AA; 230954 MW; 3208AB65E51AEDF6 CRC64;

2.2%; Score 12; DB 5; Length 2310;
 arity 100.0%; Pred. No. 0.28;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPQPQ 232
 |||||
 QPPPPQPQ 1825

RELIMINARY; PRT; 129 AA.

TrEMBLrel. 06, Created)
 TrEMBLrel. 06, Last sequence update)
 TrEMBLrel. 22, Last annotation update)
 ar ataxia 7 (Fragment).
 (Human).
 tazia; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Primates; Catarrhini; Hominidae; Homo.
 06;

N.A.
 nzw K.A., Bird T.D., Moseley M.L., Panum L.P.W.;
 9 of expanded trinucleotide repeat sequences.";
 0-0(1997).
 6; AAB87863.1; -;
 29 129
 9 AA; 14076 MW; B42FCB5972A34B3B CRC64;

2.0%; Score 11; DB 4; Length 129;
 arity 100.0%; Pred. No. 0.19;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

PPPPQPQ 232
 |||||
 PPPPQPQ 44

RELIMINARY; PRT; 309 AA.

TrEMBLrel. 25, Created)
 TrEMBLrel. 25, Last sequence update)
 TrEMBLrel. 25, Last annotation update)
 .9 protein.
 (Rice).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.D., Weng Q.J., Zhang L.,
 RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li
 RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.
 RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin
 RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
 RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL662996; CAE03881.1; -;
 SQ SEQUENCE 309 AA; 32281 MW; C532040DE1D47768 CRC64;

Query Match 2.0%; Score 11; DB 10; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; C

Qy 133 PPPPPAPVAAA 143
 |||||
 Db 104 PPPPPAPVAAA 114

RESULT 9

Q64812
 ID Q64812 PRELIMINARY; PRT; 317 AA.
 AC Q64812;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Autographa californica nuclear polyhedrosis virus ORF2.
 OS Autographa californica nuclear polyhedrosis virus (ACNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolydnavirus.
 OX NCBI_TaxID=46015;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1.2;
 RX MEDLINE=95137388; PubMed=7835700;
 RA Oshresser M., Morin N., Cerutti M., Delsert C.;
 RT "Sequence analysis and transcriptional mapping of the orF-z gene
 RT Autographa californica nuclear polyhedrosis virus.";
 RL Gene 152:201-204(1995).
 DR EMBL; X78446; CAA55206.1; -;
 SQ SEQUENCE 317 AA; 36304 MW; 7C6DD5342355DE5A CRC64;

Query Match 2.0%; Score 11; DB 12; Length 317;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; C

Qy 212 PPPPPAPPQ 222
 |||||
 Db 108 PPPPPAPPQ 118

RESULT 10

Q8LP98
 ID Q8LP98 PRELIMINARY; PRT; 422 AA.
 AC Q8LP98;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transcription factor PCF3 (Fragment).
 GN PCF3.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

M N.A.
 lponbare;
 6562; PubMed=1200681;
 hashi Y.;
 and dimerization specificity and potential targets for
 ein family.";
 337-348 (2002).
 04; BAB92951.1; -.
 P98; -.
 R005333; TCP.
 4; TCP; 1.
 22 AA; 42877 MW; 2589B5553D5789E CRC64;
 larity 100.0%; Score 11; DB 10; Length 422;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAPPPT 130
 |||||
 AAAAPPPT 302

PRELIMINARY; PRT; 438 AA.
 (TREMBLrel. 20, Created)
 (TREMBLrel. 20, Last sequence update)
 (TREMBLrel. 24, Last annotation update)
 oite protein (Fragment).
 inckei.
 lveolata; Apicomplexa; Haemosporida; Plasmodium.
 860;
 M N.A.
 Costa F., Letourner F., Walliker D., Landau I., Renia L.;
 n the circumsporozoite protein genes of Plasmodium vinckei
 ;
 UL-1999) to the EMBL/GenBank/DBJ databases.
 04; AAL36457.1; -.
 93; F:defense/immunity protein activity; IEA.
 R003067; Crmsprzoite.
 R000884; TSPI.
 0; tsp 1; 1.
 303; CRMSPRZOITE.
 09; TSPI; 1.
 0092; TSPI; 1.
 438 438
 38 AA; 45943 MW; 4BF92AB97F59B9F3 CRC64;
 larity 100.0%; Score 11; DB 5; Length 438;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DDEDEEE 341
 |||||
 DDEDEEE 83

PRELIMINARY; PRT; 442 AA.
 (TREMBLrel. 20, Created)
 (TREMBLrel. 20, Last sequence update)
 (TREMBLrel. 24, Last annotation update)
 oite protein.
 inckei petteri.
 lveolata; Apicomplexa; Haemosporida; Plasmodium.
 38298;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Sounou G., Costa F., Letourner F., Walliker D., Landau I., Ren
 RT "diversity in the circumsporozoite protein genes of Plasmodium
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AFI62332; AAL36454.1; -.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR003067; Crmsprzoite.
 DR InterPro; IPR000884; TSPI.
 DR Pfam; PF00090; tsp_1; 1.
 DR PRINTS; PR01303; CRMSPRZOITE.
 DR SMART; SM00209; TSPI; 1.
 DR PROSITE; PS00092; TSPI; 1.
 SQ SEQUENCE 442 AA; 45626 MW; D7918F094AB25A0B CRC64;
 Query Match 2.0%; Score 11; DB 5; Length 442;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 11; Conservative 0; Mismatches 0; Indels 0;
 QY 331 EEDDEDEEE 341
 |||||
 Db 73 EEDDEDEEE 83

RESULT 13
 Q98174
 ID Q98174 PRELIMINARY; PRT; 445 AA.
 AC Q98174;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MC0031.
 GN MC0031.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirir
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; PubMed=8670425;
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;
 RT "Genome sequence of a human tumorigenic poxvirus: Prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U60315; AAC55131.1; -.
 DR PIR; T30604; T30604.
 SQ SEQUENCE 445 AA; 49447 MW; 2B3C59936F0058DE CRC64;
 Query Match 2.0%; Score 11; DB 12; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 11; Conservative 0; Mismatches 0; Indels 0;
 QY 127 PPPTAPPPPP 137
 |||||
 Db 353 PPPTAPPPPP 363

RESULT 14
 Q8WSL4
 ID Q8WSL4 PRELIMINARY; PRT; 464 AA.
 AC Q8WSL4;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 GN CS.

```

OS nckeil lentum.
OC veolata; Apicomplexa; Haemosporida; Plasmodium.
CX 8297;
EN N.A.
EP osta F., Letourneur F., Walliker D., Landau I., Renia I.;
ET the circumsporozoite protein genes of Plasmodium vinckei
ET the circumsporozoite protein genes of Plasmodium vinckei
FL N-1999) to the EMBL/GenBank/DBJ databases.
DR 1; AAL36453.1; -.
DR 3; F:defense/immunity protein activity; IEA.
DR 003067; Crcmsprzoite.
DR 000884; TSPL.
DR 1; tspl.1; 1.
DR 03; Crcmsprzoite.
DR 9; TSPL; 1.
DR 092; TSPL; 1.
DR 4 AA; 48476 MW; 8AA595D8D6E97CF0 CRC64;
SQ
    2.0%; Score 11; DB 5; Length 464;
    arity 100.0%; Pred. No. 0.55;
    conservative 0; Mismatches 0; Indels 0; Gaps 0;
    DEDEDEE 341
    |||||
    DEDEDEE 83

RELIMINARY; PRT; 468 AA.

TremBLrel. 15, Created)
TremBLrel. 15, Last sequence update)
TremBLrel. 25, Last annotation update)
rane protein.
D8A.15C.
coelicol.
inobacteria; Actinobacteridae; Actinomycetales;
ae; Streptomycetaceae; Streptomycetes.
02;
N.A.
/ M145;
410; PubMed=12000953;
Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
James K.D., Harris D.E., Quail M.A., Kieser H.,
Teman A., Brown S., Chandra G., Chen C.M., Collins M.,
aser A., Goble A., Hidalgo J., Horneby T., Howarth S.,
Kieser T., Lark L., Murphy L., Oliver K., O'Neill S.,
E., Rajandream M.A., Rutherford K., Rutter S.,
nders D., Sharp S., Squares R., Squares S., Taylor K.,
tzorrek A., Woodward J., Barrell B.G., Parkhill J.,
ome sequence of the model actinomycete Streptomycetes
(2).";
1-147(2002).
3; CAB7336.1; -.
08979; Gal_bind_like.
ome.
3 AA; 48544 MW; COFD487AA341CAC0 CRC64;
SQ
    2.0%; Score 11; DB 16; Length 468;
    arity 100.0%; Pred. No. 0.56;
    conservative 0; Mismatches 0; Indels 0; Gaps 0;
    APPAVAP 192
    |||||
    APPAVAP 195

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ID O15411 PRELIMINARY; PRT; 556 AA.
AC O15411;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE CAGH32 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369492; PubMed=9225980;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
RT "cDNAs with long CAG trinucleotide repeats from human brain.";
RL Hum. Genet. 100:114-122(1997).
DR EMBL; U0743; AAB91441.1; -.
FT NON TER 1
SQ SEQUENCE 556 AA; 57588 MW; AAAF9DFEF77EE9E CRC64;

Query Match 2.0%; Score 11; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 225 QPPPPQPPPP 235
DB 80 QPPPPQPPPP 90
|||||

RESULT 17
Q9R101 PRELIMINARY; PRT; 763 AA.
ID Q9R101
AC Q9R101;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Hormone-sensitive lipase.
GN HSL.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Bauer V.W., Andrews M.T.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF177401; AAD51122.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002168; Lipolytic enzyme.
DR InterPro; IPR000379; Ser-estr.
DR PROSITE; PS01173; LIPASE_GDXG_HIS; 1.
DR PROSITE; PS01174; LIPASE_GDXG_SER; 1.
SQ SEQUENCE 763 AA; 83125 MW; E5516B02EFB8BE4D CRC64;

Query Match 2.0%; Score 11; DB 11; Length 763;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 11; Conservative 0; Mismatches 0; Indels 0; G

QY 119 PAAAAAAPP 129
DB 752 PAAAAAAPP 762
|||||

RESULT 18
Q8B916 PRELIMINARY; PRT; 810 AA.
ID Q8B916
AC Q8B916;
DT 01-MAR-2003 (TremBLrel. 23, Created)

```

(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
protein.
ou multiple nucleopolyhedrovirus.
na viruses, no RNA stage; Baculoviridae;
drovirus.
0366;

M N.A.

, Harrison R.L.;
usia ou multiple nucleopolyhedrovirus genome sequence.";
UG-2002) to the EMBL/GenBank/DBJ databases.
71; AAN28017.1; -.
protein.
10 AA; 94066 MW; 717CDB04EC226FE CRC64;

2.0%; Score 11; DB 12; Length 810;

larity 100.0%; Pred. No. 0.89; Indels 0; Gaps 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPAPQP 222

|||||
PQPAPQP 120

PRELIMINARY; PRT; 1157 AA.

(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
protein KIAA1818 (Fragment).

(Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A.

5130; PubMed=11347906;
akayama M., Nakajima D., Kikuno R., Ohara O.;
of the coding sequences of unidentified human genes. XX.
sequences of 100 new cDNA clones from brain which code
teins in vitro.";

5-95(2001).

21; BAB47447.1; -.

34; C:nucleus; IEA.

77; F:DNA binding; IEA.

001005; Myb_DNA_binding.

17; SANT; 1.

0090; MYB_3; 1.

protein.

1

157 AA; 125525 MW; B08A6AE50B1A9E01 CRC64;

2.0%; Score 11; DB 4; Length 1157;

larity 100.0%; Pred. No. 1.2;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PQPAPQP 235

|||||

PQPAPQP 549

PRELIMINARY; PRT; 3124 AA.

(TrEMBLrel. 19, Created)

(TrEMBLrel. 19, Last sequence update)

(TrEMBLrel. 25, Last annotation update)

DE P400 SW12/SNF2-related protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21400441; PubMed=11509179;

RA Fuchs M., Gerber J., Drapkin R., Sif S., Ikura T., Ogryzko V.,

RA Lane W.S., Nakatani Y., Livingston D.M.;

RT "The p400 complex is an essential E1A transformation target.";

RL Cell 106:297-307(2001).

DR EMBL; AY044869; AAK97789.1; -.

DR Genbank; HGNC:11958; EP400.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR006562; HSA.

DR InterPro; IPR001005; Myb_DNA_binding.

DR InterPro; IPR000330; SNF2_N.

DR Pfam; PF00271; helicase_C; 1.

DR Pfam; PF00176; SNF2_N; 2.

DR SMART; SM00487; DEXDc; 1.

DR SMART; SM00573; HSA; 1.

DR SMART; SM00717; SANT; 1.

DR PROSITE; PS50090; MYB_3; 1.

DR ATP-binding; Helicase; Hydrolase.

SK SEQUENCE 3124 AA; 340146 MW; B8F57FD6C7BD01E9 CRC64;

Query Match 2.0%; Score 11; DB 4;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 225 QPPPPQPQPPP 235

|||||

Db 2506 QPPPPQPQPPP 2516

RESULT 21

Q9VTD0

ID Q9VTD0 PRELIMINARY; PRT; 96 AA.

AC Q9VTD0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE CG14148 protein.

DE CG14148.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Berkeley;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.I

RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.I

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Fabrics B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W., Brielan A.E., Garg N.S., Gelbart W.M., Glasser K., ng F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Helman T.J., Hernandez J.R., Houck J., uston K.A., Howland T.J., Wei M.-H., Ibegwan C., lueh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., i B., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., i B., McIntosh T.C., McLeod M.P., McPherson D., y M., Murphy B., Mobarry C., Morris J., Moshrefi A., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., emington K., Saunders R.D.C., Scheeler F., Shen H., den-Kiamos I., Simpson M., Skupski M.P., Smith T., adling A.C., Stapleton M., Strong R., Sun E., rector C., Turner R., Venter E., Wang A.H., Wang X., asarman D.A., Weinstein G.M., Weissbach J., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., hong F.N., Zhong W., Zhou X., Zhao Q., Zheng L., yers E.W., Rubin G.M., Venter J.C.; equence of *Drosophila melanogaster*; 185-2195 (2000). 5; AAF50122.1; 3040821; CG14148. AA; 10884 MW; A17E2752CE1DCA7D CRC64;

1.9%; Score 10; DB 5; Length 96;
arity 100.0%; Pred. No. 1.1;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPPP 129
|||||
AAAPPP 32

RELIMINARY; PRT; 166 AA.

TrEMBLrel. 21, Created)
TrEMBLrel. 21, Last sequence update)
TrEMBLrel. 25, Last annotation update)
.2 protein.
.2.
(japonica cultivar-group).
cidiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzae; Oryza.
347;

N.A.
pponbare;
sumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 1, BAC
63G05.";
V-2001) to the EMBL/GenBank/DBJ databases.
); BAB90493.1; -.
36; -.

7; F:DNA binding; IEA.
5; P:regulation of transcription, DNA-dependent; IEA.
300910; HMG_12_box.
3; HMG; 1.
118; HMG_BOX.2; 1.
5 AA; 18791 MW; 3D4E911025FEAFCA CRC64;

1.9%; Score 10; DB 10; Length 166;
arity 100.0%; Pred. No. 1.8;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 PPPPQQPPPP 235
| | | | | | | | | |
Db 74 PPPPQQPPPP 83
| | | | | | | | | |
RESULT 23
Q8W2X4 PRELIMINARY; PRT; 172 AA.
AC Q8W2X4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0060105.14 OR OSJNBA0040D23.6.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa; STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Taitrin T., Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kaib E., Quackenbus
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0060105 genomic sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Taitrin T., Krol M.I., Jarrabi B.B.,
RA Jin S.S., Koo H., Ziemann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Sun B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
RT "Oryza sativa chromosome 10 BAC OSJNB0040D23 genomic sequence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
chromosome 10.";
RL Science 300:1566-1569(2003).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092697; AAL58119.1; -.
DR EMBL; AC074196; AAM76345.1; -.
DR EMBL; AE017115; AAP54812.1; -.
DR Gramene; Q8W2X4; -.
DR GO; GO:0004185; F:serine carboxypeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001563; Peptidase_S10.
DR PROSITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 17950 MW; 049DF2321C0E4D12 CRC64;

Query Match 1.9%; Score 10; DB 10; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G.

Qy 13 AAAATTAATAA 22
| | | | | | | | | |
Db 12 AAAATTAATAA 21
| | | | | | | | | |

RESULT 24

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PRELIMINARY;          PRT;    212 AA.
(TREMBLrel. 17, Created)
(TREMBLrel. 25, Last sequence update)
(TREMBLrel. 25, Last annotation update)
protein.
3.2.
  iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  a; Oryzae; Oryza.
530;

4 N.A.
  ipponbare;
  Juan O., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
  Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
  Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
  J., White O., Salzberg S.L., Fraser C.M.;
  a chromosome 10 BAC OSUNBA0003019 genomic sequence.;
  3B-2001) to the EMBL/GenBank/DBJ databases.
55; AAK00445.1; -.
  VL5; -.
protein.
12 AA; 23084 MW; BBAID03553465083 CRC64;

  1.9%; Score 10; DB 10; Length 212;
  100.0%; Pred. No. 2.2;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  AAAAPP 129
  |||||
  AAAAPP 205

PRELIMINARY;          PRT;    212 AA.
(TREMBLrel. 25, Created)
(TREMBLrel. 25, Last sequence update)
(TREMBLrel. 25, Last annotation update)
protein.
3.2.
  (Japonica cultivar-group).
  iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  a; Oryzae; Oryza.
9947;

4 N.A.
  ipponbare;
  smosome 10 Sequencing Consortium;
  sw of structure, activity, and evolution of rice
  0.;
  1566-1569(2003).

  N N.A.
  ipponbare;
  Wing R.A., McCombie W.R., Messing J., Yuan Q.;
  AY-2003) to the EMBL/GenBank/DBJ databases.
  21; AAP55122.1; -.
protein.
12 AA; 23084 MW; BBAID03553465083 CRC64;

  1.9%; Score 10; DB 10; Length 212;
  100.0%; Pred. No. 2.2;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  AAAAPP 129
  |||||
  AAAAPP 205

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RESULT 26
052494
ID 052494          PRELIMINARY;          PRT;    301 AA.
AC 052494;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HrpF protein.
GN HRPF.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OC NCBI_TaxID=305;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=20253307; PubMed=10792715;
RA Gueneron M., Timmers A.C.J., Boucher C., Arlat M.;
RT "Two novel proteins, PopB, which has functional nuclear localiza
RT signals, and PopC, which has a large leucine-rich repeat domain,
RT secreted through the Hrp-secretion apparatus of Ralstonia
RT solanacearum."
RL Mol. Microbiol. 36:261-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=95349395; PubMed=7623665;
RA Van Gijsegem F., Gough C.L., Zischek C., Genin S., Niqueux E.,
RA Arlat M., Barberis P., German S., Castello P., Boucher C.A.;
RT "The hrp gene locus of Pseudomonas solanacearum which controls a
RT III secretion system, encodes eight proteins related to component
RT the flagellar biogenesis complex."
RL Mol. Microbiol. 15:1095-1114(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=93125128; PubMed=1479894;
RA Genin S., Gough C.L., Zischek C., Boucher C.A.;
RT "Evidence that the hrpB gene encodes a positive regulator of
RT pathogenicity genes from Pseudomonas solanacearum."
RL Mol. Microbiol. 6:3065-3076(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=93113006; PubMed=1472716;
RA Gough C.L., Genin S., Zischek C., Boucher C.A.;
RT "hrp genes of Pseudomonas solanacearum are homologous to pathoge
RT determinants of animal pathogenic bacteria and are conserved amon
RT plant pathogenic bacteria."
RL Mol. Plant Microbe Interact. 5:384-389(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=93302711; PubMed=8316211;
RA Gough C.L., Genin S., Lopes V., Boucher C.A.;
RT "Homology between the HrpO protein of Pseudomonas solanacearum a
RT bacterial proteins implicated in a signal peptide-independent sec
RT mechanism."
RL Mol. Gen. Genet. 239:378-392(1993).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=96347139; PubMed=8736546;
RA Bogdanove A.J., Beer S.V., Bonas U., Boucher C.A., Collmer A.,
RA Coplin D.L., Cornelis G.R., Huang H.C., Hutcheson S.W.,
RA Panopoulos N.J., Van Gijsegem F.;
RT "Unified nomenclature for broadly conserved hrp genes of
RT phytopathogenic bacteria."
RL Mol. Microbiol. 20:681-683(1996).
RN [7]
RP SEQUENCE FROM N.A.

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```

> ;
> 01; PubMed=8313899;
> Gijsegem F., Huet J., Pernollet J., Boucher C.A.;
> ein which induces a hypersensitivity-like response on
> ia genotypes, is secreted via the Hrp pathway of
> anacearum.";
> 3-553(1994).
>
> N.A.
> ;
> 349; PubMed=8190064;
> ther C.A.;
> / of proteins involved in different secretion pathways in
> bacteria: modular structure and specificity of N-terminal
> st. 243:112-118(1994).
> l; CAB58256.1; -.
> 362087.
> l AA; 32331 MW; F3DA387F2CF95464 CRC64;
>
> arity 1.9%; Score 10; DB 2; Length 301;
> nservative 0; Mismatches 0; Indels 0; Gaps 0;
>
> EDEDD 343
> |||||
> EDEDD 300
>
> RELIMINARY; PRT; 301 AA.
>
> TrEMBLrel. 20, Created)
> TrEMBLrel. 20, Last sequence update)
> TrEMBLrel. 24, Last annotation update)
>
> 69 OR RS01640.
> anacearum (Pseudomonas solanacearum).
> laamid.
> teobacteria; Betaproteobacteria; Burkholderiales;
> ae; Ralstonia.
> 5;
>
> N.A.
> ;
> 379; PubMed=11823852;
> , Genin S., Artiguenave F., Gouzy J., Mangenot S.,
> lault A., Bröttier P., Camus J.C., Cattolico L.,
> Choisine N., Claudel-Renard C., Gunnac S., Demange N.,
> vie M., Moisan A., Robert C., Saurin W., Schiex T.,
> ebault P., Whalen M., Wincker P., Levy M.,
> , Boucher C.A.;
> ace of the plant pathogen Ralstonia solanacearum.";
> 7-502(2002).
> l; CAD18020.1; -.
> l; C:extrachromosomal DNA; IEA.
> lete proteome.
> l AA; 32732 MW; 5ED1E267293C2967 CRC64;
>
> 1.9%; Score 10; DB 16; Length 301;
> arity 100.0%; Pred.No.2.9;
> nservative 0; Mismatches 0; Indels 0; Gaps 0;
>
> EDEDD 343
> |||||
> EDEDD 300
>
> RELIMINARY; PRT; 308 AA.

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DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Substrate of serine protease (Cpsid).
GN U26.5.
OS Bovine herpesvirus type 1 (strain Jura).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
RA Schwyz M., Vlcek C., Lowery D.E., Bello L.J., Meyer G., Misra V
RT "Gene contents in a 37-kb segment centered in the UL part of the
RL bovine herpesvirus 1 genome: the last gap.";
RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Jura;
RA Schwyz M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vlcek C.;
RT "Complete DNA sequence of bovine herpesvirus 1.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ004801; CAA06108.1; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001847; Peptidase_S21.
DR Pfam; PF00716; Peptidase_S21; I.
DR SQ SEQUENCE 308 AA; 31187 MW; 676CD234E3D8C8D3 CRC64;

Query Match 1.9%; Score 10; DB 12; Length 308;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAPPP 129
Db |||||
55 AAAAAAAAAPPP 64

RESULT 29
Q7X9M6 PRELIMINARY; PRT; 320 AA.
ID Q7X9M6
AC Q7X9M6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Yabv10 protein
OS Zea mays (Maize)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73; TISSUE=Vegetative apex;
RA Juarez M.T., Twigg R.W., Timmermans M.C.P.;
RT "Reversal of dorsoventral polarity in the maize leaf.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY13904; AAP79887.1; -.
DR SQ SEQUENCE 320 AA; 33396 MW; FB65FCB8CDD4C6E6 CRC64;

Query Match 1.9%; Score 10; DB 10; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAPPP 129
Db |||||
103 AAAAAAAAAPPP 112

RESULT 30
Q7WEQ2 PRELIMINARY; PRT; 326 AA.
ID Q7WEQ2

```

(TReMBLrel. 25, Created)
 (TReMBLrel. 25, Last sequence update)
 (TReMBLrel. 25, Last annotation update)
 chromosome c.
 conchiseptica (Alcaligenes bronchisepticus).
 teobacteria; Betaproteobacteria; Burkholderiales;
 ae; Bordetella.

4 N.A.
 / ATCC BAA-588;
 7954; PubMed=12910271;
 Sebahia M., Preston A., Murphy L.D., Thomson N.,
 Holden M.T.G., Churcher C.M., Bentley S.D., Mungall
 K.L., Aggarwal A., James K., Harris B., Quail M.A.,
 Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 Collins M., Cronin A., Davis P., Doggett J.,
 Goble A., Hamlin N., Hauser H., Holroyd S., Jagels
 K., Mould S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Whitehead S., Barrall B.G., Maskell D.J.,
 analysis of the genome sequences of Bordetella pertussis,
 arapertussis and Bordetella bronchiseptica.";
 35:32-40(2003).
 51; CAB34944.1; -.
 genome.
 26 AA; 32865 MW; 1B1AD7E9FEC191B8 CRC64;

1.9%; Score 10; DB 16; Length 326;
 larity 100.0%; Pred. No. 3.2;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAAP 127
 |||||
 AAAAAAP 236

PRELIMINARY; PRT; 327 AA.

(TReMBLrel. 23, Created)
 (TReMBLrel. 23, Last sequence update)
 (TReMBLrel. 24, Last annotation update)
 protein (Fragment).
 K.

(Mouse).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 0090;

M N.A.
 /6J; TISSUE=Brain, and Hypothalamus;
 4683; PubMed=12466851;
 onsortium,

name Exploration Research Group Phase I & II Team;
 the mouse transcriptome based on functional annotation of
 length cDNAs.";
 53-573(2002).
 96; BAC32675.1; -.
 48; BAC37680.1; -.
 PT0675.
 4804; A230054D04Rik.
 protein.
 327 327

27 AA; 34826 MW; 20320E4E36DE7E8B CRC64;

1.9%; Score 10; DB 11; Length 327;
 larity 100.0%; Pred. No. 3.2;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 PPPPQQPPPP 235
 |||||
 Db 16 PPPPQQPPPP 25

RESULT 32

Q7W3D2 PRELIMINARY; PRT; 334 AA.
 ID Q7W3D2;
 AC Q7W3D2;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Putative cytochrome c.
 GN BPP4111.
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=519;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=12822 / ATCC BAA-587;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall
 K.L., Aggarwal A., James K., Harris B., Quail M.A.,
 Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 Collins M., Cronin A., Davis P., Doggett J.,
 Goble A., Hamlin N., Hauser H., Holroyd S., Jagels
 K., Mould S., Norberczak H., O'Neill S., Ormond D., Price C.,
 Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 Whitehead S., Barrall B.G., Maskell D.J.,
 analysis of the genome sequences of Bordetella pertussis,
 arapertussis and Bordetella bronchiseptica.";
 35:32-40(2003).
 51; CAB34944.1; -.
 genome.
 26 AA; 32865 MW; 1B1AD7E9FEC191B8 CRC64;

Query Match 1.9%; Score 10; DB 16; Length 334;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 118 AAAAAAAAP 127
 |||||
 Db 235 AAAAAAAAP 244

RESULT 33

Q8PFD1 PRELIMINARY; PRT; 336 AA.
 ID Q8PFD1;
 AC Q8PFD1;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE TonB-like protein.
 GN XAC4052.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN=306 / ATCC 13902 / XV 101;
 RC MEDLINE=22022145; PubMed=12024217;
 RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.,
 Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.,
 Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 Amaral G., Cannavan F., Cardoso J., Chambergo F., Chapina L.P.,
 Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

, Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D., Santos M., Truffi D., Tsai S.M., White F.F., Kitajima J.P.;
the genomes of two Xanthomonas pathogens with differing ties";
-463(2002).
; AM38887.1; --
; Ciperiplasmic space (sensu Gram-negative Bact. . . ; IEA.
; F:iron ion transporter activity; IEA.
; P:iron ion transport; IEA.
03538; TonB.
06260; TonB_C.
TonB; 1.
4; TONBPROTEIN.
01352; tonB_Cterm; 1.
ome.
AA; 35660 MW; BDD21658DABFE475 CRC64;
1.9%; Score 10; DB 16; Length 336;
rity 100.0%; Pred.No.3.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAAP 127
|||||
AAAAAP 250
RELIMINARY; PRT; 337 AA.
T:EMBLrel. 13, Created)
T:EMBLrel. 13, Last sequence update)
T:EMBLrel. 24, Last annotation update)
; filament outer layer polypeptide.
ochaetes; Spirochaetales; Spirochaetaceae; Spirochaeta.
N.A.
48; PubMed=8454190;
Greenberg E.P.;
he Spirochaeta aurantia flaA gene and transcript.";
.. Lett. 106:245-251(1993).
; Ciperiplasmic space (sensu Gram-negative Bact. . . ; IEA.
; P:ciliary/flagellar motility; IEA.
06714; FlaA.
FlaA; 1.
AA; 36772 MW; 3326E4B096618635 CRC64;
1.9%; Score 10; DB 2; Length 337;
rity 100.0%; Pred.No.3.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAAAP 127
|||||
AAAAAP 334
RELIMINARY; PRT; 368 AA.
T:EMBLrel. 23, Created)
T:EMBLrel. 23, Last sequence update)
T:EMBLrel. 25, Last annotation update)
rved protein.

OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud K., Mobley H.L.F., Donnenberg M.S., Blattner F.R.;
RA "Extensive mosaic structure revealed by the complete genome sequen-
RT of uropathogenic Escherichia coli";
RT Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RL EMBL; AE016767; AAN82264.1; --
DR InterPro; IPR009043; RNA_pol_sigma.
DR InterPro; IPR007631; Sigma70_ner.
DR InterPro; IPR007127; Sigma70_r1.1.
DR InterPro; IPR009042; Sigma70_r1.2.
DR Pfam; PF04546; sigma70_ner; 1.
DR Pfam; PF03979; sigma70_r1.1; 1.
DR Pfam; PF00140; sigma70_r1.2; 1.
KW Complete proteome.
SQ SEQUENCE 368 AA; 41966 MW; FED7AC7A0E7640BE CRC64;
Query Match 1.9%; Score 10; DB 16; Length 368;
Best Local Similarity 100.0%; Pred.No.3.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 333 DDDEDEDED 342
Db 191 DDDEDEDED 200
RESULT 36
Q8PAJ7 PRELIMINARY; PRT; 404 AA.
ID Q8PAJ7
AC Q8PAJ7;
DT 01-OCT-2002 (T:EMBLrel. 22, Created)
DT 01-OCT-2002 (T:EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T:EMBLrel. 25, Last annotation update)
DE Dihydrolipoamide S-succinyltransferase.
GN SUCB OR XCCL486.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chamergo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with differ-
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL; AE012249; AAM40782.1; --
DR GO; GO:0045252; C:oxoglutarate dehydrogenase complex; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.

49; F: dihydrolipoamide S-succinyltransferase acti. . . ; IEA.
 15; F: protein binding; IEA.
 40; F: transferase activity; IEA.
 52; P: metabolism; IEA.
 99; P: tricarboxylic acid cycle; IEA.
 R001078; 2-oxoacid dh.
 R000089; biotin_lipoyl.
 R004167; E3_binding.
 R003016; Lipoyl_BS.
 R006255; SucB.
 9; 2-oxoacid dh; 1.
 4; biotin_lipoyl; 1.
 7; e3_binding; 1.
 1115; 2-oxoacid dh; 1.
 GR01347; sucB; 1.
 0189; LIPOYL; 1.
 Complete proteome.
 04 AA; 42414 MW; B4FED8E9556D1977 CRC64;
 1.9%; Score 10; DB 16; Length 404;
 larity 100.0%; Pred. No. 3.8;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAAAP 127
 |||||
 AAAAAAP 115
 PRELIMINARY; PRT; 406 AA.
 (TrEMBLrel. 16, Created)
 (TrEMBLrel. 16, Last sequence update)
 (TrEMBLrel. 19, Last annotation update)
 actural protein.
 rium wolfei.
 yarchaeota; Methanobacteria; Methanobacteriales;
 riaceae; Methanothermobacter.
 45261;
 M N.A.
 9258; PubMed:11544247;
 cer P., Leisinger T., Wasserfallen A.;
 of Archaeal Prophage PsiM100 Encodes the Lytic Enzyme
 for Autolysis of Methanothermobacter wolfei.;
 . 183:5788-5792(2001).
 M N.A.
 UG-2000) to the EMBL/GenBank/DBJ databases.
 75; AAG39960.1; -.
 06 AA; 46062 MW; 30B27CB36A6428A6 CRC64;
 1.9%; Score 10; DB 1; Length 406;
 larity 100.0%; Pred. No. 3.8;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DDEDED 339
 |||||
 DDEDED 356
 PRELIMINARY; PRT; 406 AA.
 (TrEMBLrel. 25, Created)
 (TrEMBLrel. 25, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 mide succinyltransferase component of 2-oxoglutarate
 e complex (2-oxoglutarate dehydrogenase complex, E2
 EC 2.3.1.61).

GN ODHB OR SUBC OR B33668.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=RB50 / ATCC BAA-588;
 RC MEDLINE=22827954; PubMed=12910271;
 RX Parkhill J., Sebaihia M., Preston A., Churcher C.M., Bentley S.D., Mungall
 RA Harris D.E., Holden M.T.G., Churcher C.M., James K., Harris B., Quail M.A.
 RA Cardeno-Tarraga A.M., Temple L., Bason N., Cherevach I
 RA Achtmann M., Atkin R., Baxer S., Basham D., Bason N., Cherevach I
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels
 RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steve
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RA "Comparative analysis of the genome sequences of Bordetella pert
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL: BX640448; CAE35641.1; -.
 KW Acyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 406 AA; 41997 MW; 723C1E8E82FFD81A CRC64;
 Query Match 1.9%; Score 10; DB 16; Length 406;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 118 AFAAAAAAAP 127
 Db 93 AFAAAAAAAP 102
 RESULT 39
 O65215 PRELIMINARY; PRT; 436 AA.
 ID O65215; PRELIMINARY; PRT; 436 AA.
 AC O65215;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein ID1.
 GN ID1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Immature leaf;
 RC MEDLINE=98265970; PubMed=9604934;
 RX Colasanti J., Yuan Z., Sundaresan V.;
 RA "The indeterminate gene encodes a zinc finger protein and regula
 RT leaf-generated signal required for the transition to flowering i
 RT maize.";
 RL Cell 93:593-603(1998).
 DR EMBL: AF058757; AAC18941.1; -.
 DR PIR: T01652; T01652.
 DR TRANSFAC; T03994; -.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR SMART; SM00355; Znf_C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 436 AA; 46746 MW; 6A9AD06320413BD5 CRC64;
 Query Match 1.9%; Score 10; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

POPPA 219
|||||
POPPA 54

RELIMINARY; PRT; 466 AA.

TrEMBLrel. 22, Created)
TrEMBLrel. 22, Last sequence update)
TrEMBLrel. 23, Last annotation update)

lanogaster (Fruit fly).

tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.

27;

N.A.

ey; PubMed=10731132;

006; Holt R.A., Evans C.A., Gocayne J.D.,
elniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
S., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Worham J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
ghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
otchan M.R., Bouck J., Brokstein P., Brottier P.,
Susam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahlke C., Davenport L.B., Davies P.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Bretellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
uston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
lueh F., Karpn G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i B., McIntosh A.A., Li J., Li Z., Liang Y., Lin X.,
Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
emington K., Saunders R.D.C., Scheeler F., Shen H.,
den-Kiamos I., Simpson M., Skupski M.P., Smith T.,
adling A.C., Stapleton M., Strong R., Sun E.,
Tector C., Turner R., Venter E., Wang A.H., Wang X.,
assarman D.A., Weinstein G.M., Weissbach J.,
Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
, F., Zaveri J.S., Zhan M., Zhang Q., Zhou X., Zheng L.,
hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
yers E.W., Rubin G.M., Venter J.C.;
equence of *Drosophila melanogaster*.;
185-2195(2000).

N.A.

, Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
ocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
Center A., Champe M., Davenport L.B., Dietz S.M.,
rsett V., Doup I.E., Doyle C., Dresnek D., Farfan D.,
Frise E., Galle R.F., Garg N.S., George R.A.,
Houck J., Hoskins R.A., Hostin D., Howland T.J.,
alali M., Kruse D., Li P., Mattei B., Moshrefi A.,
Moy M., Murphy B., Nelson K.A., Nelson K.A., Nunoo J.,
ragas V., Park S., Patel S., Pfeiffer B.,

Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of *Drosophila melanogaster* genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN

RP SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smtniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
"Annotation of *Drosophila melanogaster* genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RT

RN

RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;

RL

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN

RP SEQUENCE FROM N.A.

RA FlyBase;

RL

Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AB003816; AAM68569.1; -;

DR

FlyBase; FBgn0050482; CG30482.

SQ

SEQUENCE 466 AA; 53179 MW; 22EA4D68BDD64BEA CRC64;

Query Match

Best Local Similarity 1.9%; Score 10; DB 5; Length 466;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 14 AAATTAAAS 23

Db 276 AAATTAAAS 285

RESULT 41

Q86XT7

ID Q86XT7 PRELIMINARY; PRT; 489 AA.

AC Q86XT7;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to forkhead box O1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;

RL EMBL; BC050072; AAH50072.1; -;

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA

DR InterPro; IPR001766; TF_Fork_head.

DR Pfam; PF00250; Fork head; 1.

DR PRINTS; PR00053; FORKHEAD.

DR ProDom; PD000425; TF_Fork_head; 1.

DR SMART; SM00339; FH; 1.

DR PROSITE; PS00657; FORK HEAD_1; 1.

DR PROSITE; PS00658; FORK HEAD_2; 1.

DR PROSITE; PS00339; FORK HEAD_3; 1.

SQ SEQUENCE 489 AA; 52369 MW; 3EB55F4E503E058C CRC64;

Query Match

Best Local Similarity 1.9%; Score 10; DB 4; Length 489;

Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Oy 220 PPQQQPPPP 229

|||||
 QQQPPPP 77

PRELIMINARY; PRT; 489 AA.

(TREMBlrel. 25, Created)
 (TREMBlrel. 25, Last sequence update)
 (TREMBlrel. 25, Last annotation update)

12.5 protein.

12.5.

(Rice).

Aridiplantae; Streptophyta; Embryophyta; Tracheophyta;

a; Magnoliophyta; Liliopsida; Poales; Poaceae;

e; Oryzae; Oryza.

530;

M N.A.

(Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,

J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,

S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,

H., Jia P.X., Qian Y.M., Yang K., Zhou B., Chen Z.H.,

G.L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,

G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,

Li Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,

Wang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,

Wang S.T., Ni L., Zhu F.H., Hong G.F.;

EC-2001) to the EMBL/GenBank/DBJ databases.

105; CAE02257.1; - 126F4480EBB0B1D CRC64;

89 AA; 54725 MW; 126F4480EBB0B1D CRC64;

1.9%; Score 10; DB 10; Length 489;

Identity 100.0%; Pred. No. 4.5;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAPPP 129

|||||

AAAAPPP 14

PRELIMINARY; PRT; 513 AA.

(TREMBlrel. 16, Created)
 (TREMBlrel. 16, Last sequence update)
 (TREMBlrel. 25, Last annotation update)
 o unknown protein (Hypothetical protein)

12B11.2 OR ATSG64430.

thaliana (Mouse-ear cress).

iridiplantae; Streptophyta; Embryophyta; Tracheophyta;

a; Magnoliophyta; eudicotyledons; core eudicots; rosids;

Brassicales; Brassicaceae; Arabidopsis.

702;

M N.A.

bia;

Atoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,

analysis of Arabidopsis thaliana chromosome 5. XI.;

PR-1999) to the EMBL/GenBank/DBJ databases.

M N.A.

, Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

ower L., Jones T., Bann J., Carninci P., Chen H.,

ung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

elologis A., Davis R.W.;

(OV-2001) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,

RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kaw

RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K

RA Ecker J., Theologis A., Davis R.W.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,

RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusa

RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat

RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K.,

RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

RT "Arabidopsis ORF clones";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB025640; BAB11604.1; -

DR EMBL; AY062534; AAL32612.1; -

DR EMBL; AY092962; AAM12961.1; -

DR EMBL; AY093313; AAM13312.1; -

DR EMBL; BT008878; AAF68317.1; -

DR InterPro; IPR000270; OPR_PBI.

DR Pfam; PF00564; PBI; 1.

DR SMART; SM00666; PBI; 1.

KW Hypothetical protein.

SQ SEQUENCE 513 AA; 56441 MW; 255A63F2079726AA CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 513;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 222 QQQQPPPPQ 231

Db 414 QQQQPPPPQ 423

RESULT 44

Q9LWQ9

ID Q9LWQ9 PRELIMINARY; PRT; 525 AA.

AC Q9LWQ9;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Similar to Arabidopsis thaliana chromosome II BAC T9T22 genomic

DE sequence.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC

RT clone: P0431F01.1";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP001550; BAA92994.1; -

DR Gramine; Q9LWQ9; -

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 7.

DR PRINTS; PR00320; GPROTEINRPT.

DR SMART; SM00320; WD40; 5.

DR PROSITE; PSS0082; WD_REPEATS_2; 3.

DR PROSITE; PSS00294; WD_REPEATS_REGION; 1.

KW Repeat; WD repeat.

SQ SEQUENCE 525 AA; 55187 MW; 8C302D45D6EA5BC1 CRC64;

Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 525;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

conservative 0; Mismatches 0; Indels 0; Gaps 0;
DDDD 337
|||||
DDDD 453

RELIMINARY; PRT; 544 AA.
TrEMBLrel. 01, Created)
TrEMBLrel. 01, Last sequence update)
TrEMBLrel. 25, Last annotation update)

rsaria chlorella virus 1 (PBCV-1).
A viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
506;

N.A.
167; PubMed=7831789;
Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;
45 kb of DNA located at the left end of the chlorella
genome.";
339-352(1995).

N.A.
326; PubMed=10544099;
Ilmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Ickerson K.W., Van Etten J.L.;
PBCV-1 encodes a functional homosperridine
254-262(1999).

N.A.
354; PubMed=11021991;
J.R., Adams B.J., Graves M.V., Van Etten J.L.;
ion of a beta-1,3-glucanase encoded by chlorella virus
27-36(2000).

N.A.
; 1995) to the EMBL/GenBank/DBJ databases.

N.A.
; 1997) to the EMBL/GenBank/DBJ databases.

N.A.
; 1997) to the EMBL/GenBank/DBJ databases.

N.A.
; 1998) to the EMBL/GenBank/DBJ databases.

N.A.
; 1999) to the EMBL/GenBank/DBJ databases.

N.A.
Graves M.V., Van Etten J.L.;
2-2000) to the EMBL/GenBank/DBJ databases.
AAC96425.1; -.
117547.
1 AA; 59361 MW; 6680655754F034E5 CRC64;

arity 1.9%; Score 10; DB 12; Length 544;
arity 100.0%; Pred.No.4.9;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 PPPTAPPPPP 136
| | | | | | | | | |
Db 379 PPPTAPPPPP 388

RESULT 46
Q8S7N6 PRELIMINARY; PRT; 570 AA.
AC Q8S7N6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative pyruvate kinase (EC 2.7.1.40) (PK).
GN OSUNBA0095C07.5.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Ganeberg K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
vanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbus
Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUNBA0095C07 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
chromosome 10.";
RL Science 300:1566-1569(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + PYRUVATE = ADP + PHOSPHOENOLPYRUVAT
CC -1- COFACTOR: REQUIRES MAGNESIUM AND POTASSIUM (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS; FINAL STEP.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PYRUVATE KINASE FAMILY.
DR EMBL; AC077693; AAL86487.1; -.
DR EMBL; AE017121; AAP55104.1; -.
DR Gramene; Q8S7N6; -.
DR GO; GO:000287; F:magnesium ion binding; IEA.
DR GO; GO:0004743; F:pyruvate kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001697; Pyruvate_kinase.
DR Pfam; PF00224; PK; 1.
DR Pfam; PF02887; PK_C; 1.
DR PRINTS; PR01050; PYRUVTKINASE.
DR ProDom; PD001009; Pyruvate kinase; 1.
DR TIGRFAMs; TIGR01064; pyruv_kin; 1.
DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
KW Glycolysis; Kinase; Magnesium; Pyruvate; Transferase.
SQ SEQUENCE 570 AA; 61645 MW; 00CA46020AFF6D8A CRC64;

Query Match 1.9%; Score 10; DB 10; Length 570;
Best Local Similarity 100.0%; Pred.No.5.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

Qy 119 PAAAAAAPP 128
| | | | | | | | | |
Db 26 PAAAAAAPP 35

RESULT 47

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PRELIMINARY;      PRT;      580 AA.

(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 25, Last annotation update)
(E60543) corresponds to a region of the predicted
(Rice).
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
e; Oryzeae; Oryza.
530;

M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare (GA3) genomic DNA, chromosome 6, PAC
04.";
AY-2000) to the EMBL/GenBank/DBJ databases.
69; BAA95818.1; -.
WJ7; -.
R001026; ENTH.
R008943; PI_bind_N.
7; ENTH; 1.
73; ENTH; 1.
80 AA; 64048 MW; 7E26B931100A7144 CRC64;

1.9%; Score 10; DB 10; Length 580;
larity 100.0%; Pred.No.5.1;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAPPP 129
|||||
AAAAPPP 531

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PRELIMINARY;      PRT;      607 AA.

(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)
(TREMBLrel. 24, Last annotation update)
protein.

iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Panicoideae; Andropogoneae; Zea.
577;

M N.A.
SS953;
3764; PubMed=12368247;
ca V., Messing J.;
nization of Orthologous Sequences in Grass Genomes.";
121549-1555(2002).
65; AAN40027.1; -.
R005516; Remorin_C.
3; Remorin_C; 1.
protein.
07 AA; 64780 MW; 8C699253452700EF CRC64;

1.9%; Score 10; DB 10; Length 607;
larity 100.0%; Pred.No.5.3;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EEDDED 337
|||||
EEDDED 296

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RESULT 49
Q7UBI5
ID Q7UBI5      PRELIMINARY;      PRT;      608 AA.

AC Q7UBI5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sigmad(70) factor of RNA polymerase.
GN RPOD OR S3913.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016988; AAP18396.1; -.
SQ SEQUENCE 608 AA; 69601 MW; E07A9E0169699DA1 CRC64;

Query Match      1.9%; Score 10; DB 16; Length 608;
Best Local Similarity 100.0%; Pred.No.5.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 333 DDEDEDEED 342
DB 191 DDEDEDEED 200
|||||

RESULT 50
Q8XAN5
ID Q8XAN5      PRELIMINARY;      PRT;      613 AA.

AC Q8XAN5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNA polymerase, sigma(70) factor, regulation of proteins induced
DE high temperatures (RNA polymerase sigma 70 factor RpoD).
GN RPOD OR Z4420 OR ECS3950.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Rosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).

```

6; AAG58201.1; -;
 4; BAB37373.1; -;
 B85967.
 F91122.
 9; P:DNA-directed RNA polymerase activity; IEA.
 0; P:sigma factor activity; IEA.
 0; P:transcription factor activity; IEA.
 5; P:regulation of transcription, DNA-dependent; IEA.
 2; P:transcription initiation; IEA.
 009043; RNA pol sigma.
 007631; Sigma70_ner.
 007127; Sigma70_r1.1.
 009042; Sigma70_r1.2.
 007627; Sigma70_r2.
 007624; Sigma70_r3.
 007630; Sigma70_r4.
 000943; Sigma70.
 ; sigma70_ner; 1.
 ; sigma70_r1.1; 1.
 ; sigma70_r1.2; 1.
 ; sigma70_r2; 1.
 ; sigma70_r3; 1.
 ; sigma70_r4; 1.
 146; SIGMA70FCT.
 1715; SIGMA70.1; 1.
 1716; SIGMA70.2; 1.
 come.
 3 AA; 70207 MW; 6B4CC1D0CA82AA9E CRC64;
 1.9%; Score 10; DB 16; Length 613;
 arity 100.0%; Pred.No. 5.4;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DEDED 342
 |||||
 DEDED 200
 PRELIMINARY; PRT; 613 AA.
 TREMBLrel. 24, Created)
 TREMBLrel. 24, Last sequence update)
 TREMBLrel. 25, Last annotation update)
 e, sigma(70) factor, regulation of proteins induced at
 ures.
 8.
 neri.
 teobacteria; Gammaproteobacteria; Enterobacteriales;
 aceae; Shigella.
 3;
 N.A.
 Serotype 2a;
 406; PubMed=12384590;
 Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 nce of Shigella flexneri 2a: insights into pathogenicity
 rison with genomes of Escherichia coli K12 and O157.";
 Res. 30:4432-4441(2002).
 2; AAN44584.1; -;
 9; P:DNA-directed RNA polymerase activity; IEA.
 7; P:sigma factor activity; IEA.
 0; P:transcription factor activity; IEA.
 5; P:regulation of transcription, DNA-dependent; IEA.
 2; P:transcription initiation; IEA.
 009043; RNA pol sigma.
 007631; Sigma70_ner.
 007127; Sigma70_r1.1.

DR InterPro; IPR009042; Sigma70_r1.2.
 DR InterPro; IPR007627; Sigma70_r2.
 DR InterPro; IPR007624; Sigma70_r3.
 DR InterPro; IPR007630; Sigma70_r4.
 DR InterPro; IPR000943; Sigma70.
 DR Pfam; PF04546; sigma70_ner; 1.
 DR Pfam; PF03979; sigma70_r1.1; 1.
 DR Pfam; PF00140; sigma70_r1.2; 1.
 DR Pfam; PF04542; sigma70_r2; 1.
 DR Pfam; PF04539; sigma70_r3; 1.
 DR Pfam; PF04545; sigma70_r4; 1.
 DR PRINTS; PR00046; SIGMA70FCT.
 DR PROSITE; PS00715; SIGMA70.1; 1.
 DR PROSITE; PS00716; SIGMA70.2; 1.
 KW Complete proteome.
 SQ SEQUENCE 613 AA; 70207 MW; 6B4CC1D0CA82AA9E CRC64;
 Query Match 1.9%; Score 10; DB 16; Length 613;
 Best Local Similarity 100.0%; Pred.No. 5.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 333 DDEDEDED 342
 |||||
 DB 191 DDEDEDED 200
 RESULT 52
 096151 PRELIMINARY; PRT; 635 AA.
 AC 096151;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN PF80250W.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed=9804551;
 RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind I
 Koonin E.V., Shalton S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perte M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H
 Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
 RA "Chromosome 2 sequence of the human malaria parasite Plasmodium
 falciparum.";
 RT Science 282:1126-1132(1998).
 RL Science 282:1126-1132(1998).
 DR EMBL; AE001382; AAC71839.1; -.
 DR PIR; A71620; A71620.
 KW Hypothetical protein.
 SQ SEQUENCE 635 AA; 76449 MW; DDB063DC15C15459 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 635;
 Best Local Similarity 100.0%; Pred.No. 5.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 334 DDEDEDED 343
 |||||
 DB 577 DDEDEDED 586
 RESULT 53
 08DC21 PRELIMINARY; PRT; 636 AA.
 ID 08DC21
 AC 08DC21;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide
 acyltransferase component.
 GN WV11631.

ficus.
 oteobacteria; Gammaproteobacteria; Vibrionales;
 ; Vibrio.
 72;
 M N.A.
 ;
 im S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 nome sequence of *Vibrio vulnificus* CMCP6.";
 EC-2002) to the EMBL/GenBank/DBJ databases.
 02; AA010050.1; -.
 54; F:pyruvate dehydrogenase complex; IEA.
 15; F:acyltransferase activity; IEA.
 42; F:diacylglycerol kinase activity; IEA.
 15; F:protein binding; IEA.
 96; P:glycolysis; IEA.
 52; P:metabolism; IEA.
 R001078; 2-oxoacid dh.
 R006256; AceF.
 R000089; Biotin lipoyl.
 R004167; E3 binding.
 R003016; Lipoyl BS.
 8; 2-oxoacid dh; 1.
 4; biotin lipoyl; 3.
 7; e3 binding; 1.
 1115; 2-oxoacid dh; 1.
 GR01348; PDHac trf_long; 1.
 0189; LIPOYL; 3.
 teome.
 36 AA; 65712 MW; 845B61BDB8CA23327 CRC64;
 laxity 1.9%; Score 10; DB 16; Length 636;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRELIMINARY; PRT; 660 AA.

(TrEMBLrel. 13, Created)
 (TrEMBLrel. 13, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)

4.
 elanogaster (Fruit fly).
 stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 dopterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 227;
 M N.A.
 lev;
 PubMed=10731132;
 Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Achayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Baeu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 oup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischma
 RA Posler C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003609; AAF52249.1; -.
 DR HSSP; P24781; 1XBR.
 DR FlyBase; FBgn0016660; H15.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IE
 DR InterPro; IPR008967; P53-like.
 DR InterPro; IPR001699; TF T-box.
 DR Pfam; PF00907; T-box; 1.
 DR PRINTS; PR00937; TBOX.
 DR SMART; SM00425; TBOX; 1.
 DR PROSITE; PS01283; TBOX_1; 1.
 DR PROSITE; PS0252; TBOX_3; 1.
 SQ SEQUENCE 660 AA; 72370 MW; 904BEF9AE684B58F CRC64;

Query Match 1.9%; Score 10; DB 5; Length 660;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 13 AAAATTAATAA 22
 Db 141 AAAATTAATAA 150

RESULT 55

Q9U0N1 PRELIMINARY; PRT; 673 AA.
 ID Q9U0N1
 AC Q9U0N1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical gap protein.
 GN GARP.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RC STRAIN=3D7;
 RP SEQUENCE FROM N.A.
 RA Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M
 RA Barrell B.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031746; CAB63561.1; -.
 SQ SEQUENCE 673 AA; 79795 MW; 7A7FFE921D83DA26 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 673;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;

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QY DEDEDE 340
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   DEDEDE 645

RELIMINARY;      PRT;      714 AA.

TREMBlrel. 22, Created)
TREMBlrel. 22, Last sequence update)
TREMBlrel. 24, Last annotation update)
rotein.

(japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzaeae; Oryza.
947;

N.A.
pponbare;
tsumoto T., Yamamoto K.;
nipponbare (GA3) genomic DNA, chromosome 1, PAC
7.";
V-2000) to the EMBL/GenBank/DBJ databases.
0; BAB92117.1; -.
1; C:integral to membrane; IEA.
004695; C4dc/mal transpt.
; C4dic mal tran_1.
4 AA; 78219 MW; A52C833843B619FE CRC64;

1.9%; Score 10; DB 10; Length 714;
arity 100.0%; Pred. No. 6.1;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAT 157
|||||
AAAAAT 167

RELIMINARY;      PRT;      759 AA.

TREMBlrel. 23, Created)
TREMBlrel. 23, Last sequence update)
TREMBlrel. 25, Last annotation update)
assium channel Kv3.3.

uniculus (Rabbit).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Lagomorpha; Leporidae; Oryctolagus.
86;

N.A.
1 endothelium;
629; PubMed=10712820;
pard A.R.;
ium channels in lens epithelium and corneal
; 70:339-348(2000).

N.A.
1 endothelium;
pard A.R.;
3-2002) to the EMBL/GenBank/DBJ databases.
9; AAN15930.1; -.
1; C:integral to membrane; IEA.
6; C:voltage-gated potassium channel complex; IEA.
5; F:protein binding; IEA.
9; F:voltage-gated potassium channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel pore.
DR InterPro; IPR005404; KV3.3 channel.
DR InterPro; IPR003968; KV_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M-channel nlg.
DR InterPro; IPR003974; Shaw channel.
DR Pfam; PF00520; ion_trans_1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01582; KV33CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR PRINTS; PR01498; SHAWCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Ionic channel.
SQ SEQUENCE 759 AA; 80499 MW; 746486F967D6E7AF CRC64;

Query Match      1.9%; Score 10; DB 6; Length 759;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; C

QY 226 PPPPQPQPPPP 235
   |||||
   DB 36 PPPPQPQPPPP 45

RESULT 58
Q9AB02
ID Q9AB02 PRELIMINARY; PRT; 762 AA.
AC Q9AB02;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Chemotaxis protein CheA.
GN CC0433.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Ely
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Sait J., Craven M.B., Khouri H., Shetty J., Berry K
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whit
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
CC EMBL; AE005716; AAK22420.1; -.
DR PTR; H87302; H87302.
DR HSPP; Q56310; I33Q.
DR TIGR; CC0433; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:kinase activity; IEA.
DR GO; GO:0016301; F:sugar porter activity; IEA.
DR GO; GO:0005351; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0000455; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.

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R002545; Chew.
R004105; H-kinase dim.
R005467; His Kinase.
R002114; Hpr_Serp_S.
R008207; Hpt_N.
R008208; Hpt_N.
4; Chew; 1.
5; H-kinase_dim; 1.
8; HATPase_c; 1.
7; Hpt; 1.
344; BCTRLSENSOR.
3142; Hpt_N; 1.
60; Chew; 1.
87; HATPase_c; 1.
73; HPT; 1.
0851; CHEW; 1.
0109; HIS_KIN; 1.
0894; HPT; 1.
0589; PTS_HPR_SER; 1.
phorylation; Sensory transduction; Transferase;
teome.
62 AA; 80149 MW; 95E9D16BE4F5AC2A CRC64;
1.9%; Score 10; DB 16; Length 762;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
larity 100.0%; Pred. No. 6.5;
AAAAAAP 127
|||||
AAAAAAP 347
PRELIMINARY; PRT; 806 AA.
(TREMBLrel. 13, Created)
(TREMBLrel. 13, Last sequence update)
(TREMBLrel. 24, Last annotation update)
in (Zinc finger transcription factor).
7.
elanogaster (Fruit fly).
etazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
dopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
227;
M N.A.
ley;
606; PubMed=10731132;
Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
yle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahlke C., Davenport L.B., Davies P.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
oup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
Evangelista C.C., Ferraz C., Ferreira S., Fleischmann M.,
abrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
ouston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
ei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.I
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese N
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP Ruiz-Gomez M., Coutts N., Suster M.L., Landgraf M., Bate M.;
RA "myoblasts incompetent encodes a zinc finger transcription factor
RT required to specify fusion competent myoblasts in Drosophila";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003741; AAF56082.1; -.
DR EMBL; AJ311850; CAC51080.1; -.
DR HSP; P08151; 2GLI
DR FlyBase; FBgn0039039; lmd.
DR GO; GO:0007525; P:somatic muscle development; IMP.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 806 AA; 89406 MW; CD2F5254D934EBD7 CRC64;
Query Match 1.9%; Score 10; DB 5; Length 806;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0;
QY 20 AAASSSAASP 29
|||||
DB 214 AAASSSAASP 223
RESULT 60
Q96210
ID Q96210 PRELIMINARY; PRT; 866 AA.
AC Q96210;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
GN Zn finger transcription factor lame duck (LD47926p) (CG4677-PB).
LN LMD OR CG4677.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP Duan H., Nguyen H.T.;
RT "A novel Zn finger protein that is essential for myogenesis";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M
RA Celniker S.;
Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

N.A. PubMed=10731132;
 elniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.H., Blazer R.G., Zhang M., Pfeiffer B.D.,
 le C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 Gbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Otchan M.R., Bouck J., Brokstein P., Brotter P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 orielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Iston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 Iush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 i B., McIntosh T.C., McLeod M.F., McPherson D.,
 Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 cy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 emington K., Saunders R.D., Scheeler F., Shen H.,
 den-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 adling A.C., Stapleton M., Strong R., Sun E.,
 rector C., Turner R., Venter E., Wang A.H., Wang X.,
 ssarman D.A., Weinstock G.M., Weissbach J.,
 Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 eri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 hong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 yers E.W., Rubin G.M., Venter J.C.;
 sequence of *Drosophila melanogaster*.";
 185-2195(2000).
 N.A.
 Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 ccayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
 Center A., Champagne M., Davenport L.B., Dietz S.M.,
 rsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Frise E., Galle R.F., Garg N.S., George R.A.,
 Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 alali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 ragas V., Park S., Patel S., Pfeiffer B.,
 S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Strong R., Svirska R., Tector C., Tyler D.,
 Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Drosophila melanogaster genome.";
 3-2000) to the EMBL/GenBank/DBJ databases.
 N.A.
 sby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 tuang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 rgan C., Herman B., Carlson J.W., Ceinkner S.E.,
 sdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Marshall B., Millburn G., Richter J., Russo S.,
 Smith E., Shu S., Smutniak F., Whitfield E.,
 Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Drosophila melanogaster genome.";
 R-2000) to the EMBL/GenBank/DBJ databases.
 N.A.
 elniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 R-2000) to the EMBL/GenBank/DBJ databases.

[7]
 RN SEQUENCE FROM N.A.
 RP FlyBase;
 RL Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.
 RM EMBL; AY032609; AAK39641.1; -
 DR EMBL; AY121651; AAM51978.1; -
 DR EMBL; AB003741; AANI3923.1; -
 DR FlyBase; FBGN0039039; lmd.
 DR GO; GO:0007525; P:somatic muscle development; IMP.
 DR InterPro; IPR007087; Znf C2H2.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR ProDom; PD000003; Znf C2H2; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
 DR Metal-binding; Zinc; Zinc-finger.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 866 AA; 96040 MW; 596394F14F4BA0EC CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 866;
 Best Local Similarity 100.0%; Pred.No. 7.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G
 Oy 20 AAASSSAASP 29
 Db 235 AAASSSAASP 244
 |||||
 RESULT 61
 Q8LIF6 PRELIMINARY; PRT; 888 AA.
 ID Q8LIF6
 AC Q8LIF6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE QJ1316 A04.5 protein (P0503D09.22 protein).
 GN QJ1316 A04.5 OR P0503D09.22
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
 clone:OJ1316 A04.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
 clone:P0503D09.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003822; BAC06989.1; -
 DR EMBL; AP005455; BAC16733.1; -
 DR Gramene; Q8LIF6; -
 DR InterPro; IPR007527; Znf_SWIM.
 DR Pfam; PF04434; SWIM; 1.
 DR SEQUENCE 888 AA; 100868 MW; AA78854BF338E542 CRC64;
 Query Match 1.9%; Score 10; DB 10; Length 888;
 Best Local Similarity 100.0%; Pred.No. 7.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G
 Oy 151 AAAAAATAPP 160
 Db 119 AAAAAATAPP 128
 |||||
 RESULT 62
 Q8BK12 PRELIMINARY; PRT; 943 AA.
 ID Q8BK12

(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
K. proline-rich region containing protein.

(Mouse).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0090;

M N.A.
/6J; TISSUE=Eye;
4683; PubMed=12466851;
Ensembl;

name Exploration Research Group Phase I & II Team;
the mouse transcriptome based on functional annotation of
length cDNAs";
53-573(2002).;

22; BAC34813.1; -;
P10698.
3730; D230019K20Rik.
protein.

43 AA; 99939 MW; 8B2D3326D09B5426 CRC64;

1.9%; Score 10; DB 11; Length 943;
larity 100.0%; Pred. No. 7.8;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPPQP 231
|||||
QPPPPQP 832

PRELIMINARY; PRT; 1038 AA.

(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)

ris (Yeast).
ungi; Ascomycota; Saccharomycotina; Saccharomycetes;
tales; Saccharomycetaceae; Pichia.
922;

M N.A.

2858; PubMed=10923020;
Kaiser C.A., Bevis B.J., Soderholm J., Fu D., Sears I.B.,
f Pichia pastoris genes involved in ER-to-Golgi

-993(2000).
60; AAF27636.1; -;
R000886; ER_target_S.
R001680; WD40.
20; WD40; 1.

0014; ER_TARGET; 1.
epest.
038 AA; 114600 MW; FE23F286859EBB36 CRC64;

1.9%; Score 10; DB 3; Length 1038;
larity 100.0%; Pred. No. 8.4;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EDDDEDE 338
|||||
EDDDEDE 1019

RESULT 64
P97496

ID P97496 PRELIMINARY; PRT; 1100 AA.
AC P97496;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SRG3.
GN SMARCC1 OR SRG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI_TaxID=10090;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Jeon S.H., Kang M.G., Kim Y.H., Lee C., Park S.D., Seong R.H.;
RT "A new mouse gene, SRG3, related to the SWI3 of Saccharomyces
RT cerevisiae";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR EMBL; U85614; AAB42085.1; -;
DR PIR; T30967; T30967.
DR MGD; MGI:1203524; Smarcc1.
DR GO; GO:0009887; P.organoogenesis; IMP.
DR InterPro; IPR001357; BRCT.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR001005; Myb DNA_binding.
DR InterPro; IPR007526; SWIRM.
DR Pfam; PF00533; BRCT; 1.
DR Pfam; PF00249; myb DNA-binding; 1.
DR Pfam; PF04433; SWIRM; 1.
DR SMART; SM00298; CHROMO; 1.
DR SMART; SM00717; SANT; 1.
DR PROSITE; PS50030; MYB 3; 1.
KW DNA-binding; Nuclear Protein.
SQ SEQUENCE 1100 AA; 123276 MW; 0321A9E95FDBAB4A CRC64;

Query Match 1.9%; Score 10; DB 11; Length 1100;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 220 PQQQQPPPP 229
DB 1073 PQQQQPPPP 1082

RESULT 65
Q9VY88

ID Q9VY88 PRELIMINARY; PRT; 1250 AA.
AC Q9VY88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RDGB protein.
GN RDGB OR CG1111.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Gallie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.
RA Wan X.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin

BA Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 BA Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 BA Otchan M.R., Bouck J., Brokstein P., Brothier P.,
 BA Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 BA Cawley S., Dahlke C., Davenport L.B., Davies P.,
 BA Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 BA up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 BA Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 BA briellan M.E., Garg N.S., Gelbart W.M., Glasser K.,
 BA ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 BA Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 BA uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 BA lush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 BA Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 BA Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 BA i B., McIntosh T.C., McLeod M.P., McPherson D.,
 BA Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 BA oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 BA Nelson K.A., Nixon K., Nuskearn D.R., Pacleb J.M.,
 BA Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 BA emington K., Saunders R.D.C., Scheeler F., Shen H.,
 BA den-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 BA adling A.C., Stapleton M., Strong R., Sun E.,
 BA Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 BA assarman D.A., Weinstock G.M., Weissbach J.,
 BA , Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 BA -F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 BA hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 BA yers E.W., Rubin G.M., Venter J.C.;
 BA sequence of *Drosophila melanogaster*;
 BA 185-2195(2000).
 BA 3; AAF48315.1; -;
 BA 0003218; rdgB.
 BA 9; C:subrhabdomeral cisterna; NAS.
 BA 5; P:phosphatidylcholine transporter activity; IDA.
 BA 6; P:phosphatidylcholine transporter activity; IDA.
 BA 9; P:deactivation of rhodopsin mediated signaling; IMP.
 BA 8; P:olfaction; IMP.
 BA 6; P:rhodopsin mediated signaling; IMP.
 BA 004177; DDHD dom.
 BA 001666; PI transfer.
 BA ; DDHD; 1.
 BA ; IP trans; 1.
 BA 91; PITRANSFER.
 BA 50 AA; 137840 MW; E4E78525D1BDAE2A CRC64;
 BA 1.9%; Score 10; DB 5; Length 1250;
 BA arity 100.0%; Pred. No. 9.9;
 BA nservative 0; Mismatches 0; Indels 0; Gaps 0;
 BA 00DEDE 338
 BA |||||
 BA 00DEDE 333
 BA
 BA RELIMINARY; PRT; 1250 AA.
 BA
 BA TrEMBLrel. 04, Created)
 BA TrEMBLrel. 04, Last sequence update)
 BA TrEMBLrel. 25, Last annotation update)
 BA eration B protein.
 BA 11.
 BA lanogaster (fruit fly).
 BA tzoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 BA pterygota; Diptera; Brachycera; Muscomorpha;
 BA Drosophilidae; Drosophila.
 BA 27;
 BA N.A.
 BA -R; TISSUE=Head;
 BA 389; PubMed=9680295;

RA Rubboli F., Bulfone A., Bogni S., Marchitelli A., Zollo M.,
 RA Borsani G., Ballabio A., Banfi S.;
 RA "A mammalian homologue of the *Drosophila* retinal degeneration B,
 RA implications for the evolution of phototransduction mechanisms.",
 RA Genes Funct. 1:205-214(1997).
 RA [2]
 RA SEQUENCE FROM N.A.
 RA RP STRAIN=ORCON-R; TISSUE=Head;
 RA RX MEDLINE=91231170; PubMed=1903119;
 RA Vitelic T.S., Hyde D.R., O'Tousa J.E.;
 RA "Isolation and characterization of the *Drosophila* retinal degene;
 RA B (rdgB) gene.",
 RA Genetics 127:761-768(1991).
 RA EMBL; Y08035; CAA69291.1; -;
 RA FlyBase; FBgn0003218; rdgB.
 RA GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
 RA GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
 RA GO; GO:0008536; F:phosphatidylcholine transporter activity; IDA.
 RA GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; I
 RA GO; GO:0007608; P:olfaction; IMP.
 RA GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
 RA InterPro; IPR004177; DDHD_dom.
 RA InterPro; IPR001666; PI_transfer.
 RA Pfam; PF02862; DDHD; 1.
 RA Pfam; PF02121; IP_trans; 1.
 RA PRINTS; PR00391; PITRANSFER.
 RA SQ SEQUENCE 1250 AA; 137777 MW; 3CC926ABBA40AGF28 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 1250;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G
 QY 329 EEEEDDEDE 338
 DB 324 EEEEDDEDE 333
 RESULT 67
 Q28224 PRELIMINARY; PRT; 1251 AA.
 ID Q28224
 AC Q28224
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE IRS-1(COS).
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96067568; PubMed=7488107;
 RA Wang L., Hayashi H., Mitani Y., Ishii K., Ohnishi T., Niwa Y.,
 RA Kido H., Ebina Y.;
 RA "Cloning of a cDNA encoding a 190-kDa insulin receptor substrate-
 RA like protein of simian COS cells.",
 RA Biochem. Biophys. Res. Commun. 216:321-328(1995).
 RL -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC EMBL; D64157; BAAL1026.1; -;
 DR HSSP; P35568; IIRS.
 DR GO; GO:0005158; F:insulin receptor binding; IEA.
 DR InterPro; IPR002404; Insulin_receptor_S1.
 DR InterPro; IPR001849; PH.
 DR Pfam; PF02174; IRS; 1.
 DR Pfam; PF00169; PH; 1.
 DR PRINTS; PR00628; INSULINRS1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00310; PTBI; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR SQ SEQUENCE 1251 AA; 133054 MW; 924CCAC3BE68EB98 CRC64;
 Query Match 1.9%; Score 10; DB 6; Length 1251;

larity 100.0%; Pred. No. 9.9;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 JASSNAAS 28
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 JASSNAAS 1050

PRELIMINARY; PRT; 1259 AA.
 (TREMELrel. 19, Created)
 (TREMELrel. 19, Last sequence update)
 (TREMELrel. 25, Last annotation update)
 |||||
 (1111-PA).
 111.
 melanogaster (Fruit fly).
 etazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 dpterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 227;
 M N.A.
 ley;
 Brokstein P., Hong L., Aghayani A., Carlson J.,
 havez C., Dorsett V., Farfan D., Frise E., George R.,
 Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 cleb J., Faragas V., Park S., Phouanavong S., Wan K.,
 S.E., Rubin G.M., Celnik S.
 UG-2001) to the EMBL/GenBank/DBJ databases.
 M N.A.
 6006; PubMed=10731132;
 Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 .G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 yle C., Baxter A.G., Helt G., Nelson C.R., Gabor G.L.,
 Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
 Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Belcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 cup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 abrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,
 ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 uston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 i Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 ai B., McIntosh T.C., McLeod M.P., McPherson D.,
 Malshina N.V., Mobarry C., Morris J., Moshrefi A.,
 moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Remington K., Saunders R.D., Scheeler F., Shen H.,
 iden-Klamas I., Simpson M., Skupski M.P., Smith T.,
 radling A.C., Stapleton M., Strong R., Sun E.,
 Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 asarman D.A., Weinstein G.M., Weissbach J.,
 Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 veri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Myers E.W., Rubin G.M., Venter J.C.;
 sequence of *Drosophila melanogaster*.;
 2185-2195 (2000).

SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers
 RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busan D.A.
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan I
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo
 RA Pacleb J., Faragas V., Park S., Patel S., Pfeiffer B., Scheeler I
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler I
 RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
 RA Hradscky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.
 RA "Annotation of *Drosophila melanogaster* genome.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY051422; AAK92846.1; -
 DR EMBL; AE003493; AAF48316.2; -
 DR FlyBase; Fgn0003218; rdgb.
 DR GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
 DR GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
 DR GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
 DR GO; GO:0016059; P:deactivation of rhodopsin mediated signaling;
 DR GO; GO:0007608; P:olfaction; IMP.
 DR GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
 DR InterPro; IPR004177; DDHD dom.
 DR InterPro; IPR001666; PI_transfer.
 DR Pfam; PF02862; DDHD; 1.
 DR Pfam; PF02121; IP_trans; 1.
 DR PRINTS; PR00391; PITRANSFER.
 SQ SEQUENCE 1259 AA; 138895 MW; 9DD40B76EB1079F7 CRC64;
 Query Match 1.9%; Score 10; DB 5; Length 1259;
 Best Local Similarity 100.0%; Pred. No. 9.9;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 QY 329 EEEEDDEDE 338
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 Db 324 EEEEDDEDE 333

RESULT 69
 Q9ESU6 PRELIMINARY; PRT; 1400 AA.
 AC Q9ESU6
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Cell proliferation related protein CAP.
 GN BRD4 OR CAP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mur
 OC NCBI_TaxID=10090;


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AC Q8NMS0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3-oxoacyl-(acyl-carrier-protein) synthase (EC 2.3.1.85).
GN CGL2495.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005281; BAB99888.1; -
DR GO; GO:0005835; C:fatty-acid synthase complex; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact.
DR GO; GO:0004312; F:fatty-acid synthase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001227; Ac trans.
DR InterPro; IPR003965; Fatty acid synth.
DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR002539; Maoc dehydratase.
DR InterPro; IPR001638; SBP_bac_3.
DR Pfam; PF00698; Acyl_transf; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR Pfam; PF01575; Maoc dehydratase; 1.
DR PRINTS; PR01483; FASYNTHASE.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS01039; SBP_BACTERIAL_3; 1.
KW Transferase; Acyltransferase; Complete proteome.
SQ SEQUENCE 2993 AA; 316347 MW; 14CCEA44FAC3561B CRC64;

Query Match 1.9%; Score 10; DB 16; Length 2993;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 137 PAPVAAAPAA 146
Db 1696 PAPVAAAPAA 1705
|||||

RESULT 75
Q9BMP6 PRELIMINARY; PRT; 78 AA.
AC Q9BMP6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ribosomal P0 protein (Fragment).
OS Culicoides nubeculosus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Ceratopogonidae; Ceratopogoninae; Culicoides.
OX NCBI_TaxID=144565;
RN [1]
RP SEQUENCE FROM N.A.
RA Althaus H., Marti E., Mueller N.;
RT "Cloning and sequencing of a partial cDNA expressing a recombinat
RT Culicoides nubeculosus ribosomal P0 protein.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314650; AAK00899.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

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31 N2; PubMed=9851916;
ence of the nematode C.elegans: A platform for
3 biology";
2012-2018(1998).
4 N.A.
31 N2;
AY-2003) to the EMBL/GenBank/DBJ databases.
04; CAC35852.2; -
1B2A.23; CE34109.
24; F:ATP binding; IEA.
26; F:ATP dependent helicase activity; IEA.
77; F:DNA binding; IEA.
R001410; DEAD.
R001650; Helicase_C.
R006562; HSA.
R000330; SNF2_N.
1; helicase_C; 1.
6; SNF2_N; 1.
87; DEXDC; 1.
90; HELICC; 1.
73; HSA; 1.
Protein.
722 AA; 196920 MW; B6B864925F31B643 CRC64;
1.9%; Score 10; DB 5; Length 1722;
latity 100.0%; Pred. No. 13;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TPAPPPP 136
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TPAPPPP 163

PRELIMINARY; PRT; 2980 AA.
(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
membrane protein 1 (PFEMP1).
alciparum (isolate 3D7).
Iveolata; Apicomplexa; Haemosporida; Plasmodium.
5329;

4 N.A.
Irphy L., Harris D., Berriman M., Pain A., Hall N.,
crell B.;
3P-2002) to the EMBL/GenBank/DBJ databases.
07; CAD51361.1; -
39; F:glycosaminoglycan binding; IEA.
05; P:pathogenesis; IEA.
3004258; PFEMP.
1; PFEMP; 2.
380 AA; 340609 MW; 52B1B2CD078DB34C CRC64;
1.9%; Score 10; DB 5; Length 2980;
latity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEEDD 343
|||||
DEDEEDD 1670

PRELIMINARY; PRT; 2993 AA.

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1; P:translational elongation; IEA.
001813; Ribosomal_60S.
1
AA; 8372 MW; A2C63F35E38F124A CRC64;
arity 1.7%; Score 9; DB 5; Length 78;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

AATAP 159
|||||
AATAP 48

RELIMINARY; PRT; 100 AA.

TrEMBLrel. 13, Created)
TrEMBLrel. 13, Last sequence update)
TrEMBLrel. 25, Last annotation update)
protein.
AT4G09270 OR AT4G09220.
Maliana (Mouse-ear cress).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
brassicales; Brassicaceae; Arabidopsis.
02;

N.A.
Der Schueren J., Chuang Y.J., Voet M., Robben J.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
p-1999) to the EMBL/GenBank/DBJ databases.

N.A.
ymonprez B., Volckaert G., Spiegel L.A., Huang E.N.,
J., de la Bastide M., Vil D.M., Preston R.R., Matero A.,
ughnessy A., Rodriguez M., Shekher M., Schutz K.,
oy I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
s sequencing project;
r-2000) to the EMBL/GenBank/DBJ databases.

N.A.
Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
chutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
smcke K., Mayer K.F.X.;
r-2000) to the EMBL/GenBank/DBJ databases.
5; CAB55630.1; -.
4; CAB78050.1; -.
4; CAB78046.1; -.
I17126.
protein.
0 AA; 10935 MW; C6FD13466A73F754 CRC64;
arity 1.7%; Score 9; DB 10; Length 100;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPP 229
|||||
QPPPP 73

RESULT 77
Q7XNS7 PRELIMINARY; PRT; 102 AA.
AC Q7XNS7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB OSJNB0085H1.10 protein.
GN OSJNB0085H1.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu Y.F., Jia J., Yin
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606995; CAB03961.1; -.
SQ SEQUENCE 102 AA; 11560 MW; 1C9C896BD238CAFC CRC64;

Query Match 1.7%; Score 9; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AAAATTAA 21
Db 84 AAAATTAA 92

RESULT 78
Q8LN81 PRELIMINARY; PRT; 103 AA.
AC Q8LN81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OSJNB0091N21.34.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.
RA "Oryza sativa chromosome 10 BAC OSJNB0091N21 genomic sequence."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;

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Y-2003) to the EMBL/GenBank/DBDJ databases.
 2; AM94936.1; -;
 1; AAP54558.1; -;
 91; -;
 protein.
 3 AA; 11065 MW; 3296B0DB35681B7F CRC64;
 1.7%; Score 9; DB 10; Length 103;
 arity 100.0%; Pred. No. 9.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAATA 158
 |||||
 AAATA 56

RELIMINARY; PRT; 105 AA.
 (TrEMBLrel. 22, Created)
 (TrEMBLrel. 22, Last sequence update)
 (TrEMBLrel. 23, Last annotation update)
 protein.
 124.17.
 thaliana (Mouse-ear cross).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 '02;
 I.N.A.
 K.M.K., Ishmael N., Kumar N., Redman J., Riedmuller S.,
 Whitelaw C.A., Fraser C.M., Town C.D.;
 Sequencing of Full-length cDNAs for Hypothetical Genes
 me 2 of Arabidopsis thaliana."
 Y-2002) to the EMBL/GenBank/DBDJ databases.
 8; AM96823.1; -;
 Protein.
 15 AA; 11920 MW; 068D2845C47BC58F CRC64;
 1.7%; Score 9; DB 10; Length 105;
 arity 100.0%; Pred. No. 9.3;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 EEDDD 335
 |||||
 EEDDD 85

RELIMINARY; PRT; 112 AA.
 (TrEMBLrel. 15, Created)
 (TrEMBLrel. 15, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 active acidic ribosomal protein P1).
 WIG01100.
 thaliana (Mouse-ear cross).
 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 '02;
 I.N.A.
 N.P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Lam B.,
 way A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 Li J., Liu A., Liu K., Liu S., Mukharezy N.,
 m C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
 Ecker J.R.;

RT "Genomic sequence for Arabidopsis thaliana BAC T25K16 from chrom:
 I.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBDJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam I.
 Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.,
 Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E
 Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 "Full length cDNA of gene T25K16.9 (GI:6715644).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBDJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones
 Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki
 Davis R.W., Ecker J.R., Theologis A.;
 "Arabidopsis Open Reading Frame (ORF) Clones."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBDJ databases.
 DR EMBL; AC007323; AAF26471.1; -;
 DR EMBL; AY050975; AAK93652.1; -;
 DR EMBL; AY091176; AAM14115.1; -;
 DR PIR; E86141; E86141
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
 DR GO; GO:006414; P:translational elongation; IEA.
 DR InterPro; IPR001813; Ribosomal 60S.
 DR Pfam; PF00428; 60s_ribosomal; I.
 KW Ribosomal protein.
 QY SEQUENCE 112 AA; 11162 MW; 6D086DD332205E7A CRC64;
 DB SEQUENCE 112 AA; 11162 MW; 6D086DD332205E7A CRC64;

Query Match 1.7%; Score 9; DB 10; Length 112;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 138 APVAAAAPA 146
 |||||
 DB 71 APVAAAAPA 79

RESULT 81
 QBLCW9 PRELIMINARY; PRT; 112 AA.
 AC QBLCW9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acidic ribosomal protein, putative.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; ros;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovsky N., Town C.D., Troughan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation."
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;

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DNA from Arabidopsis thaliana.;
?-2002) to the EMBL/GenBank/DBJ databases.
; AM64427.1; -.
; C:intracellular; IEA.
; C:ribosome; IEA.
; P:structural constituent of ribosome; IEA.
; P:translational elongation; IEA.
01813; Ribosomal 60S.
; 60s_ribosomal; I.
ein.
2 AA; 11192 MW; 6D087D8277245E7A CRC64;
1.7%; Score 9; DB 10; Length 112;
arity 100.0%; Pred.No.9.8;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPA 146
|||||
AAPA 79

ELIMINARY; PRT; 113 AA.

EMBLrel. 22, Created)
EMBLrel. 25, Last annotation update)
osomal protein P1-like protein.
aliana (Mouse-ear cress).
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; Brassicales; Brassicaceae; Arabidopsis.
2;
N.A.
fovsky N., Town C.D., Troukhan M., Alexandrov N.,
Flavell R.B., White O., Salzberg S.L.;
essenger RNA sequences greatly improve genome
):0-0(2002).
N.A.
ukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
DNA from Arabidopsis thaliana.;
?-2002) to the EMBL/GenBank/DBJ databases.
; AM62534.1; -.
; C:intracellular; IEA.
; C:ribosome; IEA.
; P:structural constituent of ribosome; IEA.
; P:translational elongation; IEA.
01813; Ribosomal 60S.
; 60s_ribosomal; I.
ein.
1 AA; 11270 MW; 1A2D792A052DA8B9 CRC64;
1.7%; Score 9; DB 10; Length 113;
arity 100.0%; Pred.No.9.9;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAPA 146
|||||
AAPA 79

ELIMINARY; PRT; 113 AA.

EMBLrel. 16, Created)
EMBLrel. 16, Last annotation update)
EMBLrel. 25, Last annotation update)

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DE Putative 60S acidic ribosomal protein P1.
GN AT5G47700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosi
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia.
EX MEDLINE=99156233; PubMed=10048488;
RA Aamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seven
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:379-391(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.
RA Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At5g47700 (GI:15238170).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Shinn P., Southwick A., Shinozaki
RA Sakurai T., Satou M., Seki M., Shinn P., Shinn P., Palm C.J.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016886; BAB1317.1; -.
DR EMBL; AY070049; AAL49806.1; -.
DR EMBL; AY096430; AAM20070.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR001813; Ribosomal_60S.
DR Pfam; PF00428; 60s_ribosomal; I.
KW Ribosomal protein.
SQ SEQUENCE 113 AA; 11247 MW; FAB300CD9B5D3FB6 CRC64;
Query Match 1.7%; Score 9; DB 10; Length 113;
Best Local Similarity 100.0%; Pred.No.9.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 138 APVAAAAPA 146
DB 71 APVAAAAPA 79
|||||
RESULT 84
Q852J2 PRELIMINARY; PRT; 118 AA.
AC Q852J2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OSJNB0060J21.32.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

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THE

RELIMINARY; PRT; 137 AA.

trEMBLrel. 16, Created)
trEMBLrel. 22, Last sequence update)
3C32, a novel gene induced by complement activation in
(tes).

(Human).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
06;

N.A.

1-2000) to the EMBL/GenBank/DBJ databases.
3; CAC13101.1; --
7 AA; 14559 MW; 7626567DBCD9525 CRC64;

1.7%; Score 9; DB 4; Length 137;
arity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127
|||||
AAAP 18

RELIMINARY; PRT; 145 AA.

trEMBLrel. 19, Created)
trEMBLrel. 22, Last sequence update)
protein (Fragment).
(Human).

tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
06;

N.A.

and Embryonic carcinoma;
1-2001) to the EMBL/GenBank/DBJ databases.
; AAH16788.1; --
protein.
1
; AA; 15325 MW; BA2AFB79A1120A7E CRC64;

1.7%; Score 9; DB 4; Length 145;
arity 100.0%; Pred. No. 12;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

IPARA 148
|||||
IPARA 87

RELIMINARY; PRT; 148 AA.

trEMBLrel. 23, Created)
trEMBLrel. 23, Last sequence update)
trEMBLrel. 24, Last annotation update)

anogaster (Fruit fly).
tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
Ariel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.
Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman
Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Y
Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell I
Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

```

RA      melniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RE      (R-2000) to the EMBL/GenBank/DBJ databases.
KE      1 N.A.
RA
RA
RA      RF-2002) to the EMBL/GenBank/DBJ databases.
RE      1; AAN10846.1; -
DE      10051845; CG31845.
DE      18 AA; 15757 MW; DD9BC290DA87A1D0 CRC64;
SQ
      1.7%; Score 9; DB 5; Length 148;
      Identity 100.0%; Pred.No.12;
      Conservative 0; Mismatches 0; Indels 0; Gaps
      0;
      AAAAAA 126
      |||||
      AAAAAA 116
      |
      PRELIMINARY; PRT; 149 AA.
      |
      TREMBLrel. 17, Created)
      TREMBLrel. 17, Last sequence update)
      TREMBLrel. 22, Last annotation update)
      ; protein.
      ;
      (Mouse).
      Chazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1090;
      1 N.A.
      6J; TISSUE=Tongue;
      860; PubMed=11217851;
      nagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
      Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
      Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
      Izaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
      Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
      J., Gaasterland T., Gissi C., King B., Kochiwa H.,
      Vis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
      Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
      do T., Furuno M., Aono H., Baldarelli R., Barsh G.,
      Fellini D., Bojunga N., Carninci P., de Bonaldo M.F.,
      J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
      Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
      Chiommi L., Mashima J., Mazzarelli J., Mombauts P.,
      King B., Ringwald M., Rodriguez I., Sakamoto N.,
      Ito K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
      Iyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
      A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
      ;
      unnotation of a full-length mouse cDNA collection.";
      15-690(2001).
      16; BAB26045.1; -;
      5728; 2300009A05Rik.
      19 AA; 15818 MW; B3CD4BD0BA454F0E CRC64;
      |
      1.7%; Score 9; DB 11; Length 149;
      Identity 100.0%; Pred.No.12;
      Conservative 0; Mismatches 0; Indels 0; Gaps
      0;
      AAAAAA 126
      |||||
      AAAAAA 47
      |
      PRELIMINARY; PRT; 151 AA.
      |
      68
      69
      70

```

060; PubMed=12534463;
 Weinert C., Paulsen I.T., Dodson R.J., Hilbert H.,
 Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 Eanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 Lison W., White O., Peterson J., Kouri H., Hance I.,
 Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 Jendancic D., Hohenseil J., Straetz W., Heim S.,
 Isen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 ome sequence and comparative analysis of the
 versatile Pseudomonas putida KT2440.";
 Biol. 4:799-808(2002).
 6; AAN66186.1; --.
 7; C:acetyl-CoA carboxylase complex; IEA.
 9; F:acetyl-CoA carboxylase activity; IEA.
 4; P:biotin binding; IEA.
 3; P:fatty acid biosynthesis; IEA.
 001249; ACoA_biotinCC.
 001882; Biotin_BS.
 000089; Biotin_lipoyl.
 71; biotin lipoyl; 1.
 71; ACOABiotinCC.
 188; BIOTIN; 1.
 some.
 3 AA; 16186 MW; 9CFEPB311AA3DB54 CRC64;
 1.7%; Score 9; DB 16; Length 153;
 arity 100.0%; Pred.No.13;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAPA 146
 |||||
 AAAPA 65
 RELIMINARY; PRT; 154 AA.
 TrEMBLrel. 21, Created)
 TrEMBLrel. 21, Last sequence update)
 TrEMBLrel. 22, Last annotation update)
 protein.
 (japonica cultivar-group).
 cidipiantae; Streptophyta; Embryophyta; Tracheophyta;
 ; Magnoliophyta; Liliopsida; Poales; Poaceae;
 ; Oryzaeae; Oryza.
 347;
 N.A.
 sponbare;
 sumoto T., Yamamoto K.;
 (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 009.";
 4-2001) to the EMBL/GenBank/DBJ databases.
 2; BAB89199.1; --.
 32; --.
 1 AA; 15967 MW; 173BD51BFC478013 CRC64;
 1.7%; Score 9; DB 10; Length 154;
 arity 100.0%; Pred.No.13;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TTAAA 21
 |||||
 TTAAA 41

ID Q8H056 PRELIMINARY; PRT; 155 AA.
 AC Q8H056;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OSUNBA0014006.16.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
 RA Currie J., Collura K.;
 RT "Rice Genomic Sequence."
 RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC105928; AAN77309.1; --.
 KW Hypothetical protein.
 SQ SEQUENCE 155 AA; 15618 MW; A4D4E0C8ACA320CC CRC64;
 Query Match 1.7%; Score 9; DB 10; Length 155;
 Best Local Similarity 100.0%; Pred.No.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 Qy 120 AAAAAAAPP 128
 |||||
 Db 127 AAAAAAAPP 135
 RESULT 96
 Q9DHL7
 ID Q9DHL7 PRELIMINARY; PRT; 168 AA.
 AC Q9DHL7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 96R protein.
 GN 96R.
 OS Yaba-like disease virus (YLDV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirina
 OC Yatapoxvirus.
 OX NCBI_TaxID=132475;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee H.J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21176366; PubMed=11277691;
 RA Lee H.J., Essani K., Smith G.L.;
 RT "The genome sequence of Yaba-like disease virus, a yatapoxvirus."
 RL Virology 281:170-192(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lee H.J.;
 RL Thesis (2000), Sir William Dunn School of Pathology, University o
 DR EMBL; AJ293568; CAC21334.1; --.
 DR InterPro; IPR007984; Pox_RNA_Pol_19.
 DR Pfam; PF05320; Pox_RNA_Pol_19; 1.
 SQ SEQUENCE 168 AA; 19253 MW; 19FA374984C8AE2D CRC64;
 Query Match 1.7%; Score 9; DB 12; Length 168;
 Best Local Similarity 100.0%; Pred.No.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 Qy 331 EDDDEDED 339
 |||||
 Db 13 EDDDEDED 21
 RESULT 97

PRELIMINARY; PRT; 172 AA.

(TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 24, Last annotation update)

haliana (Mouse-ear cress).
ridiplantae; Scrophophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
02;

4 N.A.
olumbia;
Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G.,
Conway A.B., Conway A.R., Dewar K., Feng J., Kim C.,
Y., Shinn P., Sun H., Davis R.W., Ecker J.R.,
A., Theologis A.;
of BAC F19P19 from Arabidopsis thaliana chromosome 1.;
AN-1997) to the EMBL/GenBank/DBJ databases.

4 N.A.
olumbia;
AR-1999) to the EMBL/GenBank/DBJ databases.
04; AAE70430.1; -.
F86176.
R007087; Znf_C2H2.
5; Zf-C2H2; 1.
35; Znf_C2H2; 1.
028; ZINC_FINGER_C2H2_1; 1.
1157; ZINC_FINGER_C2H2_2; 1.
3; Zinc; Zinc-finger.
72 AA; 19204 MW; 03473071616E37FF CRC64;

1.7%; Score 9; DB 10; Length 172;
larity 100.0%; Pred. No. 14;
Conservative 0; Mismatches 0; Indels 0; Gaps

AAAAAP 127
|||||
AAAAAP 50

PRELIMINARY; PRT; 173 AA.

(TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
protein FLJ38877.
(Human).
stazosa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
506;

4 N.A.
Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.
to T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
iki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
wai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
agai K., Isogai T.;
cDNA sequencing project."
JL-2002) to the EMBL/GenBank/DBJ databases.
36; BAC04724.1; -.
protein.
73 AA; 18626 MW; A0D11696F08F211B CRC64;

Query Match 1.7%; Score 9; DB 4; Length 173;
Best Local Similarity 100.0%; Pred.No.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAPP 128
|||||
DB 61 AAAAAAPP 69

RESULT 99
Q9ZQ24 PRELIMINARY; PRT; 183 AA.
AC Q9ZQ24
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AT2G24440 protein (Hypothetical protein).
GN AT2G24440 OR AT2G24440/T28124.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; ros
OC eurosidia II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RT [1]
RT SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.
RA Ruell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat
RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill
RA Adams M.D., Garrera A.J., Czaaszy T.H., Goodman H.M., Somerville
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768 (1999).
RT [2]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RT [3]
RP SEQUENCE FROM N.A.
RP Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.B.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RT [4]
RP SEQUENCE FROM N.A.
RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RT [5]
RP SEQUENCE FROM N.A.
RA Xiao Y., Ishmael N., Kumar N., Redman J., Riedmuller S., Utterba
RA Whitelaw C.A., Fraser C.M., Town C.D.;
RT "Cloning and sequencing of full-length cDNAs for hypothetical ge;
RT from chromosome 2 of Arabidopsis thaliana.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006403; AAD18115.1; -;
DR EMBL; AY085501; AAM62725.1; -;
DR EMBL; AY102544; AAM76749.1; -;
DR FIR; F84636; F84636.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20712 MW; 3CA61F0BD0B33F82 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 183;
Best Local Similarity 100.0%; Pred.No.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

```

BEDDD 335
|||||
BEDDD 85

RELIMINARY; PRT; 185 AA.
TReMBLrel. 10, Created)
TReMBLrel. 10, Last sequence update)
TReMBLrel. 25, Last annotation update)
somal protein L12.
67ID01.16.
(Rice), and
(Japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzaeae; Oryza.
30, 39947;

N.A.
iva; STRAIN=cv. Nipponbare; TISSUE=Green leaf;
Arimura S.;
N-1999) to the EMBL/GenBank/DBJ databases.

N.A.
iva; STRAIN=cv. Nipponbare; TISSUE=Green leaf;
rashige M., Hirai A., Tautumi N.;
tion of two rice genes for nuclear-encoded chloroplast
tein L12 and phylogenetic analysis of the acquisition of
gen and gene duplication.";
Genet. 97:110-115(1998).

N.A.
iva (japonica cultivar-group); STRAIN=cv. Nipponbare;
sumoto T., Yamamoto K.;
(japonica cultivar-group) genomic DNA, chromosome 1, PAC
1.";
3-2001) to the EMBL/GenBank/DBJ databases.
4; BAA37171.1; -
4; BAB91739.1; -
PC4267.
ICTF.
34; -.
2; C:intracellular; IEA.
0; C:ribosome; IEA.
3; P:structural constituent of ribosome; IEA.
2; P:protein biosynthesis; IEA.
00206; Ribosomal L12.
08932; Ribos L12/7_olig.
; Ribosomal L12; 1.
326; Ribosomal L12; 1.
R00855; L12; 1.
tein.
5 AA; 18590 MW; EBF7A7FFC98609AB CRC64;
arity 1.7%; Score 9; DB 10; Length 185;
nservative 100.0%; Pred. No. 15;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 127
|||||
AAAAA 29

RELIMINARY; PRT; 187 AA.
TReMBLrel. 16, Created)
TReMBLrel. 16, Last sequence update)

01-OCT-2003 (TReMBLrel. 25, Last annotation update)
Y59A8B.9 protein.
Y59A8B.9.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoic
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RA Sulston J.E.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; ALI32898; CAC14409.1; -.
DR WormPep; Y59A8B.9; CE26218.
DR GO; GO:0008017; F:microtubule binding; IEA.
DR InterPro; IPR004953; EB1.
DR Pfam; PF03271; EB1; 1
DR SEQUENCE 187 AA; 19601 MW; B869998562FA1340 CRC64;
SQ

Query Match 1.7%; Score 9; DB 5; Length 187;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAAAAPP 128
Db 89 AAAAAAAAAAPP 97

RESULT 102
Q96BU2 PRELIMINARY; PRT; 194 AA.
AC Q96BU2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015174; AAH15174.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05C8D3C CRC64;

Query Match 1.7%; Score 9; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 227 PPPQPQPPP 235
Db 127 PPPQPQPPP 135

RESULT 103
Q8H083 PRELIMINARY; PRT; 198 AA.
AC Q8H083;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.

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2.8.
(japonica cultivar-group).
  (ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  3947; Oryzae; Oryza.

M.N.A.
  1.Y.; Soderlund C., Kim H.-R., Rambo T., Saski C.,
  Allura K.;
  "Sequence.";
  SC-2002) to the EMBL/GenBank/DBJ databases.
  34; AAN87736.1; -.
  3007087; Znf.C2H2.
  5; Zf.C2H2.1.
  0028; ZINC_FINGER_C2H2_1; 1.
  0157; ZINC_FINGER_C2H2_2; 1.
  protein.
  38 AA; 21161 MW; 753E11BECF71D7E5 CRC64;

  1.7%; Score 9; DB 10; Length 198;
  arity 100.0%; Pred.No.16;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  TPAPPP 135
  |||||
  TPAPPP 99

PRELIMINARY; PRT; 214 AA.

(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 24, Last annotation update)
  UNA for DREB1A.
  (Rice).
  ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  330; Oryzae; Oryza.

1.N.A.
  Pponbare;
  Tsunamoto T., Yamamoto K.;
  (nipponbare (GA3) genomic DNA, chromosome 6, PAC
  12.";
  18; BAA90812.1; -.
  2GCC.
  IV3; -.
  14; C:nucleus; IEA.
  10; F:transcription factor activity; IEA.
  15; P:regulation of transcription, DNA-dependent; IEA.
  1001471; TF.ERF.
  167; AP2-domain: 1.
  167; ETHRSPELEMT.
  423; TF.ERF; 1.
  10; AP2; 1.
  4 AA; 23110 MW; 883D48CBB151F69 CRC64;

  1.7%; Score 9; DB 10; Length 214;
  arity 100.0%; Pred.No.17;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  ASSSAA 27
  |||||
  ASSSAA 135

2.8.
(japonica cultivar-group).
  (ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  3947; Oryzae; Oryza.

M.N.A.
  1.Y.; Soderlund C., Kim H.-R., Rambo T., Saski C.,
  Allura K.;
  "Sequence.";
  SC-2002) to the EMBL/GenBank/DBJ databases.
  34; AAN87736.1; -.
  3007087; Znf.C2H2.
  5; Zf.C2H2.1.
  0028; ZINC_FINGER_C2H2_1; 1.
  0157; ZINC_FINGER_C2H2_2; 1.
  protein.
  38 AA; 21161 MW; 753E11BECF71D7E5 CRC64;

  1.7%; Score 9; DB 10; Length 198;
  arity 100.0%; Pred.No.16;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  TPAPPP 135
  |||||
  TPAPPP 99

PRELIMINARY; PRT; 214 AA.

(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 24, Last annotation update)
  UNA for DREB1A.
  (Rice).
  ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  a; Magnoliophyta; Liliopsida; Poales; Poaceae;
  330; Oryzae; Oryza.

1.N.A.
  Pponbare;
  Tsunamoto T., Yamamoto K.;
  (nipponbare (GA3) genomic DNA, chromosome 6, PAC
  12.";
  18; BAA90812.1; -.
  2GCC.
  IV3; -.
  14; C:nucleus; IEA.
  10; F:transcription factor activity; IEA.
  15; P:regulation of transcription, DNA-dependent; IEA.
  1001471; TF.ERF.
  167; AP2-domain: 1.
  167; ETHRSPELEMT.
  423; TF.ERF; 1.
  10; AP2; 1.
  4 AA; 23110 MW; 883D48CBB151F69 CRC64;

  1.7%; Score 9; DB 10; Length 214;
  arity 100.0%; Pred.No.17;
  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  ASSSAA 27
  |||||
  ASSSAA 135

Query Match 1.7%; Score 9; DB 10; Length 214;
Best Local Similarity 100.0%; Pred.No.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 19 AAAASSSAA 27
|||||
DB 127 AAAASSSAA 135

RESULT 106
P93426
ID P93426 PRELIMINARY; PRT; 217 AA.
AC P93426;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Leucine zipper protein.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Tainung 67; TISSUE=Seed;
RA Hsing Y.C., Tsao C.V., Chow T., Hsieh J., Chen Z.;
RT "Rice early embryogenesis gene.";
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
DR EMBL; U25283; AAB39320.1; -.
DR PIR; T04353; T04353.
DR Gramene; P93426; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
DR InterPro; IPR008917; Euk_transcr_DNA.

```

04827; TF_BZIP.

bZIP; 1.

BRLZ; 1.

17; BZIP; 1.

36; BZIP_BASIC; 1.

nuclear protein.

AA; 23178 MW; C71B4189FAFFAF8 CRC64;

1.7%; Score 9; DB 10; Length 217;

identity 100.0%; Pred. No. 17;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127

|||||

AAAP 60

ELIMINARY; PRT; 217 AA.

REMBLrel. 15, Created)

REMBLrel. 15, Last sequence update)

REMBLrel. 25, Last annotation update)

Rice).

idiplantae; Streptophyta; Embryophyta; Tracheophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae;

Oryzae; Oryza.

0;

N.A.

4;

Chow T.-Y., Chang Z.-T., Chen Z.-Y., Chung M.-C.,

ieh J.-S.;

ion of a rice early embryogenesis specific gene OSE2.;

-2000) to the EMBL/GenBank/DBJ databases.

; BELONGS TO THE BZIP FAMILY.

; AAF65459.1; -

5; -

; C:nucleus; IEA.

; F:DNA binding; IEA.

; P:regulation of transcription, DNA-dependent; IEA.

08917; Euk transcr_DNA.

04827; TF_BZIP.

bZIP; 1.

; BRLZ; 1.

17; BZIP; 1.

36; BZIP_BASIC; 1.

nuclear protein.

AA; 23192 MW; CE6F8BACE7C3C203 CRC64;

1.7%; Score 9; DB 10; Length 217;

identity 100.0%; Pred. No. 17;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAP 127

|||||

AAAP 60

ELIMINARY; PRT; 217 AA.

REMBLrel. 24, Created)

REMBLrel. 24, Last sequence update)

REMBLrel. 25, Last annotation update)

protein.

japonica cultivar-group).

idiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzae; Oryza.

OC NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Katayose Y.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC

clone:OJ9990 A01.1";

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005847; BAC65071.1; -

DR InterPro; IPR004893; DUF260.

DR PROSITE; PS0891; LOB; 1.

SQ SEQUENCE 217 AA; 23641 MW; 1D6EC23E52DFBC3C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 217;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEE 341

|||||

Db 163 DDEDEDEE 171

RESULT 109

Q90764

ID Q90764 PRELIMINARY; PRT; 218 AA.

AC Q90764;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Transcriptional regulator.

GN ASH.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Wang S., Kirby M.L.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

CC -! SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMIL

CC TRANSCRIPTION FACTORS.

DR EMBL; L11871; AAA03722.1; -

DR InterPro; IPR001092; HLH_basic.

DR Pfam; PF00010; HLH; 1.

DR SMART; SM00353; HLH; 1.

DR PROSITE; PS00038; HLH 1; 1.

DR PROSITE; PS0888; HLH 2; 1.

SQ SEQUENCE 218 AA; 22884 MW; A80B11AEC09B8211 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 218;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Ga

QY 120 AAAAAAAPP 128

|||||

Db 28 AAAAAAAPP 36

RESULT 110

Q90575

ID Q90575 PRELIMINARY; PRT; 219 AA.

AC Q90575;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Achaete-scute homologue.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian

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OC      31;
CX      [ N.A.
RX      365; PubMed=7600956;
RA      Walker M.B., Morris M.D., Reh T.A.;
RI      haete-scute homolog (CASH-1) is expressed in a temporally
RI      discrete manner in the developing nervous system.";
RL      20:769-783(1994).
CC      Y: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC      ION FACTORS.
DE      AAC59658.1; -.
DE      I51382; HLH_basic.
DE      001092; HLH_basic.
DE      ); HLH; 1.
DE      038; HLH; 1.
DE      038; HLH; 1.
DE      088; HLH; 2; 1.
DE      09 AA; 22980 MW; 31AE76764BC58B43 CRC64;
SQ      1.7%; Score 9; DB 13; Length 219;
      .arity 100.0%; Pred. No. 17;
      conservative 0; Mismatches 0; Indels 0; Gaps 0;
      AAAPP 128
      |||||
      AAAPP 36

PRELIMINARY; PRT; 231 AA.
(TREMBLrel. 08, Created)
(TREMBLrel. 08, Last sequence update)
(TREMBLrel. 24, Last annotation update)
sembly and synthesis protein precursor.
aromaticivorans.

teobacteria; Alphaproteobacteria; Sphingomonadales;
aceae; Novosphingobium.
1935;
4 N.A.

Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
Gaasterland T., Saffer J.D., Fredrickson J.K.;
nence of a 184 kb catabolic plasmid from Sphingomonas
ns strain F199.";
IL-1998) to the EMBL/GenBank/DBJ databases.
7; AAD03955.1; -.
11; C:extrachromosomal DNA; IEA.
1. 27 POTENTIAL.
11 AA; 24710 MW; 27F3C1F6664F258B CRC64;
      .arity 1.7%; Score 9; DB 2; Length 231;
      conservative 0; Mismatches 0; Indels 0; Gaps 0;
      APARAP 149
      |||||
      APARAP 222

PRELIMINARY; PRT; 235 AA.
(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)

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DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Bcl-2 protein.
GN      BCL-2.
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yamazaki J., Sano J., Kano R., Hasegawa A.;
RT      "Felis catus mRNA for bcl-2, complete cds.";
RL      Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB096611; BAC24136.1; IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR      GO; GO:0006915; P:apoptosis; IEA.
DR      InterPro; IPR00712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; BCL2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.
DR      SMART; SM00265; BH4; 1.
DR      TIGRFAMs; TIGR00865; bcl-2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01258; BH2; 1.
DR      PROSITE; PS01259; BH3; 1.
DR      PROSITE; PS00063; BH4_2; 1.
DR      PROSITE; PS00063; BH4_2; 1.
SQ      SEQUENCE 235 AA; 25621 MW; 2320B57C96B64548 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY      118 APAAAAAA 126
DB      |||||
      70 APAAAAAA 78

RESULT 113
Q9AX02 PRELIMINARY; PRT; 239 AA.
AC Q9AX02;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P0492F05.10 protein (P0443E07.2 protein).
GN P0492F05.10 OR P0443E07.2.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=O. sativa; STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0492F05.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases;
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=O. sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0443E07.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002902; BAB32708.1; -.
DR EMBL; AP002900; BAB92099.1; -.
DR Gramene; Q9AX02; -.

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AA; 25914 MW; ACECLIFE77F78339 CRC64;
1.7%; Score 9; DB 10; Length 239;
rity 100.0%; Pred. No. 19;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAT 157
|||||
AAAT 194

RELIMINARY; PRT; 239 AA.

TREMBlrel. 25, Created)
TREMBlrel. 25, Last sequence update)
TREMBlrel. 25, Last annotation update)
protein.

nchiseptica (Alcaligenes bronchisepticus).
eobacteria; Betaproteobacteria; Burkholderiales;
; Bordetella.
;

N.A.
ATCC BAA-588;
954; PubMed=12910271;
Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A.A.M., Temple L., James K., Harris B., Quail M.A.,
Atkin R., Baker S., Basham D., Davis P., Doggett J.,
T., Collins M., Cronin A., Hauser H., Holroyd S., Jagels K.,
Goble A., Norberczak H., O'Neill S., Ormond D., Price C.,
Rutter S., Saunders M., Saunders D., Seeger K.,
Nelson D.R., Skelton J., Squares R., Squares S., Stevens K.,
Whithead S., Barrell B.G., Maskell D.J.;
analysis of the genome sequences of Bordetella pertussis,
capertussis and Bordetella bronchiseptica."
5:32-40(2003).
3; CAE30891.1; -.
protein; Complete proteome.
9 AA; 24495 MW; 5F6AB75BA5856581 CRC64;

arity 1.7%; Score 9; DB 16; Length 239;
rity 100.0%; Pred. No. 19;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
|||||
AAAPA 161

RELIMINARY; PRT; 241 AA.

TREMBlrel. 25, Created)
TREMBlrel. 25, Last sequence update)
TREMBlrel. 25, Last annotation update)
protein.

apertussis.
eobacteria; Betaproteobacteria; Burkholderiales;
; Bordetella.
9;

N.A.
/ ATCC BAA-587;
954; PubMed=12910271;
Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

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RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Hauser H., Holroyd S., Jagels K
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Saunders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steven
RA Unwin L., Whithead S., Barrell B.G., Maskell D.J.;
RA "Comparative analysis of the genome sequences of Bordetella pertu
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640424; CAE35975.1; -.
KW Hydrothermal protein; Complete proteome.
SQ SEQUENCE 241 AA; 24663 MW; 5E49B6BL6F8A326F CRC64;

Query Match 1.7%; Score 9; DB 16; Length 241;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 138 APVAAAAPA 146
Db 153 APVAAAAPA 161
|||||

RESULT 116
Q9VET8 Q9VET8 PRELIMINARY; PRT; 248 AA.
AC Q9VET8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG11769 protein.
GN CG11769.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
RA Balw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA assman D.A., Weinstock G.M., Weissenbach J.,
RA Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA -F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA yers E.W., Rubin G.M., Venter J.C.;
RA sequence of Drosophila melanogaster."
RA 185-2195(2000).
RA 3; AAF55330.1; -.
RA 0038441; CG11769.
RA 8 AA; 26831 MW; 1E55A2CFE296C0F1 CRC64;
RA 1.7%; Score 9; DB 5; Length 248;
RA arity 100.0%; Pred. No. 19;
RA Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA
RA AAAS 23
RA |||||
RA AAAS 41
RA
RA PRELIMINARY; PRT; 248 AA.
RA
RA (TREMBLrel. 20, Created)
RA (TREMBLrel. 20, Last sequence update)
RA (TREMBLrel. 24, Last annotation update)
RA jellar assembly protein FLIH.
RA 192 OR RS00820.
RA anacearum (Pseudomonas solanacearum).
RA blasmid.
RA reobacteria; Betaproteobacteria; Burkholderiales;
RA eae; Ralstonia.
RA 05;
RA 4 N.A.
RA 00;
RA 1879; PubMed=11823852;
RA Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA ilault A., Bottier P., Camus J.C., Cattolico L.,
RA Choise N., Claudel-Renard C., Cunnac S., Demange N.,
RA vie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA thebault P., Whalen M., Wincker P., Levy M.,
RA J., Boucher C.A.;
RA ence of the plant pathogen Ralstonia solanacearum."
RA 97-502(2002).
RA 78; CAD17543.1; -.
RA 21; C:extrachromosomal DNA; IEA.
RA 88; C:flagellum (sensu Bacteria); IEA.
RA 74; F:motor activity; IEA.
RA 39; P:ciliary/flagellar motility; IEA.
RA R000563; Flag_FliH.
RA 8; FliH; 1.
RA 003; FLGFLIH.
RA plete proteome.
RA 48 AA; 26993 MW; 9CA196E0BC549D47 CRC64;
RA 1.7%; Score 9; DB 16; Length 248;
RA larity 100.0%; Pred. No. 19;
RA Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA
RA AAAPPP 129
RA |||||
RA AAAPPP 38
RA
RA PRELIMINARY; PRT; 252 AA.
RA
RA (TREMBLrel. 22, Created)
RA (TREMBLrel. 22, Last sequence update)
RA (TREMBLrel. 25, Last annotation update)

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DE P0524E08.25 protein.
GN P0524E08.25.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytæ;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RL clone:P0524E08."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004341; BAC10856.1; -.
DR Gramene; Q8LHK1; -.
DR InterPro; IPR008889; VQ.
DR Pfam; PF05678; VQ; 1.
SQ SEQUENCE 252 AA; 25166 MW; 9453D1A134A6634C CRC64;
Query Match 1.7%; Score 9; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 120 AAAAAAAPP 128
DB |||||
DB 191 AAAAAAAPP 199
RESULT 119
Q89LR9 PRELIMINARY; PRT; 262 AA.
ID Q89LR9;
AC Q89LR9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE B1r4474 protein.
GN B1r4474.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada
RA Tabata S.;
RA "Complete genomic sequence of nitrogen-fixing symbiotic bacteriu
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005951; BAC49739.1; -.
KW Complete proteome.
SQ SEQUENCE 262 AA; 27675 MW; 1F590E2B275473E9 CRC64;
Query Match 1.7%; Score 9; DB 16; Length 262;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 131 PAPPPPAP 139
DB |||||
DB 81 PAPPPPAP 89
RESULT 120
Q9A8M0 PRELIMINARY; PRT; 273 AA.
ID Q9A8M0;
AC Q9A8M0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

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A polymerase-related protein.
 centus.
 eobacteria; Alphaproteobacteria; Caulobacterales;
 ae; Caulobacter.
 5892;
 N.A.
 3089 / CBJ5;
 598; PubMed=11259647;
 Feldblyum T.V., Laub M.R.T., Paulsen I.T., Nelson K.E.,
 elberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 elson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 odson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 Venter J.C., Shapiro L., Fraser C.M.;
 me sequence of *Caulobacter crescentus*.
 cad. Sci. U.S.A. 98:4136-4141(2001).
 8; AAK23314.1; --
 F87414.
 --
 005273; SPOLpolNrel.
 005122; UDNA_glycylseSF.
 ; UDG; 1.
 R00758; SPOLpolNrel; 1.
 some.
 3 AA; 29214 MW; CR54307D81568194 CRC64;
 1.7%; Score 9; DB 16; Length 273;
 arity 100.0%; Pred.No.21;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PAPVA 141
 |||||
 PAPVA 55
 RELIMINARY; PRT; 274 AA.
 TREMBLrel. 13, Created
 TREMBLrel. 13, Last sequence update)
 TREMBLrel. 22, Last annotation update)
 in.
 lanogaster (Fruit fly).
 tazona; Arthropoda; Hexapoda; Insecta; Pterygota;
 opterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 27;
 N.A.
 ey;
 006; PubMed=10731132;
 elinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 le C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 ghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 otchan M.R., Bouck J., Brokstein P., Brotter P.,
 Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahlke C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 briellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 ng F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Snue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003730; AAP55762.1; --
 DR FlyBase; FBgn0038794; CG17205.
 SQ SEQUENCE 274 AA; 30624 MW; 1AA91C5120C2DDF7 CRC64;
 Query Match 1.7%; Score 9; DB 5; Length 274;
 Best Local Similarity 100.0%; Pred.No.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; C
 Qy 335 DEDEDEDD 343
 |||||
 Db 129 DEDEDEDD 137
 RESULT 122
 Q9SNS1
 ID Q9SNS1 PRELIMINARY; PRT; 276 AA.
 AC Q9SNS1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
 RT clone:F0535G04.1";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP000399; BAA8355.1; --
 DR Gramene; Q9SNS1; --
 KW Hypothetical protein.
 SQ SEQUENCE 276 AA; 29463 MW; 62B4AA1069536447 CRC64;
 Query Match 1.7%; Score 9; DB 10; Length 276;
 Best Local Similarity 100.0%; Pred.No.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; C
 Qy 121 AAAAAAPP 129
 |||||
 Db 79 AAAAAAPP 87
 RESULT 123
 Q9SLP7
 ID Q9SLP7 PRELIMINARY; PRT; 278 AA.
 AC Q9SLP7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)

TREMBLrel. 21, Last sequence update)
TREMBLrel. 25, Last annotation update)
binding protein.

(japonica cultivar-group).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Oryzaeae; Oryza.
947;

[N.A.
pponbare;
tsumoto T., Yamamoto K.;
(nipponbare (GA3) genomic DNA, chromosome 1, PAC
8";
B-2001) to the EMBL/GenBank/DBJ databases.
Y: BELONGS TO THE BZIP FAMILY.
6; BAB9789.1; -.
P7; -.
4; C:nucleus; IEA.
7; P:DNA binding; IEA.
5; P:regulation of transcription, DNA-dependent; IEA.
004827; TF_BZIP.
; BZIP; 1.
8; BRLZ; 1.
0217; BZIP; 1.
0036; BZIP BASIC; 1.
Nuclear protein.
18 AA; 29688 MW; 9425F64C16D2A0FA CRC64;

1.7%; Score 9; DB 10; Length 278;
larity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 127

|||||
AAAAAP 108

PRELIMINARY; PRT; 278 AA.

(TREMBLrel. 01, Created)
(TREMBLrel. 01, Last sequence update)
(TREMBLrel. 25, Last annotation update)
ise.

virus (strain Kaplan) (PRV).
NA viruses, no RNA stage; Herpesviridae;
irinae; Varicellovirus.
3703;

4 N.A.

1;
9740; PubMed=8806172;
bras F., Vende P., Simonet B., Nguyen X., Flamand A.,

ragment 9 of pseudorabies virus contains genes homologous
UL25, UL26, and UL26.5 genes of herpes simplex virus

2:27-39(1996).
; CAA65010.1; -.
001; -.
33; F:peptidase activity; IEA.

78 AA; 28198 MW; E0AD4E74C395273F CRC64;

1.7%; Score 9; DB 12; Length 278;
larity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAA 126

Db 212 APAAAAAA 220
|||||

RESULT 125

O15415 PRELIMINARY; PRT; 279 AA.

AC O15415;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CAGH3.
GN CAGH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369492; PubMed=9225980;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
RT "CDNAs with long CAG trinucleotide repeats from human brain."
RL Hum. Genet. 100:114-122(1997).
DR EMBL; U80747; AAB91445.1; -.
DR Genew; HGNC:11966; TNRC3.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0007393; P:neurogenesis; TAS.
SQ SEQUENCE 279 AA; 31630 MW; 3C571297D422DA04 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 222 QQQQPPPPQ 230

Db 175 QQQQPPPPQ 183
|||||

RESULT 126

Q86NQ6 PRELIMINARY; PRT; 280 AA.

AC Q86NQ6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE RE01075P.
GN ECT.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Friese E
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT003781; AAC41462.1; -.
SQ SEQUENCE 280 AA; 29519 MW; 73BECA0FC7A7C10 CRC64;

Query Match 1.7%; Score 9; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 330 EEDDEDE 338

|||||
DEDE 87

ELIMINARY; PRT; 281 AA.

EMBLrel. 12, Created)
EMBLrel. 12, Last sequence update)
EMBLrel. 24, Last annotation update)
ative SWI/SNF complex subunit BAF170.
(Rice).
diplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzae; Oryza.
N.A.
ponbare;
sumoto T., Yamamoto K.;
Nipponbare (GA3) genomic DNA, chromosome 2, PAC
(contig b).";
1-1999) to the EMBL/GenBank/DBJ databases.
7; BAA82389.1; -.
15; -.
007526; SWIRM.
SWIRM; 1.
1 AA; 28773 MW; AACCE096AC53156 CRC64;
arity 100.0%; Score 9; DB 10; Length 281;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 79

ELIMINARY; PRT; 282 AA.

EMBLrel. 22, Created)
EMBLrel. 22, Last sequence update)
EMBLrel. 24, Last annotation update)
tein L4.
haliana (Mouse-ear cress).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
02;

N.A.
lfovsky N., Town C.D., Troukhan M., Alexandrov N.,
Flavell R.B., White O., Salzberg S.L.;
messenger RNA sequences greatly improve genome

0:0-0(2002).

N.A.
oukhan M., Alexandrov N., Lu Y.-P., Flavell R.,

CDNA from Arabidopsis thaliana";
R-2002) to the EMBL/GenBank/DBJ databases.
1; AAM61637.1; -.
2; C:intracellular; IEA.
0; C:ribosome; IEA.
5; F:structural constituent of ribosome; IEA.
2; P:protein biosynthesis; IEA.
002136; Ribosomal_L4/LuE.
; Ribosomal_L4; 1.
12 AA; 30584 MW; 0809CC09EA60E79C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G.

QY 330 EEEDEDEDE 338
DB 267 EEEDEDEDE 275

RESULT 129

Q9RBF9 PRELIMINARY; PRT; 283 AA.
ID Q9RBF9
AC Q9RBF9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Alcaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=335;
RA Seibert V., Schloemann M.;
RT "Characterization of a Gene Cluster Encoding the Maleylacetate
RT Reductase from Ralstonia eutropha 335, an Enzyme Recruited for Gr
RT with 4-Fluorobenzoate.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130250; AAD55888.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact.;
DR GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR InterPro; IPR001853; DSBa.
DR Pfam; PF01323; DSBa; 1.
KW Hypothetical protein.
SQ SEQUENCE 283 AA; 31479 MW; 4FCD36A6C0C70518 CRC64;

Query Match 1.7%; Score 9; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 117 GAPAAAAA 125
DB 20 GAPAAAAA 28

RESULT 130

Q8IQD9 PRELIMINARY; PRT; 283 AA.
ID Q8IQD9;
AC Q8IQD9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE CG6611-PC.
GN ECT OR CG6611 OR CG11965.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin I.
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N.
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 Busam D.A., Bulter H., Cadieu E., Center A., Chandra I.,
 Cawley S., Dahle C., Davenport L.B., Davies P.,
 Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Ibriclian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Jing F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Jostan K.A., Howland T.J., Wei M.H., Ibegwam C.,
 Kallush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 Li Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Li B., McIntosh T.C., McLeod M.P., McPherson D.,
 Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Remington K., Saunders R.D., Scheeler F., Shen H.,
 Iden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Tector C., Stapleton M., Strong R., Sun E.,
 Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Assarman D.A., Weinstock G.M., Weissenbach J.,
 Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 Veri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Myers E.W., Rubin G.M., Venter J.C.;
 sequence of *Drosophila melanogaster*.;
 2185-2195(2000).
 N.A.
 Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 An H., Baldwin D., Benson J., Beeson K.Y., Busam D.A.,
 Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Frise E., Galle R.F., Garg N.S., George R.A.,
 Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 Paragas V., Park S., Patel S., Pfeiffer B.,
 Pittman G.S., Puri V., Richards S., Scheeler F.,
 Strong R., Swirskas R., Tector C., Tyler D.,
 Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 of *Drosophila melanogaster* genome.;
 MAR-2000) to the EMBL/GenBank/DBJ databases.
 N.A.
 roshy M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
 Rysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 B., Marshall B., Millburn G., Richter J., Russo S.,
 J., Smith E., Shu S., Smutniak F., Whitfield E.,
 Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 of *Drosophila melanogaster* genome.;
 MAR-2000) to the EMBL/GenBank/DBJ databases.
 N.A.
 Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 MAR-2000) to the EMBL/GenBank/DBJ databases.
 N.A.
 (SEP-2002) to the EMBL/GenBank/DBJ databases.
 1549; AAN11922.1; -;
 3900000451; ect.
 283 AA; 30272 MW; 3E7B16C02CEB1C2C CRC64;
 1.7%; Score 9; DB 5; Length 283;
 nilarity 100.0%; Pred. No. 22; 0; Indels 0; Gaps 0;
 Conservative 0; Mismatches 0;

QY 330 EEDDEDE 338
 Db 79 EEDDEDE 87
 RESULT 131
 Q814H9 PRELIMINARY; PRT; 287 AA.
 ID Q814H9
 AC Q814H9
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE C. elegans sdn-1 protein (corresponding sequence F57C7.3b).
 GN F57C7.3 OR SDN-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditos
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA White S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:212-2018(1998).
 DR EMBL; Z69646; CAD44142.1; -;
 DR WormPep; F57C7.3b; CE32681.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008032; F:cytoskeletal protein binding; IEA.
 DR InterPro; IPR001050; Syndecan.
 DR Pfam; PF01034; Syndecan; 1.
 DR PROSITE; PS00964; SYNDECAN; 1.
 SQ SEQUENCE 287 AA; 30851 MW; C947CF0A7FC95BC5 CRC64;
 Query Match 1.7%; Score 9; DB 5; Length 287;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 332 EDDDEDE 340
 Db 144 EDDDEDE 152
 RESULT 132
 Q9BUP6 PRELIMINARY; PRT; 306 AA.
 ID Q9BUP6
 AC Q9BUP6
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler C
 RA Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.I
 RA Altschul S.F., Zeeberg B., Buetow K.H., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne I
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly


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PRELIMINARY; PRT; 316 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 25, Last annotation update)
ribosomal protein P0.
casipalpis.
stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
ipterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
3; Sarcophaga.
3312;

M N.A.
0706; PubMed=11024299;
Denlinger D.L.;
a transcription patterns of 60S ribosomal protein P0, a
ulated AP endonuclease in the flesh fly, Sarcophaga
";
-388(2000).
39; AAF31449.1; -.
22; C:intracellular; IEA.
40; C:ribosome; IEA.
35; F:structural constituent of ribosome; IEA.
14; P:translational elongation; IEA.
R001813; Ribosomal_L10.
R001790; Ribosomal_L10.
8; 60S ribosomal; I.
5; Ribosomal_L10; I.
otein.
16 AA; 34095 MW; 0EF6152DA9A77572 CRC64;

1.7%; Score 9; DB 5; Length 316;
larity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATAP 159
|||||
AAATAP 284

PRELIMINARY; PRT; 316 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 24, Last annotation update)
rabidopsis thaliana chromosome 5 BAC clone F21E10.
(Rice).
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
e; Oryzae; Oryza.
530;

M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare(GA3) genomic DNA, chromosome 1, PAC
'05.";
UN-2000) to the EMBL/GenBank/DBJ databases.

M N.A.
ipponbare;
atsumoto T., Yamamoto K.;
a nipponbare(GA3) genomic DNA, chromosome 1, PAC
'01.";
UN-2000) to the EMBL/GenBank/DBJ databases.
ILAR LOCATION: NUCLEAR (BY SIMILARITY).
TY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
;80; BAA96556.1; -.

DR EMBL; AP002070; BAA95850.1; -.
DR Gramene; Q9LD92; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PRO0404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regul
SQ SEQUENCE 316 AA; 34240 MW; DB4E00CD509EF819 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 131 PAPPPPPPAP 139
Db 179 PAPPPPPPAP 187

RESULT 138
Q9AYL3 PRELIMINARY; PRT; 316 AA.
AC Q9AYL3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative carnitine/acylcarnitine translocase.
GN OSUNBA003019.8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL "Oryza sativa chromosome 10 BAC OSUNBA003019 genomic sequence."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC060755; AAK00443.1; -.
DR Gramene; Q9AYL3; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 316 AA; 31554 MW; 61B69BB6012BCB86 CRC64;

Query Match 1.7%; Score 9; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAA 126
Db 142 APAAAAAA 150

RESULT 139
Q7XBY4 PRELIMINARY; PRT; 316 AA.
ID Q7XBY4
AC Q7XBY4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative carnitine/acylcarnitine translocase.

```

```

26 1.8.
27 (japonica cultivar-group).
28 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
29 ; Magnoliophyta; Liliopsida; Poales; Poaceae;
30 ; Oryzae; Oryza.
31 947;
32 N.A.
33 pponbare;
34 mosome 10 Sequencing Consortium;
35 w of structure, activity, and evolution of rice
36 ;
37 566-1569(2003).
38 N.A.
39 pponbare;
40 ing R.A., McCombie W.R., Messing J., Yuan Q.;
41 Y-2003) to the EMBL/GenBank/DBJ databases.
42 1; AAP5124.1; -.
43 6 AA; 31554 MW; 61B69BB6012BCB86 CRC64;
44 1.7%; Score 9; DB 10; Length 316;
45 arity 100.0%; Pred. No. 24;
46 conservative 0; Mismatches 0; Indels 0; Gaps 0;
47
48 AAAAA 126
49 |||||
50 AAAAA 150
51
52 RELIMINARY; PRT; 317 AA.
53
54 TREMBLrel. 15, Created)
55 TREMBLrel. 15, Last sequence update)
56 TREMBLrel. 25, Last annotation update)
57 bosomal protein PO (Fragment).
58 lla (leafy spurge).
59 ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
60 ; Magnoliophyta; eudicotyledons; core eudicots; rosids;
61 Malpighiales; Euphorbiaceae; Euphorbiaceae; Euphorbiaceae;
62 193;
63
64 N.A.
65 , Horvath D.P.;
66 on of mRNAs expressed in underground adventitious buds of
67 lla (leafy spurge).";
68 N-2000) to the EMBL/GenBank/DBJ databases.
69 2; AAF34767.1; -.
70 2; C:intracellular; IEA.
71 0; C:ribosome; IEA.
72 5; F:structural constituent of ribosome; IEA.
73 4; P:translational elongation; IEA.
74 001813; Ribosomal_L10.
75 001790; Ribosomal_L10.
76 3; 60s ribosomal; 1.
77 ; Ribosomal_L10; 1.
78 stein.
79 1
80 1
81 7 AA; 33738 MW; 3761F2EE62AF4F4A CRC64;
82 1.7%; Score 9; DB 10; Length 317;
83 larity 100.0%; Pred. No. 24;
84 conservative 0; Mismatches 0; Indels 0; Gaps 0;
85
86 AAAAA 146
87 |||||
88 AAAAA 288
89
90 Query Match 1.7%; Score 9; DB 5; Length 322;
91
92 Q7XM58 PRELIMINARY; PRT; 320 AA.
93 ID Q7XM58;
94 AC Q7XM58;
95 DT 01-OCT-2003 (TREMBLrel. 25, Created)
96 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
97 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
98 DE OSJNB0020011.15 protein.
99 GN OSJNB0020011.15.
100 OS Oryza sativa (Rice).
101 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
102 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
103 OC Euphorbiaceae; Oryzae; Oryza.
104 NCBI_TaxID=4530;
105 RN [1]
106 RP SEQUENCE FROM N.A.
107 RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
108 RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
109 RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li
110 RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.
111 RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
112 RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin
113 RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
114 RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
115 RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
116 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
117 DR EMBL; AL662998; CAE04786.1; -.
118 SQ SEQUENCE 320 AA; 33224 MW; B230739AD8EDC0DA CRC64;
119
120 Query Match 1.7%; Score 9; DB 10; Length 320;
121 Best Local Similarity 100.0%; Pred. No. 24;
122 Matches 9; Conservative 0; Mismatches 0; Indels 0;
123
124 QY 13 AAAATTAAA 21
125 DB 13 AAAATTAAA 21
126
127 RESULT 142
128 Q95S20
129 ID Q95S20 PRELIMINARY; PRT; 322 AA.
130 AC Q95S20;
131 DT 01-DEC-2001 (TREMBLrel. 19, Created)
132 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
133 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
134 DE HL01227p.
135 GN CG32423 OR CG10647 OR CG10649 OR CG10668.
136 OS Drosophila melanogaster (Fruit fly).
137 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
138 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
139 OC Ephydroidea; Drosophilidae; Drosophila.
140 NCBI_TaxID=7227;
141 RN [1]
142 RP SEQUENCE FROM N.A.
143 RC STRAIN=Berkeley;
144 RA Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R.
145 RA Champe M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.
146 RA Gonzalez M., Pacleb J., Paragas V., Park S., Phouanavong S., Wan
147 RA Nunoo J., Lewis S.E., Rubin G.M., Celniker S.;
148 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
149 DR EMBL; AY060995; AAL28543.1; -.
150 DR FlyBase; FBgn0052423; CG32423.
151 DR GO; GO:0003723; F:RNA binding; IEA.
152 DR InterPro; IPR002343; Hud Sxl RNA.
153 DR InterPro; IPR000504; RNA_rec_mot.
154 DR Pfam; PF00076; rrm; 2.
155 DR PRINTS; PR00961; HUDSLRNA.
156 DR SMART; SM00360; RRM; 2.
157 DR PROSITE; PS00102; RRM; 2.
158 DR PROSITE; PS00030; RRM_RNP_1; 1.
159 SQ SEQUENCE 322 AA; 34158 MW; C861E594FACD31BE CRC64;
160
161 Query Match 1.7%; Score 9; DB 5; Length 322;

```

larity 100.0%; Pred. No. 24;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 39

PRELIMINARY; PRT; 322 AA.

(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)

elanogaster (Fruit fly).
stazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
227;

M N.A.
ley;
Brokstein P., Hong L., Agbayani A., Carlson J.,
havez C., Dorsett V., Farfan D., Frise E., George R.,
Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
cleb J., Fargas V., Park S., Phouanavong S., Wan K.,
S.E., Rubin G.M., Celnikier S.;
UG-2001) to the EMBL/GenBank/DBJ databases.
36; AAK93060.1; -
n0031965; CG7093.
22 AA; 35090 MW; 8D70B7CCE322EA4F CRC64;

larity 1.7%; Score 9; DB 5; Length 322;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEDEED 342
|||||
DEDEED 151

PRELIMINARY; PRT; 325 AA.

(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
expressed 10.
(Human).

etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A.
heral Nervous System;

..;
PR-2003) to the EMBL/GenBank/DBJ databases.
59; AAH50659.1; -
76; P-nucleic acid binding; IEA.
R005162; Retrotrans_gag.
R001878; Znf_CCHC.
2; Retrotrans_gag; 1.
18; zf-CCHC; 1.
1939; C2HCZNFINGER.
10158; ZF_CCHC; 1.
125 AA; 36965 MW; 118E4CFAF97F2A76 CRC64;

larity 1.7%; Score 9; DB 4; Length 325;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 121 AAAAAAPPP 129
|||||
DB 64 AAAAAAPPP 72

RESULT 145

Q7XPH4
ID Q7XPH4 PRELIMINARY; PRT; 325 AA.
AC Q7XPH4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE OSJNB0003B01.9 protein.
GN OSJNB0003B01.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RX [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
Liu Y.L., Wu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., L
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606649; CAE03618.1; -
SQ SEQUENCE 325 AA; 35096 MW; 3F1C483A61C0FCAD CRC64;

Query Match 1.7%; Score 9; DB 10; Length 325;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 19 AAAAASSAA 27
|||||
DB 33 AAAAASSAA 41

RESULT 146

Q871D4
ID Q871D4 PRELIMINARY; PRT; 328 AA.
AC Q871D4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein B8G12.135.
GN B8G12.135.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
RX [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Hollar
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX294027; CAD71073.1; -
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 34350 MW; 760420D2C40A6EB5 CRC64;

Query Match 1.7%; Score 9; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 24;

mservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPP 128
|||||
AAAPP 280

RELIMINARY; PRT; 328 AA.

TrEMBLrel. 24, Created)
TrEMBLrel. 24, Last sequence update)
TrEMBLrel. 25, Last annotation update)
tin-like protein.
appendiculatus (Brown ear tick).
azoa; Arthropoda; Chelicerata; Arachnida; Acari;
s; Ixodida; Ixodidae; Rhipicephalus.
331;

N.A.

igimoto C., Onuma M.;
s appendiculatus midgut gallectin-like protein.";
3-2002) to the EMBL/GenBank/DBJ databases.
7; AA060051.1; -.
008985; ConA like lec_gl.
001079; Galactin.
; Gal-bind lectin; 1.
5; GLECT; 2.
3 AA; 36185 MW; 90BFD7322818CAB CRC64;

1.7%; Score 9; DB 5; Length 328;
arity 100.0%; Pred.No. 24;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126
|||||
AAAAA 298

RELIMINARY; PRT; 333 AA.

TrEMBLrel. 24, Created)
TrEMBLrel. 24, Last sequence update)
TrEMBLrel. 25, Last annotation update)
form of TSLC-1.
(Human).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
06;

N.A.

y., Nagano T.;
secretory isoform of SGISF/TSLC-1.";
T-2002) to the EMBL/GenBank/DBJ databases.
6; BAC66178.1; -.
003599; IG.
007110; IG-like.
003598; IG_c2.
; IG; 3.
9; IG; 3.
8; IGC2; 3.
835; IG LIKE; 3.
3 AA; 36915 MW; D7C1102F46D08492 CRC64;

1.7%; Score 9; DB 4; Length 333;
arity 100.0%; Pred.No. 25;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 AAAAAAAPP 128
|||||
Db 14 AAAAAAAPP 22

RESULT 149
Q84J51
ID Q84J51 PRELIMINARY; PRT; 333 AA.
AC Q84J51; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative peroxisomal Ca-dependent anotate carrier protein (Hypothe
protein OJA1364E02.4).
GN OJA1364E02.15 OR OJA1364E02.4.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RT "Rice Genomic Sequence.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135208; AAP06887.1; -.
DR EMBL; AC139168; AAP06894.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Hypothetical protein.
SQ SEQUENCE 333 AA; 36347 MW; F6E61EEA3E08D45C CRC64;

Query Match 1.7%; Score 9; DB 10; Length 333;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 222 QQQQPPPPQ 230
|||||
Db 18 QQQQPPPPQ 26

RESULT 150
Q8C4L5
ID Q8C4L5 PRELIMINARY; PRT; 333 AA.
AC Q8C4L5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical SNF2 related domain containing protein.
GN BC004701 OR D330021P09RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotati
RL Nature 420:563-573(2002).
RL Nature 420:563-573(2002).
DR EMBL; AK081756; BAC38321.1; -.
DR MGI; MGI:2384292; BC004701.
DR InterPro; IPR008941; TPR-like.

11:33:42 2004

us-09-976-740-43.olig.rspt

protein.
13 AA; 36271 MW; 2B3B61EF7E32CBD1 CRC64;
1.7%; Score 9; DB 11; Length 333;
arity 100.0%; Pred.No. 25;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDED 342
|||||
DEDED 123
Se March 30, 2004, 15:02:09
JO s

11:33:41 2004

us-09-976-740-43.olig.rsp

GenCore version 5.1.6
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in search, using sw model

rch 30, 2004, 14:54:51 ; Search time 18 Seconds
(without alignments)

1556.319 Million cell updates/sec

-09-976-740-43

3

MAGPPALPPETATAAATAA.....HIKVLQGHFEDDDPDGFLG 538

IGO

pop 60.0 , Gapext 60.0

1681 seqs, 52070155 residues

ts satisfying chosen parameters: 141681

eth: 0

eth: 2000000000

isting first 150 summaries

wissProt_42:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

seq	length	DB	ID	Description
2.0	239	1	CENB_SHEEP	P49451 ovis aries
2.0	808	1	Y066 NPVAC	P41467 autographa
2.0	892	1	ATX7 HUMAN	O15265 homo sapien
1.9	75	1	MSDA DROME	Q9Vb16 drosophila
1.9	260	1	A32E MOUSE	P97822 mus musculus
1.9	275	1	HXA5 HETER	Q9ia23 heterodontu
1.9	403	1	FXQ1 HUMAN	Q9C009 homo sapien
1.9	469	1	FXGA HUMAN	P55316 homo sapien
1.9	557	1	ACH1 SCHGR	P23414 schistocerc
1.9	579	1	Z384 RAT	Q9eqj4 rattus norv
1.9	613	1	RPSD ECOLI	P00579 escherichia
1.9	615	1	RPSD SALTY	P07336 salmonella
1.9	621	1	VP40 HSVBC	P54817 bovine herp
1.9	678	1	GARP PLAFF	P13816 plasmodium
1.9	1054	1	R0GB DROME	P43125 drosophila
1.9	1362	1	BRD4 HUMAN	O60885 homo sapien
1.9	1461	1	TOP2 CANAL	P87078 candida alb
1.9	1887	1	FAS2 YEAST	P19097 s fatty aci
1.7	109	1	RLA1 MAIZE	P52855 zea mays (m
1.7	109	1	RLA1 TRYCR	P28643 trypanosoma
1.7	158	1	RL12 ORYSA	O22386 oryza sativ
1.7	178	1	RPOE LISMO	Q8Y494 listeria mo
1.7	228	1	V33P ADE02	P24939 human adeno
1.7	229	1	V33P ADE05	P24940 human adeno
1.7	254	1	BRX1 MOUSE	Q9er42 mus musculu
1.7	272	1	TRPC MYCTU	O06129 mycobacteri
1.7	282	1	RK4 ARATH	O50061 arabidopsis
1.7	288	1	SDC CAEL	P50605 caenorhabdi
1.7	376	1	HMEV DROME	P06602 drosophila
1.7	415	1	RL3 DROME	O16797 drosophila
1.7	416	1	EVX1 MOUSE	P23683 mus musculu
1.7	440	1	Y77A STRCO	Q9f1y6 streptomyce
1.7	482	1	BHB3 HUMAN	Q9c0j9 homo sapien

34	9	1.7	488	1	HLX1_HUMAN	Q14774 homo
35	9	1.7	490	1	MOT3_YEAST	P54785 sacc
36	9	1.7	507	1	PIAG_MOUSE	Q9jm05 mus
37	9	1.7	562	1	SIS2_YEAST	P36024 sacc
38	9	1.7	565	1	FXJ2_MOUSE	Q9es18 mus
39	9	1.7	574	1	FXJ2_HUMAN	Q9p0x8 homo
40	9	1.7	639	1	ZIC5_HUMAN	Q99t52 homo
41	9	1.7	864	1	ELS_RAT	Q99372 ratt
42	9	1.7	901	1	A180_MOUSE	Q61548 mus
43	9	1.7	915	1	A180_RAT	Q05140 ratt
44	9	1.7	984	1	MCR_HUMAN	P08235 homo
45	9	1.7	987	1	IF3A_ARATH	Q9ld55 arab
46	9	1.7	1065	1	KOG1_HUMAN	O75912 homc
47	9	1.7	1085	1	IFH1_YEAST	P39520 sacc
48	9	1.7	1137	1	MSH3_HUMAN	P20585 homo
49	9	1.7	1150	1	NRDC_HUMAN	O43847 homo
50	9	1.7	1461	1	IE18_PRIVIF	P11675 pseu
51	9	1.7	2004	1	MTS3_HUMAN	Q92794 homc
52	9	1.7	2063	1	NCO6_MOUSE	Q14686 h nu
53	9	1.7	2067	1	MLL4_HUMAN	Q9j119 m nu
54	9	1.7	2715	1	DY1B_CHLRE	Q9umf6 homc
55	9	1.7	4513	1	ANP3_PSEAM	Q9mbf8 chla
56	8	1.5	37	1	ANP4_PSEAM	P02733 pseu
57	8	1.5	82	1	ANP4_PSEAM	P04002 pseu
58	8	1.5	85	1	ANP4_PSEAM	P02734 pseu
59	8	1.5	91	1	ANP4_PSEAM	P07835 pseu
60	8	1.5	91	1	ANP4_PSEAM	P23699 pseu
61	8	1.5	97	1	ANP4_PSEAM	P09031 lima
62	8	1.5	99	1	CU02_BLACK	P08076 blat
63	8	1.5	99	1	RL12_METVA	P10623 meth
64	8	1.5	104	1	HSP3_RAT	Q84256 ratt
65	8	1.5	105	1	RLA2_DICDI	P22683 dict
66	8	1.5	106	1	RL12_ARCFU	O28780 arch
67	8	1.5	111	1	RLA1_CABEL	P91913 caer
68	8	1.5	112	1	RLA1_DROME	P08570 dros
69	8	1.5	114	1	RLA2_EINTE	Q967y3 eime
70	8	1.5	121	1	ASF2_HELAN	P22184 heli
71	8	1.5	131	1	SECR_PIG	P01279 sus
72	8	1.5	134	1	RS16_BRUME	Q8Yj59 bruc
73	8	1.5	136	1	SR14_HUMAN	P37108 homc
74	8	1.5	138	1	HEX9_ADE07	P03283 huma
75	8	1.5	138	1	RL34_AEDTR	Q9nb34 aede
76	8	1.5	141	1	RNS3_STRAU	P30289 stre
77	8	1.5	146	1	WHM1_WHEAT	O64392 trit
78	8	1.5	148	1	WHW2_WHEAT	O64393 trit
79	8	1.5	149	1	HMGL_VICFA	P040620 vic
80	8	1.5	165	1	RS16_CAUCR	P58122 caul
81	8	1.5	177	1	OM19_BRUME	Q44663 bruc
82	8	1.5	200	1	RMS_CHICK	Q9w611 gall
83	8	1.5	205	1	PSAD_HORVU	P36213 horc
84	8	1.5	205	1	YNP2_CABEL	P34555 caer
85	8	1.5	209	1	HS27_CANFA	P42929 cani
86	8	1.5	211	1	HM1X_HUMAN	Q9ugv6 homc
87	8	1.5	211	1	RS5_CORGL	Q8nsx5 corl
88	8	1.5	214	1	RSMB_RAT	P17136 ratt
89	8	1.5	215	1	HANI_HUMAN	Q96004 homc
90	8	1.5	231	1	RSMB_MOUSE	P27048 mus
91	8	1.5	231	1	UCRI_NEUCR	P07056 neur
92	8	1.5	240	1	RSMB_CHICK	Q9pv94 gall
93	8	1.5	240	1	RSMB_ERIEU	Q8tu67 erir
94	8	1.5	240	1	RSMB_HUMAN	P14678 homc
95	8	1.5	240	1	RSMB_MONDO	Q9tu66 monc
96	8	1.5	240	1	YPBE_BACSU	P50731 bac
97	8	1.5	243	1	AX28_SOYBN	P13089 glyc
98	8	1.5	249	1	PRA_MYCLE	P41484 mycc
99	8	1.5	251	1	RPC8_YEAST	P17890 sacc
100	8	1.5	255	1	YU95_MYCTU	Q10863 mycc
101	8	1.5	261	1	GSHI_MOUSE	P31315 mus
102	8	1.5	264	1	GSHI_HUMAN	Q9h482 homc
103	8	1.5	271	1	HXA9_MOUSE	P09631 mus
104	8	1.5	272	1	HXA9_HUMAN	P31269 homc
105	8	1.5	279	1	ASF1_YEAST	P32447 sacc
106	8	1.5	281	1	CEBE_RAT	P56261 ratt

1.5 294 1 NPM_CHICK
 1.5 299 1 PP3D_HUMAN
 1.5 303 1 ALB3_MAIZE
 1.5 304 1 RIP9_MAIZE
 1.5 311 1 CDX2_MOUSE
 1.5 313 1 HEM3_PSEPK
 1.5 317 1 RLAO_MOUSE
 1.5 320 1 TTP_RAT
 1.5 322 1 KHSE_XANCP
 1.5 323 1 OLG2_HUMAN
 1.5 323 1 OLG2_MOUSE
 1.5 323 1 HKDD_HUMAN
 1.5 335 1 INGS_HUMAN
 1.5 337 1 LIMA_PSEAE
 1.5 340 1 MBNL_MOUSE
 1.5 341 1 MBNL_MOUSE
 1.5 347 1 RLAO_METAC
 1.5 353 1 NK24_HUMAN
 1.5 354 1 ATH1_HUMAN
 1.5 354 1 SXL_DROME
 1.5 357 1 IF35_HUMAN
 1.5 359 1 WN9B_MOUSE
 1.5 372 1 GDF1_HUMAN
 1.5 376 1 HXA2_HUMAN
 1.5 377 1 CX10_CHICK
 1.5 387 1 SOX1_HUMAN
 1.5 388 1 MBNL_HUMAN
 1.5 391 1 SOX1_MOUSE
 1.5 392 1 HME1_HUMAN
 1.5 394 1 HGH1_YEAST
 1.5 394 1 K1M4_HUMAN
 1.5 395 1 IF5_SCHPO
 1.5 396 1 ARRS_XENLA
 1.5 396 1 SX11_CHICK
 1.5 399 1 HXAA_MOUSE
 1.5 401 1 HME1_MOUSE
 1.5 405 1 GDFB_MOUSE
 1.5 407 1 GDFB_HUMAN
 1.5 407 1 YOI4_CAEEL
 1.5 410 1 BHB3_MOUSE
 1.5 410 1 BHB3_RAT
 1.5 410 1 HME2_DROME
 1.5 412 1 FKBA_SPOFR
 1.5 416 1 CRTC_MOUSE
 1.5 416 1 CRTC_RAT

ALIGNMENTS

STANDARD; PRT; 239 AA.

(Rel. 33, Created)

(Rel. 33, Last sequence update)

(Rel. 41, Last annotation update)

mere autoantigen B (Centromere protein B) (CENP-B)

Sheep).

etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

riniae; Ovis.

940;

M N.A.

9078; PubMed=8893808;

Jones C.A., Burkin H.R., McGrew J.A., Broad T.E.;

and CENP genes show a high level of sequence similarity

d synteny with their human homologs.;

ell Genet. 74:86-89(1996).

; Interacts with centromeric heterochromatin in

CC chromosomes and binds to a specific subset of aliphoid satell
 CC DNA, called the CENP-B box. May organize arrays of centromer
 CC satellite DNA into a higher order structure which then direc
 CC centromere formation and kinetochore assembly in mammalian
 CC chromosomes (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 CENPB domain.
 CC This SWISS-PROT entry is copyright. It is produced through a col
 CC between the Swiss Institute of Bioinformatics and the EMBL ou
 CC the European Bioinformatics Institute. There are no restrictio
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U35655; AAA79098.1; -;
 CC InterPro: IPR004875; CENP-B.
 CC Pfam: PF03184; DDE; 1.
 CC Chromosomal protein; Nuclear protein; DNA-binding; Centromere.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 26436 MW; 259C6C72E7D9C135 CRC64;

Query Match 2.0%; Score 11; DB 1; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0;

Matches 11; Conservative 0; Mismatches 0;

QY 329 EEEEDDEDED 339

|||||

Db 158 EEEEDDEDED 168

RESULT 2

Y066 NPVAC

ID Y066 NPVAC STANDARD; PRT; 808 AA.

AC P41457;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE Hypothetical 94.0 kDa protein in POL-LEF3 intergenic region.

OS Autographa californica nuclear polyhedrosis virus (AcMNPV).

OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

OC Nucleopolyhedrovirus.

OX NCBI_TaxID=46015;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=C6;

RX MEDLINE=94303173; PubMed=8030224;

RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;

RT "The complete DNA sequence of Autographa californica nuclear

RT polyhedrosis virus.;"

RL Virology 202:586-605(1994).

CC -!- SIMILARITY: TO CORRESPONDING ORF IN OFMNPV AND LDMNPV.

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CC the European Bioinformatics Institute. There are no restrictio

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L22858; AAA66696.1; -;
 CC PIR: C72858; C72858.
 CC Hypothetical protein.
 FT DOMAIN 106 117
 SQ SEQUENCE 808 AA; 93973 MW; 76A871D2B6633F8A CRC64;

Query Match 2.0%; Score 11; DB 1; Length 808;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 11; Conservative 0; Mismatches 0; Indels 0;

PPAPPO 222
|||||
PPAPPO 118

STANDARD; PRT; 892 AA.
; 0753229; Q9Y6P8;
el. 38, Created)
el. 38, Last sequence update)
el. 42, Last annotation update)
ocerebellar ataxia type 7 protein).

Human).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;
N.A.
last;
13; PubMed=9288099;
rt G., Stevanin G., Duerr A., Yvert G., Cancel G.,
rt S.G., Saudou F., Antoniou E., Drabkin H., Gemmill R.,
omar A., Wood N., Ruberg M., Agid Y., Mandel J.-L.,
e SCA7 gene reveals a highly unstable CAG repeat
:-55-70(1997).
N.A.

68; PubMed=9425224;
Kroels L., Michalik A., Theuns J., Loefgren A.,
ehmert A., Van den Bossche D., Van Zand K.,
van Regenmortel N., Martin J.-J., Van Broeckhoven C.;
etic analysis of autosomal dominant cerebellar ataxia
eneration (ADCA type II) caused by CAG triplet repeat
t. 7:177-186(1998).

89; PubMed=12533095;
ark A.M., Townsend J.J., Ptacek L.J., Fu Y.H.;
al nervous system-enriched spinocerebellar ataxia type 7
60:97-103(2003).

CATION.
72; PubMed=10441328;
Muvick L.A., Skinner P.J., Koob M.D., Ranum L.P.,
ization of the spinocerebellar ataxia type 7 protein,
t. 8:1657-1664(1999).

TH SH3P12.
3;
mot L., Takahashi J., Spassky N., Leprince C.,
der C., Fujigasaki H., Kusel-Andermann P.,
Cannonis J.H., Brice A.;
racts with a Cbl-associated protein that it recruits
intracellular inclusions.";
t. 10:1201-1213(2001).

[TH PSMCI.
11; PubMed=11734547;
rbea C., Einum D.D., Townsend J., Michalik A.,
en C., Jensen C.C., Murphy K.J., Ptacek L.J.; Fu Y.H.;
of ataxin-7 with the proteasome subunit S4 of the 19S
plex";
t. 10:2821-2831(2001).

-I- FUNCTION: Involved in neurodegeneration.
-I- SUBUNIT: Interacts with SH3P12, PSMCI and CRX.
-I- SUBCELLULAR LOCATION: Nuclear. In addition to a diffuse
distribution throughout the nucleus, it is associated with the
nuclear matrix and the nucleolus. Isoform b is cytoplasmic.
-I- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=a; Synonyms=Ataxin-7a;
IsoId=O15265-1; Sequence=Displayed;
Note=Nuclear;
Name=b; Synonyms=Ataxin-7b, SCA7b;
IsoId=O15265-2; Sequence=VSP_007695;
Note=Cytoplasmic;
TISSUE SPECIFICITY: Isoform a and isoform b are expressed in
CNS, but isoform a is expressed predominantly in the periph-
erical tissues. Isoform b is also highly expressed in the frontal lo-
cus, skeletal muscle and spinal cord and is expressed at a lower lo-
calization in the lung, lymphoblast and intestine.
-I- PTM: Proteolytically cleaved. The cleavage may be involved in
neurodegeneration; the isoform fragments may exert distinct toxic
influences that could contribute to selective neurodegenerati-
on. POLYMORPHISM: The poly-Gln region of SCA7 is highly polymorph-
ic (to 18 repeats) in the normal population and is expanded to abo-
ve 38-130 repeats in SCA7 patients. Intermediate alleles with 28
to 35 repeats are prone to further expansion.
-I- DISBASE: Defects in SCA7 are the cause of spinocerebellar atax-
ia type 7 (SCA7) [MIM:164500]; also known as autosomal dominant
cerebellar ataxia type II (ADCA-II). SCA7 is characterized by
pigmentary macular dystrophy and retinal degeneration leading
to blindness.
-I- SIMILARITY: Belongs to the ataxin 7 family.

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ommercial entities requires a license agreement (See http://www.isb-sib.ch/
or send an email to license@isb-sib.ch).

EMBL; AJ000517; CRA04154.1; -;
EMBL; AF032105; AAC39765.1; -;
EMBL; AF032102; AAC19162.1; -;
EMBL; AF032103; AAC19163.1; -;
EMBL; AA398030; -; NOT ANNOTATED_CDS.
Genew; HGNC:10560; SCA7.
MIM; 607640; -;
MIM; 164500; -;
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0006997; P:nuclear organization and biogenesis; TAS.
GO; GO:0007601; P:vision; TAS.
KW Polymorphism; Triplet repeat expansion; Disease mutation;
Nuclear protein; Alternative splicing.
FT DOMAIN 30 49
FT PRO-RICH.
FT DOMAIN 40 65
FT SER-RICH.
FT DOMAIN 171 219
FT PRO-RICH.
FT DOMAIN 402 486
FT PRO-RICH.
FT DOMAIN 640 851
FT POLY-ALA.
FT DOMAIN 16 20
FT POLY-ALA.
FT DOMAIN 23 28
FT POLY-GLN.
FT DOMAIN 30 39
FT POLY-PRO.
FT DOMAIN 40 45
FT POLY-SER.
FT DOMAIN 51 55
FT POLY-SER.
FT DOMAIN 171 174
FT POLY-SER.
FT DOMAIN 213 219
FT POLY-SER.
FT DOMAIN 647 654
FT POLY-SER.
FT DOMAIN 717 730
FT POLY-SER.
FT DOMAIN 840 845
FT POLY-SER.
FT VARSPPLIC 888 892
FT PKARP -> DISSPCLRTGISATSPQSPDLKSKGTS
STGRNADTFEKLHLHSLWTRPCL (in isofo-
rm b).
/FTID=VSP_007695.
K -> R (in dbSNP:1053338).

VARIANT 264 264
FT FT

```

/FTid=VAR_011823.
P -> S (in dbSNP:1053340).
/FTid=VAR_011824.
P -> H (IN REF. 2; AAC19162).
29 129 C -> S (IN REF. 2; AAC19162).
52 862 V -> M (IN REF. 2).
88 892 PKARP -> VGNGL (IN REF. 2;
AAC39765/AAC19163).
2 AA; 95451 MW; 9AEAF7D77103C5F CRC64;

2.0%; Score 11; DB 1; Length 892;
arity 100.0%; Pred.No. 0.46;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

PPPPQQ 232
|||||
PPPPQQ 46

STANDARD; PRT; 75 AA.
0; Q8MSH9;
Rel. 42, Created
Rel. 42, Last sequence update)
nd-specific peptide 57Da precursor (Male accessory gland
tein 57Da)
DNA:GH19893 OR CG9074.
lanogaster (Fruit fly).
taxa; Arthropoda; Hexapoda; Insecta; Pterygota;
opterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
27;

[N.A., AND TISSUE SPECIFICITY.
-R;
188; PubMed=7711745;
chaefer M., Schaefer U.;
d regulation of a gene cluster for male accessory gland
n Drosophila melanogaster."
m. Mol. Biol. 25:127-137(1995).

[N.A.
ev;
1006; PubMed=10731132;
leiniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Heit J.G., Nelson C.R., Miklos G.L.G.,
ghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cawley S., Dahlke C., Davenport L.B., Davies P.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
up L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
ibrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
ong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
uston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
ilush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
i Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
ai B., McIntosh T.C., McLeod M.P., McPherson D.,
Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
oy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[3]
RN SEQUENCE OF 2-75 FROM N.A.
RP STRAIN=Berkley; TISSUE=Head;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan
RA George R.A., Guarin H., Krommiller B., Pacleeb J.M., Park S., Wan
RA Rubin G.M., Celniker S.E.;
RA "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -!- FUNCTION: Transferred from male to female during mating and it
CC affect egg laying and behavior after mating.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Lumen fluid of male accessory glands, bec
CC seminal fluid.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z33647; CAA83925.1; -
DR EMBL; AE003753; AAF56515.1; -
DR EMBL; AY118802; AAM50662.1; -
DR Flybase; FBgn0011668; Mst57Da.
KW Signal; Behavior.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 75 ACCESSORY GLAND-SPECIFIC PEPTIDE 57I
FT DOMAIN 39 64 ALA/PRO-RICH DOMAIN.
FT CONFLICT 39 46 MISSING (IN REF. 1).
FT CONFLICT 64 75 MISSING (IN REF. 1).
SQ SEQUENCE 75 AA; 7106 MW; BCD3D70817C98E14 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 75;
Best Local Similarity 100.0%; Pred.No. 0.38; Mismatches 0; Indels 0; C
Matches 10; Conservative 0;

QY 118 APAAATAAAP 127
Db 40 APAAATAAAP 49
|||||
|||||

RESULT 5
A32E MOUSE STANDARD; PRT; 260 AA.
ID A32E MOUSE
AC P97822; Q8BPR8; Q8C2L4; Q8C7Q8; Q9CZD2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Acidic leucine-rich nuclear phosphoprotein 32 family member E (LF
DE like protein) (LAMP-L) (Cerebellar postnatal development protein-
GN ANP32E OR CPDI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBCELLULAR LOCATION, 1
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

```

74; PubMed=11430900;
Vila-Ortiz G., Cafferata B.G.A., Di Tella M.C.,
ico A., Perandones C., Pivetta O.H., Carminatti H.,
V.P., Santa-Coloma T.A.;
expression of CPD during postnatal development in the
um.";
:162-174 (2001).
N.A. (ISOFORM 1).
; TISSUE=Brain;
-2000) to the EMBL/GenBank/DBJ databases.
N.A. (ISOFORMS 1 AND 2).
J, and NOD; TISSUE=Embryo, Spinal cord, and Thymus;
83; PubMed=12466851;
runo M., Kasukawa T., Adachi J., Bono H., Kondo S.,
ato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
u Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
adt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
ani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gariboldi M., Gissi C., Godzik A., Gough J.,
usincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
ji H., Kawasawa Y., Kedzierski R.M., King B.L.,
urochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maltais L., Marchionni L., McKenzie L., Miki H.,
Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Pillai R., Pontius J.U., Qi D., Ramachandran S.,
d J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
chenider C., Simple C.A., Setou M., Shimada K.,
kenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
gner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
Wynshaw-Boris A., Yanoigisawa M., Yang I., Yang L.,
an M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
kawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
ki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
zume Y., Imotani K., Ishii Y., Itoh M., Kagawa I.,
akai K., Sasaki D., Shibata K., Shingawa A.,
Yoshino M., Waterston R., Lander E.S., Rogers J.,
ashizaki Y.;
he mouse transcriptome based on functional annotation of
ngth cDNAs.";
-573 (2002).
N.A. (ISOFORM 1).
57; PubMed=12477932;
Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
uellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
orley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
on E., Ketterman W., Madan A., Rodrigues S., Sanchez A.,
dan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Touchman J.W., Green E.D., Dickson M.C.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinaki M.I., Skalka U., Smailus D.E.,
chein J.E., Jones S.J.M., Marra M.A.;
d initial analysis of more than 15,000 full-length human
sequences.";
ad. Sci. U.S.A. 99:16899-16903 (2002).
Inhibits activity of protein phosphatase 2A. Does not
otein phosphatase 1. May play a role in cerebellar
R. LOCATION: Nuclear and cytoplasmic.

CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P97822-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P97822-2; Sequence=VSP_007373;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed at highest levels in cerebellum
CC spleen. In the cerebellum, expressed mainly in granule cells a
CC to a lesser extent, in Purkinje cells.
CC -!- DEVELOPMENTAL STAGE: Low levels are found at postnatal day 4.
CC Levels increase from postnatal day 7 to postnatal day 17. Leve
CC decrease and remain low in the adult.
CC -!- SIMILARITY: Belongs to the ANP32 family.
CC -!- SIMILARITY: Contains 4 leucine-rich (LRR) repeats.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL out
CC the European Bioinformatics Institute. There are no restrictions
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for co
CC entities requires a license agreement (See http://www.isb-sib.ch/a
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U9345; AAB49462.2; -
CC EMBL; AB037685; BAB03507.1; -
CC EMBL; AK012759; BAB28449.1; -
CC EMBL; AK049647; BAC33858.1; -
CC EMBL; AK076049; BAC36147.1; -
CC EMBL; AK088401; BAC40331.1; -
CC EMBL; BC005690; AAB05690.1; -
CC MGD; MGI:1913721; Amp32e.
CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0019212; F:phosphatase inhibitor activity; IDA.
CC InterPro; IPR001611; LRR.
CC SMART; SM00446; LRRcap.
CC Pfam; PF00560; LRR; 3.
CC SMART; SM00446; LRRcap; 1.
CC Leucine-rich repeat; Repeat; Nuclear protein; Alternative splicing
FT REPEAT 41 63
FT REPEAT 64 86
FT REPEAT 87 111
FT REPEAT 115 138
FT VARSPLIC 208 219
FT Missing (in isoform 2).
FT CONFLICT 98 98 N -> D (IN REF. 3; BAB28449).
FT CONFLICT 199 199 S -> T (IN REF. 3; BAC33858).
SQ SEQUENCE 260 AA; 29622 MW; 7F94E46D72A04780 CRC64;
Query Match 1.9%; Score 10; DB 1; Length 260;
Best Local Similarity 100.0%; Pred.No.1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Ga
QY 329 REEEDDEDE 338
Db 187 REEEDDEDE 196
RESULT 6
HXAS_HETFR
ID HXAS_HETFR STANDARD; PRT; 275 AA.
AC Q91A23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5.
GN HOXA5.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;

[N.A.
 096; PubMed=10677514;
 miya C., Bailey W., Kawasaki K., Mezey J., Miller W.,
 Shimizu N., Wagner G., Ruddle F.;
 genomics in the horn shark, *Heterodontus francisci*.;
 Acad. Sci. U.S.A. 97:1653-1660(2000).
 Sequence-specific transcription factor which is part of
 mental regulatory system that provides cells with
 positional identities on the anterior-posterior axis (By
 Y).
 AR LOCATION: Nuclear (By similarity).
 Y: Belongs to the Antp homeobox family.

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 ail to license@isb-sib.ch).

 2; AAF44643.1; -
 1SAN.
 476; -
 001827; Antennapedia.
 001356; Homeobox.
 ; homeobox; 1.
 25; ANTENNAPEDIA.
 24; HOMEBOX.
 010; Homeobox; 1.
 9; HOX; 1.
 032; ANTENNAPEDIA; 1.
 027; HOMEBOX 1; 1.
 071; HOMEBOX 2; 1.
 -binding; Developmental protein; Nuclear protein;
 regulation.
 81 186 ANTP-TYPE HEXAPEPTIDE.
 00 259 HOMEBOX.
 75 78 POLY-ALA.
 81 84 POLY-ALA.
 34 142 POLY-SER.
 27 230 POLY-ARG.
 5 AA; 30214 MW; 51BC2720808A31B6 CRC64;

 1.9%; Score 10; DB 1; Length 275;
 arity 100.0%; Pred. No. 1.1;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TTA AAA 22
 |||||
 TTA AAA 84

 STANDARD; PRT; 403 AA.
 6;
 Rel. 41, Created
 Rel. 41, Last sequence update
 Rel. 42, Last annotation update
 Protein Q1 (Hepatocyte nuclear factor 3 forkhead homolog
 'head-like protein 1) (HNF-1).
 ..
 (Human).
 :Zooa; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Primates; Catarrhini; Hominidae; Homo.
 .06;
 [N.A., AND TISSUE SPECIFICITY.
 676; PubMed=11747606;
 asche B., Frank S., Glaeser B., Kunz J., Witt K.,

RT "Isolation and characterization of the human forkhead gene FOXQ1.
 RL DNA Cell Biol. 20:555-561(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21207067; PubMed=11309849;
 RA Hong H.-K., Noveroske J.K., Headon D.J., Liu T., Sy M.S.,
 RA Justice M.J., Chakravarti A.;
 RT "The winged helix/forkhead transcription factor Foxq1 regulates
 RT differentiation of hair in satin mice.";
 RL Genesis 29:163-171(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.I
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz J
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany E
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk E
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the stomach,
 CC trachea, bladder and salivary gland.
 CC -!- SIMILARITY: Contains 1 fork-head domain.

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 EMBL; AF225950; AAK00639.1; -
 EMBL; AF153341; AAF75586.1; -
 EMBL; BC053850; AAH53850.1; -
 HSP; Q63245; 2HFH.
 Genew; HGNC:20951; FOXQ1.
 InterPro; IPR001766; TF_Fork_head.
 Pfam; PF00250; Fork_head; 1.
 PRINTS; PR00053; FORKHEAD.
 ProDom; PDO00425; TF_Fork_head; 1.
 SMART; SMO0339; FH; 1.
 DR PROSITE; PS00657; FORK_HEAD_1; 1.
 DR PROSITE; PS00658; FORK_HEAD_2; 1.
 DR PROSITE; PS00039; FORK_HEAD_3; 1.
 XW DNA-binding; Nuclear protein; Transcription regulation.
 FT DNA_BIND 119 214 FORK-HEAD.
 FT DOMAIN 13 103 ALA/GLY-RICH.
 FT DOMAIN 221 397 PRO-RICH.
 FT CONFLICT 49 52 NSPA -> KPS (IN REF. 2).
 FT CONFLICT 60 61 PP -> TQ (IN REF. 2).
 FT CONFLICT 386 386 S -> L (IN REF. 2).
 FT CONFLICT 395 395 P -> S (IN REF. 2).
 SQ SEQUENCE 403 AA; 41491 MW; EB52255A8AC6929B CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; C

APAAP 187
 |||||
 APAAP 246

STANDARD; PRT; 469 AA.
 Rel. 34, Created
 Rel. 34, Last sequence update)
 Rel. 40, Last annotation update)
 protein G1A (forkhead-related protein FKHL2)
 1 factor BF-2 (Brain factor 2) (BF2) (HPK2).
 2.
 Human).
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 16;
 N.A.
 132; PubMed=7959731;
 Niese S., Burfeind P., Schmudt D., Mattei M.-G.,
 W. W., Thies U.;
 factor 1, a new member of the fork head gene family.";
 51-557(1994).
 N.A.
 150; PubMed=7590184;
 My D.B., Schlung A., Burfeind P., Schmudt D.,
 Mattei M.-G., Thies U.;
 human brain factor 1 and 2, members of the fork head
 are clustered on chromosome 14q.";
 WS. Acta 1262:105-112(1995)
 Plays an important role in the establishment of the
 subdivision of the developing brain and in the
 it of the telencephalon. Sequence-specific DNA-binding
 with a distinct binding specificity (By similarity).
 NR LOCATION: Nuclear (Potential).
 Contains 1 fork-head domain.
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 between the Swiss Institute of Bioinformatics and the EMBL out-
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 or send an email to license@isb-sib.ch).
 All to license@isb-sib.ch).
 CAA55038.1; -
 CAA52240.1; -
 37451.
 2HEH.
 192;
 111; FOXG1A.
 F:DNA binding; TAS.
 P:brain development; TAS.
 101766; TF_Fork_head.
 Fork_head; 1.
 125; TF_Fork_head; 1.
 FH; 1.
 157; FORK_HEAD_1; 1.
 158; FORK_HEAD_2; 1.
 159; FORK_HEAD_3; 1.
 regulation; DNA-binding; Nuclear protein;
 protein.
 13 56 HIS-RICH.
 17 79 PRO-RICH.
 0 73 POLY-GLN.

FT DOMAIN 83 88 POLY-ARG.
 FT DNA_BIND 161 252 FORK-HEAD.
 SQ SEQUENCE 469 AA; 50539 MW; 943B8BDB90008EDC CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 220 PQQQQQPPPP 229
 |||||
 Db 68 PQQQQQPPPP 77

RESULT 9
 ACHI SCHGR STANDARD; PRT; 557 AA.
 ID ACHI SCHGR STANDARD; PRT; 557 AA.
 AC P23414;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-L1 chain precursor.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Caelifera; Acridoidea; Schistocerca.
 OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
 OX NCBI_TaxID=7010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91032263; PubMed=1702381;
 RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
 Darlison M.G., Sattelle D.B., Barnard E.A.;
 "Sequence and functional expression of a single alpha subunit of
 insect nicotinic acetylcholine receptor.";
 RL EMBO J. 9:4391-4398(1990).
 CC -i- FUNCTION: After binding acetylcholine, the AChR responds by a
 extensive change in conformation that affects all subunits an
 leads to opening of an ion-conducting channel across the plas
 membrane.
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -i- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC This SWISS-PROT entry is copyright. It is produced through a coll.
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 DR EMBL; X55439; CAA39081.1; -
 DR FIR; S12359; S12359.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_chan_memb.
 DR Pfam; PF02931; Neu_chan_LBD; 1.
 DR Pfam; PF02932; Neu_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Sig
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPH
 FT CHAIN EXTRACELLULAR.
 FT DOMAIN 24 244
 FT TRANSMEM 245 286
 FT TRANSMEM 274 294
 FT TRANSMEM 308 329
 FT DOMAIN 330 500
 FT TRANSMEM 501 523
 FT TRANSMEM 501 523
 FT DISULFID 151 165
 FT DISULFID 224 225
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).

```

47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
135 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
182 400 ALA/SER-RICH.
106 422 HIS-RICH.
57 AA; 63026 MW; 168389C88/DFDF3E CRC64;
1.9%; Score 10; DB 1; Length 557;
arity 100.0%; Pred.No. 2;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SSSAAS 28
|||||
SSSAAS 399

STANDARD; PRT; 579 AA.
I2; Q9EQJ3; Q9JWJ5;
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
protein 384 (Nuclear matrix transcription factor 4)
ed zinc finger protein).
A OR CIZ.
icus (Rat).
icazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1116;
1 N.A. (ISOFORM 1), SUBCELLULAR LOCATION, DNA-BINDING, AND
WITH CAS.
1045; PubMed=10669742;
Yamagata T., Sakai R., Ogawa S., Honda H., Ueno H.,
izaki Y., Hirai H.;
finger protein that interacts with p130cas and activates
n of matrix metalloproteinases."
.01. 20:1649-1658(2000).

1 N.A. (ISOFORMS 1; 2 AND 3).
ie-Dawley;
193; PubMed=11149472;
1 P., Alvarez M., Tokunaga K., Onyia J.E., Hock J.,
ister H., Rhodes S.J., Bidwell J.P.;
functional analysis of a family of nuclear matrix
; factors (NP/NMP4) that regulate type I collagen
t osteoblasts."
. Res. 16:10-23(2001).
Transcription factor that binds the consensus DNA
[GC]AAAAA. Seems to bind and regulate the promoters of
3, MMP7 and COL1A1.
Interacts with Cas.
AR LOCATION: Nuclear.
VE PRODUCTS;
ernative splicing: Named isoforms=3;
-Additional isoforms seem to exist;
9EQJ4-1; Sequence=Displayed;
9EQJ4-2; Sequence=VSP_006921;
9EQJ4-3; Sequence=VSP_006922;
ECIFCIIV; Expressed in osteocytes, osteoblasts, and
/es in bone.
Y; BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
TEINS.
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CC -----
DR EMBL; AB019281; BAA89664.1; -
DR EMBL; AF216804; AAG40582.1; -
DR EMBL; AF216805; AAG40583.1; -
DR EMBL; AF216806; AAG40584.1; -
DR HSSP; P08153; 1ZFD.
DR TRANSFAC; T05136; -
DR TRANSFAC; T05137; -
DR TRANSFAC; T05138; -
DR TRANSFAC; T05141; -
DR TRANSFAC; T05142; -
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 8.
DR ProDom; PD000003; Znf_C2H2; 4.
DR SMART; SM00355; Znf_C2H2; 8.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 8.
KW Transcription regulation; Zinc-finger; Metal-binding; Nuclear pr
KW DNA-binding; Repeat; Alternative splicing.
FT ZN_FING 229 251
FT ZN_FING 257 279
FT ZN_FING 285 307
FT ZN_FING 318 340
FT ZN_FING 346 368
FT ZN_FING 374 398
FT ZN_FING 404 426
FT ZN_FING 434 456
FT DOMAIN 462 524
FT DOMAIN 467 506
FT VARSPPLIC 103 118
FT VARSPPLIC 301 361
FT VARSPPLIC 178 179
FT CONFLICT 576 577
FT CONFLICT LA -> WP (IN REF. 1).
SQ SEQUENCE 579 AA; 63139 MW; FBC242E0D1050C45 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 579;
Best Local Similarity 100.0%; Pred.No. 2.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; (

QY 222 QQQQPPPPPP 231
Db 511 QQQQPPPPPP 520

RESULT 11
RPSD_ECOLI
ID RPSD_ECOLI STANDARD; PRT; 613 AA.
AC P00579;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase sigma factor rpoD (Sigma-70).
GN RPOD OR ALT OR B3067.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=82014879; PubMed=6269063;
RA Burton Z.F., Burgess R.R., Lin J., Moore D., Holder S., Gross C.F
RT "The nucleotide sequence of the cloned rpoD gene for the RNA
RL polymerase sigma subunit from E. coli K12.";
RN Nucleic Acids Res. 9:2889-2903(1981).
[2]
RC SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;

```

Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Lado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
 Jis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 genome sequence of *Escherichia coli* K-12.;
 153-1474(1997).

TOGRAPHY (2.6 ANGSTROMS) OF 113-446.

145; PubMed=8858155;

Severinova E., Darst S.A.;

Structure of a sigma 70 subunit fragment from *E. coli* RNA

36(1996).

The sigma factor is an initiation factor that promotes
 the RNA polymerase to specific initiation sites and
 released. This is the primary sigma-factor of this

f: Belongs to the sigma-70 factor family.

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AAA24601.1; -

AAA89147.1; -

}; AAC76103.1; -

UNEC5

RAY-97.

12:0; 6TH EDITION.

196; rpoD.

09043; RNA_pol sigma.

07631; Sigma70 ner.

07127; Sigma70_r1_1.

09042; Sigma70_r1_2.

07627; Sigma70_r2.

07624; Sigma70_r3.

07630; Sigma70_r4.

00943; Sigma70.

sigma70_ner_1.

sigma70_r1_1; 1.

sigma70_r1_2; 1.

sigma70_r2; 1.

sigma70_r3; 1.

sigma70_r4; 1.

16; SIGMA70FCT.

15; SIGMA70_1; 1.

16; SIGMA70_2; 1.

regulation; Sigma factor; DNA-directed RNA polymerase;

1D-structure; Complete proteome.

13 416 POLYMERASE CORE BINDING (POTENTIAL).

13 592 H-T-H MOTIF (BY SIMILARITY).

13 149 D -> N (IN REF. 1).

15 115

16 134

15 136

18 148

19 154

18 160

11 161

12 165

19 182

17 190

14 234

15 236

13 256

17 258

19 261

13 292

13 294

FT HELIX 299 306
 FT TURN 307 309
 FT HELIX 313 315
 FT TURN 316 316
 FT HELIX 317 320
 FT TURN 321 322
 FT HELIX 325 329
 FT TURN 333 333
 FT HELIX 334 351
 FT TURN 352 352
 FT HELIX 355 382
 FT TURN 383 383
 FT HELIX 384 391
 FT TURN 392 393
 FT TURN 395 396
 FT HELIX 401 418
 FT HELIX 421 423
 FT HELIX 427 445
 SQ SEQUENCE 613 AA; 70263 MW; CA4F0E30DEC1703D CRC64;

Query Match 1.9%; Score 10; DB 1; Length 613;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 333 DDEDEDEED 342
 |||||
 DB 191 DDEDEDEED 200

RESULT 12

RPSD SALTY
 ID RPSD SALTY STANDARD; PRT; 615 AA.
 AC P07336; Q823M4;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE RNA polymerase sigma factor rpoD (Sigma-70).
 GN RPOD OR STM3211 OR STY3390 OR T3131.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=86337422; PubMed=3005129;
 RA Erickson B.D., Burton Z.F., Watanabe K.K., Burgess R.R.;
 RT "Nucleotide sequence of the rpoD-dnaG-rpoB operon from Salmonella
 RT typhimurium and a comparison of this sequence with the homologous
 RT operon of *Escherichia coli*.";
 RL Gene 40:67-78(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille
 RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimur:
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wair
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia I
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
sen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
utherford K., Simmonds M., Skelton J., Stevens K.,
Barrell B.G.;
ome sequence of a multiple drug resistant Salmonella
var Typhi CT18.";
8-852(2001)).

N.A.
hi; STRAIN=Ty2 / ATCC 700931;
367; PubMed=12644504;
S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
odoyanni V., Schwartz D.C., Blattner F.R.;
Genomics of Salmonella enterica serovar Typhi strains Ty2
185:2330-2337(2003).
The sigma factor is an initiation factor that promotes
t of the RNA polymerase to specific initiation sites and
released. This is the primary sigma-factor of this
Y: Belongs to the sigma-70 factor family.

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ail to license@isb-sib.ch).

AAA27242.1; -
7; AAL22085.1; ALT INIT.
8; CAD07736.1; ALT INIT.
4; AAO70674.1; ALT INIT.
RNEB8T.
1SIG.
369; rpoD.
009043; RNA pol sigma.
007631; Sigma70 ner.
007127; Sigma70 r1.1.
009042; Sigma70 r1.2.
007627; Sigma70 r2.
007624; Sigma70 r3.
007630; Sigma70 r4.
009043; Sigma70.
; sigma70 ner; 1.
; sigma70 r1.1; 1.
; sigma70 r1.2; 1.
; sigma70 r2; 1.
; sigma70 r3; 1.
; sigma70 r4; 1.
46; SIGMA70FCT.
715; SIGMA70.1; 1.
716; SIGMA70.2; 1.
regulation; Sigma factor; DNA-directed RNA polymerase;
Complete proteome.
05 418 POLYMERASE CORE BINDING (POTENTIAL).
73 592 H-T-H MOTIF (BY SIMILARITY).
5 AA; 70530 MW; 114E8D4236A3D59A CRC64;
1.9%; Score 10; DB 1; Length 615;
arity 100.0%; Pred.No.2.2;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDEED 342
|||||
DEDEED 202

STANDARD; PRT; 621 AA.
5;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid protein P40 [Contains: Assemblin (Protease) (EC 3.4.21.97);
DE Capsid assembly protein].
GN UL26.
OS Bovine herpesvirus type 1 (strain Cooper).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10323;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96013856; PubMed=7474173;
RA Haanes E.J., Thomsen D.R., Martin S., Homa F.L., Lowery D.E.;
RT "The bovine herpesvirus 1 maturational proteinase and scaffold
RT proteins can substitute for the homologous herpes simplex virus 1
RT proteins in the formation of hybrid type B capsids.";
RL J. Virol. 69:7375-7379(1995).
CC -!- FUNCTION: THE CAPSID ASSEMBLY PROTEIN IS COMPONENT OF THE CAI
CC CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA.
CC -!- FUNCTION: ASSEMBLIN IS A PROTEASE WHICH CAN PROTEOLYTICALLY (C
CC ITSELF AND THE CAPSID ASSEMBLY PROTEIN AT THE C-TERMINUS.
CC -!- CATALYTIC ACTIVITY: Cleaves -Ala-|-Ser- and -Ala-|-Ala- bonds
CC the scaffold protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, UL26 (shown here) and UL26.5, are produ
CC by alternative initiation;
CC -!- SIMILARITY: Belongs to peptidase family S21.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
CC This SWISS-PROT entry is copyright. It is produced through a coll
CC between the Swiss Institute of Bioinformatics and the EMBL out
CC the European Bioinformatics Institute. There are no restriction
CC use by non-profit institutions as long as its content is ir
CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (see <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).

EMBL; U31809; AAA91999.1; -
EMBL; U31809; AAA92000.1; -
EMBL; Z78205; CAB01599.1; -
EMBL; AJ004801; CAA06107.1; -
HSSP; P16753; 1CMV.
MEROPS; S21.001; -
DR InterPro: IPR001847; Peptidase S21.
DR Pfam: PF00716; Peptidase S21; 1.
DR PRINTS; PR00236; HSVCAPSIDP40.
KW Capsid assembly; Hydrolase; Serine protease; Coat protein;
KW Alternative initiation.
FT CHAIN 1 621 CAPSID PROTEIN P40, ISOFORM UL26.
FT CHAIN 314 621 CAPSID PROTEIN P40, ISOFORM UL26.5.
FT INIT MET 314 314 FOR ISOFORM UL26.5.
FT CHAIN 1 254 ASSEMBLIN (PROTEASE).
FT CHAIN 255 621 CAPSID ASSEMBLY PROTEIN.
FT SITE 254 255 CLEAVAGE (BY THE PROTEASE) (PROBABLE
FT ACT SITE 68 68 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 155 155 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 621 AA; 63711 MW; AEF6D7C9DBE69003 CRC64;
Query Match 1.9%; Score 10; DB 1; Length 621;
Best Local Similarity 100.0%; Pred.No.2.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G
Qy 120 AAAAAAAAAPPP 129
| | | | | | | | | |
Db 368 AAAAAAAAAPPP 377
| | | | | | | | | |

RESULT 14
GARP_PLAFF STANDARD; PRT; 678 AA.
ID_GARP_PLAFF

el. 13, Created)
 el. 13, Last sequence update)
 el. 38, Last annotation update)
 rich protein precursor.

ciparum (isolate FC27 / Papua New Guinea).
 eolata; Apicomplexa; Haemosporida; Plasmodium.
 7;

N.A.
 48; PubMed-2903445;
 ahl H.-D., Crewther P.E., Silva A., Anders R.F.,

a Plasmodium falciparum gene that encodes a glutamic
 ein (GARP).";
 Parasitol. 31:199-202(1988).

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AA29605.1; -.
 54514.
 a; Antigen; Signal.
 1 25
 6 678 GLUTAMIC ACID-RICH PROTEIN.
 0 164 15 X 3 AA TANDEM REPEATS OF K-K-X.
 2 416 9 X APPROXIMATE TANDEM REPEATS.
 7 441 5 X APPROXIMATE TANDEM REPEATS.
 6 604 POLY-GLU.
 5 653 7 X APPROXIMATE TANDEM REPEATS.
 4 663 POLY-GLU.
 AA; 80551 MW; 2AF895606496EA9E CRC64;
 1.9%; Score 10; DB 1; Length 678;
 rity 100.0%; Pred. No. 2.4;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 EDEDE 340
 EDEDE 649

STANDARD; PRT; 1054 AA.
 el. 32, Created)
 el. 32, Last sequence update)
 el. 32, Last annotation update)
 ration B protein (Probable calcium transporter RDGB).
 anogaster (Fruit fly).
 azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 pterygota; Diptera; Brachycera; Muscomorpha;
 rosophilidae; Drosophila.
 7;

N.A.
 R; TISSUE=Head;
 70; PubMed=1903119;
 Hyde D.R., O'Tousa J.E.;
 Characterization of the Drosophila retinal
 (rdgB) gene."
 61-768(1991).
 RDGB mutants undergo rapid light-induced retinal
 on. May control phosphatidylinositol concentration in
 vesicles from the subrhabdomeric cisternae (SRC) to the

CC rhabdomere. May function as a calcium transporter.
 CC -!- TISSUE SPECIFICITY: Expressed in adult heads, not detected in
 CC bodies.
 CC -!- SIMILARITY: THE N-TERMINAL IS SIMILAR TO MAMMALIAN
 CC PHOSPHATIDYLINOSITOL (PTDINS) TRANSFER PROTEINS.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL out
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@sib-sib.ch).

CC EMBL; X57978; CAA41044.1; -.
 CC PIR; A61221; A61221.
 CC FlyBase; FBgn0003218; rdgB.
 CC GO; GO:0016029; C:subrhabdomeral cisterna; NAS.
 CC GO; GO:0008525; F:phosphatidylcholine transporter activity; IDA.
 CC GO; GO:0008526; F:phosphatidylinositol transporter activity; IDA.
 CC GO; GO:0016059; P:deactivation of rhodopsin mediated signaling; IN
 CC GO; GO:0007608; P:olfaction; IMP.
 CC GO; GO:0016056; P:rhodopsin mediated signaling; IMP.
 CC InterPro; IPR004177; DDHD_dom.
 CC DR PIR; A61221; A61221.
 CC DR Pfam; PF02862; DDHD; 1.
 CC DR PRINTS; PR00391; P1TRANSFER.
 CC Transmembrane; Vision.
 KW DOMAIN 321 332 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT TRANSMEM 501 519 POTENTIAL.
 FT TRANSMEM 734 750 POTENTIAL.
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 658 658 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 852 852 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 928 928 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1054 AA; 116560 MW; 87F26EB871003CA8 CRC64;
 Query Match 1.9%; Score 10; DB 1; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 329 BEEDDEDE 338
 Db 324 BEEDDEDE 333

RESULT 16
 BRD4 HUMAN
 ID BRD4 HUMAN STANDARD; PRT; 1362 AA.
 AC O60885; Q96PD3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bromodomain-containing protein 4 (HUNK1 protein).
 GN BRD4 OR HUNK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21590020; PubMed=11733348;
 RA French C.A., Miyoshi I., Aster J.C., Kubonishi I., Kroll T.G.,
 RA Dal Cin P., Vargas S.O., Perez-Atayde A.R., Fletcher J.A.;
 RT "BRD4 bromodomain gene rearrangement in aggressive carcinoma with
 RT translocation t(15;19).";
 RL Am. J. Pathol. 159:1987-1992(2001).
 RN [2]
 RP SEQUENCE OF 1-722 FROM N.A.
 RC TISSUE=Placenta;

EA
EB
EC
ED
EE
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R-1997) to the EMBL/GenBank/DBJ databases.
AR LOCATION: Nuclear (Potential).
Y: Contains 2 bromodomains.

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9; AAL26987.1; -;
CAA72780.1; -;
1B91.
3575; BRD4.
001487; Bromodomain.
; bromodomain; 2.
03; BROMODOMAIN.
7; BROMO; 2.
633; BROMODOMAIN 1; 1.
014; BROMODOMAIN 2; 2.
Repeat; Nuclear Protein.
75 147 BROMODOMAIN 1.
68 440 BROMODOMAIN 2.
35 594 LYS-RICH.
92 717 SER-RICH.
93 714 POLY-SER.
38 743 POLY-HIS.
57 761 POLY-PRO.
64 770 POLY-PRO.
71 775 POLY-GLN.
76 783 POLY-PRO.
54 964 POLY-PRO.
74 986 POLY-PRO.
11 1014 POLY-PRO.
28 1033 POLY-PRO.
83 1300 POLY-GLN.
01 1308 POLY-ALA.
35 1338 POLY-ARG.
20 721 EM -> GP (IN REF. 2).
62 AA; 152219 MW; D52EFCF9960907 CRC64;

arity 1.9%; Score 10; DB 1; Length 1362;
conservative 0; Pred.No. 4.2;
Mismatch 0; Indels 0; Gaps 0;

QPQPPP 235
|||||
QPQPPP 986

STANDARD; PRT; 1461 AA.

Rel. 35, Created)
Rel. 35, Last sequence update)
Rel. 39, Last annotation update)
rase II (EC 5.99.1.3).

ans (Yeast).
ngi; Ascomycota; Saccharomycotina; Saccharomycetes;
ales; mitosporic Saccharomycetales; Candida.
76;

N.A.
gton 2402E;
233; PubMed=9164874;
Patel S., Fisher L.M.;
oning and expression of the Candida albicans TOP2 gene
of fungal DNA topoisomerase II inhibitors in yeast.";

Biochem. J. 324:329-339(1997).
-!- FUNCTION: Control of topological states of DNA by transient
breakage and subsequent rejoining of DNA strands. Topoisomera
makes double-strand breaks.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoin
of double-stranded DNA.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax bc
negative and positive supercoils, whereas prokaryotic enzymes
relax only negative supercoils.
-!- SIMILARITY: Belongs to the type II topoisomerase family.

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EMBL; Y10177; CAA71405.1; -;
HSSP; P08786; 1BGM.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003957; CBFA_NFYB_topis.
InterPro; IPR001241; DNA_topoisoiI.
InterPro; IPR002205; DNA_topoisoiV.
Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoiV; 1.
Pfam; PF02518; HATFase_C; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TPI2FAMILY.
ProDom; PD000742; DNA_topoisoiV; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00433; TOP2C; 1.
SMART; SM00434; TOP4C; 1.
PROSITE; PS00177; TOPOISOMERASE_II; FALSE_NEG.
Isomerase; Topoisomerase; DNA-binding; ATP-binding; Phosphorylati
Nuclear protein.
NP_BIND 190 195 ATP (POTENTIAL).
ACT_SITE 842 842 DNA_CLEAVAGE (BY SIMILARITY).
SEQUENCE 1461 AA; 165386 MW; B2F7933B05804E36 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 1461;
Best Local Similarity 100.0%; Pred.No. 4.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; G

QY 334 DDEDEDEDD 343
|||||
DB 1436 DDEDEDEDD 1445

RESULT 18

FAS2_YEAST
ID_FAS2_YEAST STANDARD; PRT; 1887 AA.
AC P19097; Q12533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes: Acyl
carrier; 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100
(Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier protein] synth
(EC 2.3.1.41) (Beta-ketoacyl synthase)].
GN FAS2 OR YPL231W OR P1409.
OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315020; PubMed=2900835;
RA Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
RT "Primary structure of the multifunctional alpha subunit protein o

id synthase derived from FAS2 gene sequence.";
263:12315-12325(1988).
N.A.
(-1994) to the EMBL/GenBank/DBJ databases.
N.A.
AB972;
71; PubMed=9169875;
rms R.K., Ahmed A., Albersmann K., Allen E., Ansonge W.,
Riccio A., Bartell B.G., Badcock K., Benes V.,
Iowman S., Bruckner M., Carpenter J., Cherry J.M.,
Cher C.M., Coster F., Davis K., Davis R.W.,
Delius H., Dipaolo T., Dubois E., Dueterhoeft A.,
eth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
ng U., Heumann K., Hilbert H., Hillier L.W.,
S., Hyman R., Johnston M., Kalman S., Klein K.,
O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
ssenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
Namath A., Nentwich U., Oefner P., Pearson D.,
hl T.M., Purnelle D., Schafer M., Scharfe M.,
chramm S., Schroeder M., Sdicu A.M., Tettelin H.,
A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
mbutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
lilner A., Vo D.H., Hani J.;
e sequence of Saccharomyces cerevisiae chromosome XVI.";
-105(1997).
GLX-1250.
98; PubMed=8041367;
omoda H., Hashimoto H., Watanabe A., Takeshima H.,
instant mutants of Saccharomyces cerevisiae with an
acid synthase gene.";
t. 244:90-96(1994).
Fatty acid synthetase catalyzes the formation of
fatty acids from acetyl-CoA, malonyl-CoA and NADPH.
subunit contains domains for: acyl carrier protein,
[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-
oate] synthase. This subunit coordinates the binding
beta subunits to the enzyme complex.
ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
acyl-CoA + N CoA + N CO(2) + 2N NADP(+).
ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
oate] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
ier protein]
ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
3-oxoacyl-[acyl-carrier protein] + NADPH.
Alpha(6)beta(6)] hexamers of two multifunctional
alpha and beta].
: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
I.
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for license agreement).

DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR004568; Pantethn trn.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF01099; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR TIGRFAM; TIGR00556; pantethn trn; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
DR PROSITE; PS00606; B KETOACYL SYNTHASE; 1.
KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
KW Transferase; NADP; Phosphopantetheine.
FT DOMAIN 1 ? ACYL CARRIER (ACP).
FT DOMAIN 675 874 BETA-KETOACYL REDUCTASE.
FT DOMAIN 1149 1363 BETA-KETOACYL SYNTHASE.
FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT ACT SITE 1305 1305 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT MUTAGEN 1250 1250 G->S: CERULENIN-RESISTANCE.
FT CONFLICT 310 310 G -> GTTGGG (IN REF. 1).
FT CONFLICT 594 594 T -> I (IN REF. 1).
FT CONFLICT 941 1019 AKIRKELVETSEVRKAVSTALEHKKVNGNSADA;
FT IOPRANIQDFFPELKYKQVKQIAPAELEGGLDLER;
FT CINCVKSWLKLLKLEKPEKSKLLMSRLSMAIAMI;
FT XNQLTFTWTSQNRNHTNRLKLLPLSLRVCWIKI
(IN REF. 1).
FT CONFLICT 1036 1041 RWMEA -> KMGNGS (IN REF. 1).
FT CONFLICT 1408 1408 A -> S (IN REF. 1).
FT CONFLICT 1671 1671 N -> T (IN REF. 1).
SQ SEQUENCE 1887 AA; 206946 MW; 08B872734CF3AEEA CRC64;
Query Match 1.9%; Score 10; DB 1; Length 1887;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gz
QY 137 PAPVAAAPAA 146
DB 125 PAPVAAAPAA 134
|||||
RESULT 19
RLAI MAIZE
ID FLAI MAIZE STANDARD; PRT; 109 AA.
AC P52855; O24414;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE 60S acidic ribosomal protein P1 (L12).
GN RPL1A.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22;
RA Hamilton D.A., Turcich M.P., Bokhari-Riza A., Mascarenhas J.P.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-21.
RC STRAIN=cv. B73; TISSUE=Ear;
RX MEDLINE=97422884; PubMed=9276949;
RA Bailey-Serres J., Vargala S., Szick K., Lee C.H.;
RT "Acidic phosphoprotein complex of the 60S ribosomal subunit of mai
seedling roots. Components and changes in response to flooding.";
RL Plant Physiol. 114:1293-1305(1997).
CC -!- FUNCTION: Plays an important role in the elongation step of
protein synthesis (By similarity).
CC -!- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subu
(By similarity).
CC -!- PTM: Phosphorylated.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the L12p family of ribosomal proteins.
CC -----

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AA91168.1; -
 AAB71079.1; -
 T02039.
 T02716.
 1; -
 001813; Ribosomal 60S.
 001859; Ribosomal_P2.
 ; 60s ribosomal; 1.
 56; RIBOSOMALP2.
 tein.
 9
 9 AA; 11096 MW; 1BEC8E34391F080 CRC64;
 1.7%; Score 9; DB 1; Length 109;
 arity 100.0%; Pred.No. 3.4;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAPA 146
 |||||
 AAAPA 77

STANDARD; PRT; 109 AA.

Rel. 23, Created)
 Rel. 23, Last sequence update)
 Rel. 34, Last annotation update)
 bosomal protein P1.
 ruzi.
 Glenczoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 93;

N.A.
 148; PubMed=1598221;
 chijman A., Levin M.;
 equence of a cDNA encoding a Trypanosoma cruzi acidic
 type protein.";
 Res. 20:2599-2599(1992).
 Plays an important role in the elongation step of
 synthesis.
 P1 and P2 exist as dimers at the large ribosomal subunit.
 Y: Belongs to the L12P family of ribosomal proteins.

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CAA46159.1; -
 R6UTP1.
 001813; Ribosomal 60S.
 001859; Ribosomal_P2.
 ; 60s ribosomal; 1.
 56; RIBOSOMALP2.
 tein; Phosphorylation.
 9 AA; 10754 MW; D674D31C102F70AF CRC64;

1.7%; Score 9; DB 1; Length 109;
 arity 100.0%; Pred.No. 3.4;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 APAAAAAA 126
 |||||
 Db 77 APAAAAAA 85
 RESULT 21
 RK12_ORYSA
 ID RK12_ORYSA STANDARD; PRT; 158 AA.
 AC O22386;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 50S ribosomal protein L12, chloroplast precursor (CL12) (Fragment
 Oryza sativa (Rice).
 OS
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ILPUM; TISSUE=Seedling;
 RA Lee J.S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
 CC
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 entities requires a license agreement (See <http://www.isb-sib.ch/>
 or send an email to license@isb-sib.ch).

CC EMBL; AF010581; AAB66886.1; -
 DR HSSP; P02392; 1CTF.
 DR Gramene; O22386; -
 DR InterPro; IPR008932; Ribos_L12/7_olig.
 DR InterPro; IPR002026; Ribosomal_L12.
 DR Pfam; PF00542; Ribosomal_L12; 1.
 DR ProDom; PD001326; Ribosomal_L12; 1.
 KW Ribosomal protein; Chloroplast; Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? >158 50S RIBOSOMAL PROTEIN L12.
 FT NON_TER 158 158
 SQ SEQUENCE 158 AA; 16313 MW; BFD1733A6AF9372A CRC64;

Query Match 1.7%; Score 9; DB 1; Length 158;
 Best Local Similarity 100.0%; Pred.No. 4.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 119 PAAAAAAP 127
 |||||
 Db 21 PAAAAAAP 29

RESULT 22

RPOE LISMO
 ID RPOE LISMO STANDARD; PRT; 178 AA.
 AC Q8Y494;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable DNA-directed RNA polymerase delta subunit (RNAP delta
 factor).
 DE factor).
 GN RPOE OR LMO2560.
 OS Listeria monocytogenes
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OC NCBI_TaxID=1639;
 OX
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;

```

ungeul L., Buchrieser C., Rusniok C., Anand A.,
Zirhe P., Bloeker H., Brandt P., Chakraborty T.,
Lévesque F., Couve E., de Daruvar A., Dehoux P.,
Linguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Fsihi H., Garcia-del Portillo F., Garrido P.,
Jebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jaerist U., Kraft J., Kuhn M., Kunst F., Kurapat G.,
Laitournam A., Mata Vicente J., Ng E., Nedjari H.,
Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
Re M., Schlueter T., Simoes N., Tierrez A.,
L. J.-A., Voss H., Wehlund J., Cossart P.;
Genomics of Listeria species.";
19-852(2001).
Participates in both the initiation and recycling phases
of transcription. In the presence of the delta subunit, RNAP
shows an increased specificity of transcription, a decreased
efficiency for nucleic acids, and an increased efficiency of RNA
transcription because of enhanced recycling (By similarity).
RNAP is composed of a core of 2 alpha, a beta and a beta'
subunit. The core is associated with a delta subunit and one of
the sigma factors (By similarity).
sigma factor; Belongs to the rpoE family.
-----
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or license@isb-sib.ch).
-----
; CAD00638.1; -
; H1394.
; 02560; -
; 7; -; 1.
; 07759; RNA pol delta.
RNA pol delta; 1.
RNA polymerase; transcription; Complete proteome.
; 0 178 ASP/GLU-RICH (ACIDIC).
; AA; 20640 MW; 241725288916148B CRC64;
1.7%; Score 9; DB 1; Length 178;
arity 100.0%; Pred.No.5.1;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
DEDER 341
|||||
|EDED 112
STANDARD; PRT; 228 AA.
el. 21, Created)
el. 21, Last sequence update)
el. 21, Last annotation update)
protein.
us type 2.
. viruses, no RNA stage; Adenoviridae; Mastadenovirus.
15;
N.A.
92; PubMed=6296434;
lerisse J., Courtois G.;
quence of the EcoRI-F fragment of adenovirus 2 genome.";
179).
[ OF PROTEIN.
92; PubMed=6296434;
n E.A., Anderson C.W.;
tructure and encoding location of the adenovirus
e, nonstructural 33k protein.";

```

ein BarH-like 1.
(Mouse).
tazoba; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
090;
[N.A.
P-2000) to the EMBL/GenBank/DBJ databases.
0-254 FROM N.A.
ilman D.B., Jones F.S.;
tion of the mouse Barx1 gene.";
IN-2000) to the EMBL/GenBank/DBJ databases.
08-254 FROM N.A.
311; PubMed=7669690;
J.P., Mucchielli M.L., Mark M., Mattei M.-G., Goridis C.,
mouse homeodomain transcription factor expressed in
ectomesenchyme and the stomach.";
3-15 (1995).
Transcription factor, which may be involved in
ial development, in ontogenesis and in stomach
esis. May have a role in the differentiation of molars
sors. Binds to a regulatory module of the NCM promoter.
AR LOCATION: Nuclear (probable).
SPECIFICITY: Expressed predominantly in the facial
t, developing stomach, and proximal limbs.
NTAL STAGE: Expressed in areas of the first and second
arches, before any apparent cellular or morphologic
iation. Later in development, all expressing tissue in
on, including the mesenchyme underlying the olfactory
m, the primary and secondary palate, the molar tooth
and the stroma of the submandibular gland, appear to be
rom ectomesenchyme of neural crest origin. By day 16.5,
except the developing molars are BARX1-negative. In
BARX1 marks the area of the future stomach in the
gut at embryonic day 9.5, and is present in the
ial wall of the stomach until embryonic day 16.5.
Y: Belongs to the BAR homeobox family.
Y: Contains 1 homeobox domain.
It is uncertain whether Met-1 or Met-30 is the initiator.
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7; CAC10357.1; -;
0; AAG18573.1; -;
CAA69257.1; -;
1B72.
2A03; -;
24; Barx1.
2001356; Homeobox.
2000047; HTH_lanbrepresr.
5; homeobox; 1.
24; HOMEBOX.
31; HTHREPRESS.
3010; Homeobox; 1.
39; HOX; 1.
3027; HOMEBOX 1; 1.
3071; HOMEBOX_2; 1.
anscription regulation; DNA-binding; Nuclear protein.
142 201 HOMEBOX.

FT DOMAIN 44 53 POLY-ALA.
SQ SEQUENCE 254 AA; 27282 MW; 48586B28FA23FCC CRC64;
Query Match 1.7%; Score 9; DB 1; Length 254;
Best Local Similarity 100.0%; Pred.No. 6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 118 APAAATAAAA 126
| | | | | | | | | |
Db 45 APAAATAAAA 53
RESULT 26
TRPC MYCTU
ID TRPC MYCTU STANDARD; PRT; 272 AA.
AC 006129;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGPS).
GN TRPC OR RV1611 OR MT1646 OR MTCY01B2.03 OR MB1637.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RC SEQUENCE FROM N.A.
RP SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr:
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy:
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RC SEQUENCE FROM N.A.
RP SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
RN [3]
RC SEQUENCE FROM N.A.
RP SPECIES=M.dovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Dutthoy S., Grondin S., Lacroix C., Monsemp C., Simon P
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P
RA Parkhill J., Barrrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.
RA "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
CC -!- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulc
phosphate = 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2);
CC -!- PATHWAY: Tryptophan biosynthesis; fourth step.
CC -!- SIMILARITY: Belongs to the trpC family.

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CAB08905.1; -;
9; AAK45915.1; ALT_INIT.
3; CAD96305.1; -;
470557.
1P11.
-;
rv1611; -;
34; -; 1.
003009; FMN enzyme.
001468; IGPS.
1; IGPS; 1.
511; IGPS; 1.
514; IGPS; 1.
0synthesis; Lyase; Decarboxylase; Complete proteome.
32 37 POLY-ALA.
34 164 T -> I (IN REF. 2).
2 AA; 28023 MW; 9CA29D0F0FAC76C2 CRC64;

1.7%; Score 9; DB 1; Length 272;
arity 100.0%; Pred. No. 7.2;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
VAPP 129
|||||
VAPP 40

STANDARD; PRT; 282 AA.
; Q9LNV1;
rel. 37, Created
rel. 41, Last sequence update)
rel. 43, Last annotation update)
protein L4, chloroplast precursor (R-protein L4).
/320 FR F22G5.34 OR F22G5.28.
ialiana (Mouse-ear cress).
diplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
Brassicales; Brassicaceae; Arabidopsis.
12;

N.A.
umbia;
05; PubMed=9461586;
at I., Gagnon J., Baera L., Lerbs-Mache S.;
P4 gene encodes a chloroplast protein that co-purifies
the transcription complex as well as plastid
273:3980-3985(1998).

N.A.
umbia;
719; PubMed=11130712;
Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
iso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
an A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
un L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
P., Feldblyum T.V., Feng J.D., Fong B., Fujii C.Y.,
demich A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
son J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
i L.J., Tambunga G., Toriumi M.J., Southwick A.M.,
Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
RT Nature 408:816-820(2000).

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=145931172;
RA Yamada K., Lim J., Dale J.M., Chen H., Nguyen M., Pham P.K., Cheuk R.
RA Southwick A.M., Wu H.C., Kim C.J., Sakano H., Wu T., Yu G.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anseli
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.
RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kaniya A., Meyers E., Nakajima M., Narusaka M., Seki M., Sakurai
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamur
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome";
RL Science 302:842-846(2003).

CC -|- FUNCTION: This protein binds directly and specifically to 23S
CC (by similarity). May play a role in plastid transcriptional
CC regulation.
CC -|- SUBCELLULAR LOCATION: Chloroplast.
CC -|- SIMILARITY: Belongs to the L4P family of ribosomal proteins.
CC -|- CAUTION: Ref.2 sequence differs from that shown due to errone
CC gene model prediction.

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CC EMBL; Y14565; CAA74894.1; -;
CC EMBL; Y14566; CAA74895.1; -;
CC EMBL; AC022464; AAF79563.1; ALT SEQ.
CC EMBL; AY063889; AAL36245.1; -;
CC InterPro; IPR002136; Ribosomal L4/L1E.
CC Pfam; PF00573; Ribosomal L4; 1.
CC Ribosomal protein; rRNA-Binding; Chloroplast; Transit peptide.
FT TRANSIT 1 49 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 50 282 50S RIBOSOMAL PROTEIN L4.
FT DOMAIN 267 282 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 192 192 F -> L (IN REF. 1).
SQ SEQUENCE 282 AA; 30558 MW; 1479CCICEA75F29C CRC64;

Query Match 1.7%; Score 9; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G;

QY 330 EEDDDDEDE 338
Db 267 EEDDDDEDE 275

RESULT 28

SDC CAEEL STANDARD; PRT; 288 AA.
ID SDC CAEEL
AC P50605;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable syndecon precursor.
GN F57C7.3.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

N.A.
 1 N2;
 B-1996) to the EMBL/GenBank/DBJ databases.
 Cell surface proteoglycan that bears heparan sulfate
 arity).
 AR LOCATION: Type I membrane protein (Potential).
 Y: Belongs to the syndecan proteoglycan family.

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 ail to license@isb-sib.ch).

 CAA93474.1; -.
 T22846.
 7.3; CE05996.
 003585; Neurexin-like.
 001050; Syndecan.
 4; 4.1m; 1.
 964; SYNDECAN; 1.
 Heparan sulfate; Transmembrane; Glycoprotein; Signal.
 POTENTIAL.
 1 26
 PROBABLE SYNDECAN.
 27 288
 EXTRACELLULAR (POTENTIAL).
 32 231
 POTENTIAL.
 53 288
 CYTOPLASMIC (POTENTIAL).
 71 71
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 86 86
 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 14 214
 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 42 161
 ASP/GLU-RICH (HIGHLY ACIDIC).
 75 181
 POLY-THR.
 8 AA; 30979 MW; 10F14F119541341F CRC64;
 1.7%; Score 9; DB 1; Length 288;
 arity 100.0%; Pred. No. 7.6;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DEDE 340
 |||||
 DEDE 153

 STANDARD; PRT; 376 AA.
 7; Q9V5B6;
 Rel. 06, Created
 Rel. 40, Last sequence update)
 Rel. 42, Last annotation update)
 protein even-skipped.

 Drosophila (Fruit fly).
 Insecta; Hexapoda; Insecta; Pterygota;
 Pterygota; Diptera; Brachycera; Muscomorpha;
 Drosophilidae; Drosophila.
 127;

 1 N.A.
 744; PubMed=2877745;
 Ingham P., Struhl G.;
 structure, and expression of even-skipped: a second pair-
 Drosophila containing a homeo box.";
 '34(1986).

 1 N.A.
 536; PubMed=2884106;

 RA Frasch M., Hoey T., Rushlow C., Doyle H., Levine M.;
 RT "Characterization and localization of the even-skipped protein of
 RL Drosophila.";
 RN EMBL J. 6:749-759 (1987).
 RP [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Amanatides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.
 RA George R.A., Lewis S.E., Zhang Q., Chen L.X.,
 RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.N.
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dur
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmar
 RA Foster C., Gabrielson A.E., Garg N.S., Gelbart M.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum
 RA Jalali M., Kalush B., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
 RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [4]
 RP SEQUENCE OF 1-58 FROM N.A.
 RC STRAIN=OR-RC; WA-F, ZM56, AP-S, and FL-S;
 RX MEDLINE=96038621; PubMed=8524036;
 RA Ludwig M.Z., Kreitman M.;
 RT "Evolutionary dynamics of the enhancer region of even-skipped in
 RL Drosophila.";
 RN Mol. Biol. Evol. 12:1002-1011 (1995).
 RP [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 70-189.
 RX MEDLINE=96134926; PubMed=8557047;
 RA Hirsch J.A., Aggarwal A.K.;
 RT "Structure of the even-skipped homeodomain complexed to AT-rich I
 RL EMBL J. 14:6280-6291 (1995).
 CC -!- FUNCTION: May play a role in determining neuronal identity. It
 CC directly involved in specifying identity of individual neuron
 CC pair-rule protein required for segmentation; involved in
 CC transforming the broad, spatial, aperiodic expression pattern
 CC the gap genes into a system of precise periodic expression
 CC patterns of the pair-rule and segmentary polarity genes.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the even-skipped homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.

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 il to license@isb-sib.ch)

AAA28522.1; -
 CAA28784.1; -
 ; AAF58865.1; -
 AAB05358.1; -
 AAB05359.1; -
 AAB05360.1; -
 AAB05361.1; -
 AAB05362.1; -
 126066.
 -JUL-01.
 172; -
 000606; eve.
 ; P-determination of anterior/posterior axis, e. . . ; NAS.
 01356; Homeobox.
 homeobox; 1.
 14; Homeobox; 1.
 110; Homeobox; 1.
 127; Homeobox 1; 1.
 171; Homeobox 2; 1.
 developmental protein; Embryo; Pair-rule protein;
 regulation; Homeobox; Nuclear protein; 3D-structure.
 0 129 HOMEBOX.
 5 179 ALA-RICH.
 10 300 L -> V (IN REF. 1).
 ; AA; 39970 MW; 59058E0634B1BED0 CRC64;
 1.7%; Score 9; DB 1; Length 376;
 100.0%; Pred. No. 9.4;
 0; Mismatches 0; Indels 0; Gaps 0;
 JAAA 126
 ||||
 JAAA 173
 STANDARD; PRT; 415 AA.
 ; Q9VGR5; Q9VGR6;
 el. 36, Created
 el. 36, Last sequence update
 el. 42, Last annotation update
 protein L3.
 anogaster (Fruit fly).
 azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 pterygota; Diptera; Brachycera; Muscomorpha;
 rosophilidae; Drosophila.
 7;
 N.A. (ISOFORM A).
 17; PubMed=9661671;
 hang Y., Hoheisel J.D., O'Kane C.J.;
 n and characterization of the gene for Drosophila L3
 ein";
 25(1998).
 N.A.
 y;
 106; PubMed=10731132;
 iniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 i., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 ortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
 e C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [3]
 RN REVISIONS, AND ALTERNATIVE SPLICING.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Croesby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -!- FUNCTION: The L3 protein is a component of the large subunit
 CC cytoplasmic ribosomes.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=A; Synonyms=B, E;
 CC IsoId=O16797-1; Sequence=Displayed;
 CC Name=D;
 CC IsoId=O16797-2; Sequence=VSP_005715, VSP_005717;
 CC Name=C;
 CC IsoId=O16797-3; Sequence=VSP_005714, VSP_005716;
 CC -!- SIMILARITY: Belongs to the L3P family of ribosomal proteins.
 CC -----
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 CC -----
 CC EMBL; AF016835; AAC26144.1; -
 DR EMBL; AF003690; AAF54609.1; -
 DR EMBL; AF003690; AAF54610.2; -
 DR EMBL; AF003690; AAF54611.1; ALT_INIT.
 DR EMBL; AF003690; AAF54612.2; -

0020910; Rpl3.
 000597; Ribosomal L3.
 009000; Translat Factor.
 ; Ribosomal L3; 1.
 474; RIBOSOMAL L3; 1.
 tein; Alternative splicing.
 0
 BY SIMILARITY.
 21 137 WYKSKKFTKSKWT -> CSSISLLRELFKSLNV
 (in isoform C).
 /FTID-VSP 005714.
 23 160 KSKKFTKSKWTDDLGKKSIENDFRMLRYCKVIR ->
 VSEDHVVLPTPEVAFPGVHTKMAADTCFLES
 (in isoform D).
 /FTID-VSP 005715.
 38 415 Missing (in isoform C).
 /FTID-VSP 005716.
 61 415 Missing (in isoform D).
 /FTID-VSP 005717.
 5 AA; 46784 MW; DE5964681PAF8A15 CRC64;
 1.7%; Score 9; DB 1; Length 415;
 arity 100.0%; Pred.No.10;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;
 TAAAA 22
 |||||
 TAAAA 408
 STANDARD; PRT; 416 AA.
 Rel. 20, Created)
 Rel. 20, Last sequence update)
 Rel. 43, Last annotation update)
 -skipped homolog protein 1 (EVX-1).
 (Mouse).
 ; Chordata; Craniata; Vertebrata; Euteleostomi;
 ; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ; 090;
 [N.A.
 ; TISSUE=Liver;
 ; 218; PubMed=1971786;
 ; P.;
 n-skipped homologue, Evx 1, is expressed during early
 ; and neurogenesis in a biphasic manner.";
 ; 9-1852(1990).
 [N.A.
 ;
 ; 649; PubMed=1349539;
 ; rtin G.R.;
 mouse Evx genes: Evx-1 displays graded expression in the
 ; "leak.";
 ; 1:273-287(1992).
 ; May play a role in the specification of neuronal cell
 ; y play a role in the dorsoventral specification of
 ; l cell fate.
 ; AR LOCATION: Nuclear.
 ; ENTPAL STAGE: Shows a graded distribution in the primitive
 ; id in cells lateral to it. It is not detected in cells
 ; A-P axis of the embryo anterior to the primitive streak,
 ; E7.5 when there is transient expression in the head
 ; The highest levels of expression are found within the
 ; (posterior) portion of the primitive streak and cells
 ; with expression levels decreasing more distally
 ; ly).
 ; Belongs to the even-skipped homeobox family.
 ; Contains 1 homeobox domain.

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 CC -----
 CC EMBL; X54239; CRA38145.1; -;
 CC HSSP; P14653; 1B72.
 CC TRANSFAC; T02023; -;
 CC MGD; MGI:95461; Evx1.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS50071; HOMEBOX_2; 1.
 CC DNA-binding; Developmental protein; Homeobox; Nuclear protein.
 CC FT DOMAIN 114 124 ASP/GLU-RICH (ACIDIC).
 CC FT DNA BIND 183 242 HOMEBOX.
 CC FT DOMAIN 289 297 ALA-RICH.
 CC FT DOMAIN 341 349 ALA-RICH.
 CC FT DOMAIN 369 375 ALA-RICH.
 CC SQ SEQUENCE 416 AA; 43198 MW; 9F0EE4F3677CD3EE CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred.No.10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; C
 QY 148 APRAAAAA 156
 Db 366 APRAAAAA 374
 |||||
 |||||
 RESULT 32
 Y77A_STRCO
 ID Y77A_STRCO STANDARD; PRT; 440 AA.
 AC Q9FIY6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein SCO7700.
 GN SCO7700 OR SCIA4.08 OR SCBAC12C8.01.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1147;
 RA Watanabe M., Kawamoto S., Ochi K.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -!- SIMILARITY: Strong, to S.griseus 47.6 kDa protein in glk 3' re
 CC -----
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NOT ANNOTATED_CDS.

AACS1346.1; JOINED.

AACS1346.1; JOINED.

AACS1346.1; JOINED.

A55180.

IFTT.

2051; -.

4978; HLX1.

75; P:development; TAS.

R001356; Homeobox.

R000047; HTH_lambrepresr.

5; homeobox; 1.

24; HOMEBOX.

331; HTHREPRESSR.

3010; Homeobox; 1.

39; HOX; 1.

3027; HOMEBOX 1; 1.

3071; HOMEBOX 2; 1.

1; regulation; DNA-binding; Homeobox; Nuclear protein.

120 123

POLY-HIS.

125 137

POLY-GLN.

138 142

POLY-PRO.

276 335

HOMEBOX.

428 431

POLY-GLY.

437 448

POLY-SER.

456 459

POLY-GLY.

MISSING (IN REF. 1).

AAALTAHLGSHVPHASFOAAARSPRLRPTVPVAPSEVPAGFP

QRSLPLP -> PPSPTWAFRTPLSKRPDPREDPPQW

WRPKSLASRSCSLRLS (IN REF. 1).

QQQ -> RRE (IN REF. 1).

SGRVVFNPHSGSA -> RDAGSEPPPPQWLC (IN

REF. 1).

38 AA; 50799 MW; ACEIA91ADA9C851A CRC64;

1.7%; Score 9; DB 1; Length 488;

larity 100.0%; Pred. No. 12;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QPPPP 229

QPPPP 141

STANDARD; PRT; 490 AA.

(Rel. 34, Created)

(Rel. 34, Last sequence update)

(Rel. 42, Last annotation update)

protein MOT3/HMS1.

OR YMR070W OR YMG916.09.

s cerevisiae (Baker's Yeast).

ungi; Ascomycota; Saccharomycotina; Saccharomycetes;

cales; Saccharomycetaceae; Saccharomycetes.

932;

N.A.

Winston F.;

PR-1995) to the EMBL/GenBank/DBJ databases.

N.A.

/ AB972;

3268; PubMed-9169872;

Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.";

RT Nature 387:90-93 (1997).

RL Nature 387:90-93 (1997).

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -!- SIMILARITY: Contains 2 C2H2-type zinc fingers.

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CC

CC EMBL; U25279; AAC49982.1; -.

DR EMBL; Z48952; CA88795.1; -.

DR PIR; S52830; S52830.

DR GerMOnline; 142736; -.

DR TRANSFAC; T03448; -.

DR TRANSFAC; T03500; -.

DR SGD; S0004674; MOT3.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0003677; F:DNA binding; IPI.

DR GO; GO:0016564; F:transcriptional repressor activity; IDA.

DR GO; GO:0006350; P:transcription; IGI.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF00096; zf-C2H2; 2.

DR SMART; SM00355; Znf_C2H2; 2.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.

KW Nuclear protein; Zinc-finger; Metal-binding; Repeat.

FT ZN_FING 346 368

C2H2-TYPE 1.

FT ZN_FING 374 397

C2H2-TYPE 2.

FT DOMAIN 8 35

POLY-GLN.

FT DOMAIN 98 104

POLY-ASN.

FT DOMAIN 143 157

POLY-ALA.

FT DOMAIN 173 177

POLY-ALA.

FT DOMAIN 240 245

POLY-HIS.

FT DOMAIN 417 420

POLY-SER.

FT DOMAIN 421 433

POLY-ASN.

FT DOMAIN 441 450

POLY-ALA.

SQ SEQUENCE 490 AA; 54362 MW; 4D0DA8DE43F171ED CRC64;

Query Match 1.7%; Score 9; DB 1; Length 490;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAAATAP 159

DB 443 AAAAAATAP 451

RESULT 36

PIAG_MOUSE

ID PIAG_MOUSE STANDARD; PRT; 507 AA.

AC Q9J005; Q8R165;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein inhibitor of activated STAT protein gamma (PIAS-gamma)

DE (PIASy).

GN PIASG.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

RC TISSUE=Brain;

089; PubMed=10854042;
 h M., White F.A.;
 analysis of a murine Pias family member, Pias-gamma, in
 in and neurons.";
 sci. 14:107-121(2000).
 N.A.
 257; PubMed=12477932;
 L., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Quallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Con E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Adan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Touchman J.W., Green E.D., Dickinson M.C.,
 Greenwood J., Schmutz J., Myers R.M.,
 S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 Schein J.E., Jones S.J.M., Marra M.A.;
 and initial analysis of more than 15,000 full-length
 cdna sequences.";
 cad. Sci. U.S.A. 99:16899-16903(2002).
 CELLULAR LOCATION, AND MUTAGENESIS OF CYS-330; CYS-335;
 340 AND 470-SER-SER-474.
 340; PubMed=11731474; 474.
 cun L., Sieber H., Pichler A., Melchior F.,
 lear matrix-associated SUMO E3 ligase, represses LEF1
 sequestration into nuclear bodies.";
 :3088-3103(2001).
 Specifically inhibits activated STAT signaling and acts
 as a transcriptional corepressor of STAT1, without blocking its
 activity. Represses the activity of a Wnt-responsive
 transcription factor, LEF1, by stimulating sumoylation and
 sequestration into nuclear bodies. Also interacts with the C-
 region of tumor suppressor protein p53 and inhibits p53-
 mediated transcriptional activity.
 AR LOCATION: Nuclear.
 ICIFICITY: During embryo development, expressed in the
 part of the neural tube (E8.5), neuroepithelium of the
 and hindbrain (E10.5), neural tube, eye, limb buds and
 arches (E11.5), hindlimbs, forelimbs and forebrain
 developing limb buds and single cells of the mesenchyme
 of future digit structures (E13.5), inner root sheath of
 hair follicle (E15.5) and epithelium of olfactory and the
 (E6.5). In adult mice, expressed in most major organs, but
 liver and lung.
 TIAL STAGE: In the embryo, expressed from day 7.5 and
 throughout development. Also expressed in the adult.
 : Contains 1 SAP domain.
 : Contains 1 MIZ-type zinc finger.

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 mail to license@isb-sib.ch).

 ; AAF72040.1; -;
 ; AAH25159.1; -;
 ; 340; Piasg.
 ; C:nuclear matrix; IDA.

DR GO; GO:0003677; F:DNA binding; IDA.
 DR GO; GO:000515; F:protein binding; IPI.
 DR GO; GO:0019789; F:SUMO ligase activity; IDA.
 DR GO; GO:0003714; F:transcription co-repressor activity; IDA.
 DR GO; GO:0016564; F:transcriptional repressor activity; IDA.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0007275; P:development; NAS.
 DR GO; GO:0001122; P:negative regulation of transcription from P.
 DR GO; GO:0016481; P:negative regulation of transcription; ISS.
 DR GO; GO:0016925; P:protein sumoylation; IDA.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 KW Transcription regulation; Repressor; Developmental protein;
 KW DNA-binding; Ubiquitination pathway; Nuclear protein; Zinc-finger
 KW Metal-binding; Zinc.
 FT DOMAIN 12 46
 FT ZN_FING 315 367
 FT MUTAGEN 330 330
 FT MUTAGEN 335 335
 FT MUTAGEN 337 337
 FT MUTAGEN 340 340
 FT MUTAGEN 470 474
 FT CONFLICT 230 230 K -> N (IN REF. 1).
 FT CONFLICT 417 417 L -> H (IN REF. 1).
 FT CONFLICT 494 494 K -> N (IN REF. 1).
 SQ SEQUENCE 507 AA; 55569 MW; A85E6E3BAC76426 CRC64;
 Query Match 1.74; Score 9; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G
 QY 332 EDDDEDEDE 340
 Db 481 EDDDEDEDE 489
 RESULT 37
 SIS2 YEAST
 ID -SIS2 YEAST STANDARD; PRT; 562 AA.
 AC P36024;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SIS2 protein (Halotolerance protein HAL3).
 GN SIS2 OR HAL3 OR YKR072C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95220693; PubMed=7705654;
 RA di Como C.J., Bose R., Arndt K.T.;
 RT "Overexpression of SIS2, which contains an extremely acidic regio:
 increases the expression of SWI4, CLN1 and CLN2 in sit4 mutants."
 RL Genetics 139:95-107(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohl T.M., Pohl F.M.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=96009574; PubMed=7565698;
 RA Ferrando A., Kron S.J., Rios G., Fink G.R., Serrano R.;
 RT "Regulation of cation transport in Saccharomyces cerevisiae by the
 salt tolerance gene HAL3.";
 RL Mol. Cell. Biol. 15:5470-5481(1995).
 RN [4]
 RP IDENTIFICATION AS INHIBITORY SUBUNIT OF PP21.

1578; PubMed-9636153;
 Clotet J., Fossas R., Serrano R., Gomez N., Arino J.;
 Alotolerance determinant Hal3p is an inhibitory subunit of
 r/Thr protein phosphatase.";
 Acad. Sci. U.S.A. 95:7357-7362(1998).
 : May stimulate expression of certain genes that are
 ally expressed during late G1. Also modulates the
 on of the enal ATPase. Interacts with the C-terminal
 f the serine-threonine protein phosphatase PP21 and acts
 inhibitory subunit of PP21.
 AR LOCATION: NUCLEAR OR CYTOPLASMIC.
 TY: TO C.TROPICALIS SIS2/HAL3 AND TO YEAST YKL088W. SOME,
 JIANA HAL3A AND HAL3B.
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 ; AAA80000.1; -;
 ; CAAG2151.1; -;
 S38149.
 ; LE20.
 140051; -;
); SIS2.
 37; C:cytoplasm; IC.
 34; C:nucleus; IDA.
 54; F:protein phosphatase inhibitor activity; IDA.
 32; P:G1/S transition of mitotic cell cycle; IGI.
 46; P:regulation of mitotic cell cycle; IGI.
 51; P:salinity response; IGI.
 3003382; Flavoprotein.
 1; Flavoprotein; 1.
 196 553 ASP/GLU-RICH (HIGHLY ACIDIC).
 52 AA; 62478 MW; 19A9A475145DA7AB CRC64;
 1.7%; Score 9; DB 1; Length 562;
 larity 100.0%; Pred. No. 13;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 DDEDE 338
 |||||
 DDEDE 504

 STANDARD; PRT; 565 AA.
 (Rel. 40, Created)
 (Rel. 40, Last sequence update)
 (Rel. 43, Last annotation update)
 protein J2 (Fork head homologous X).
 . (Mouse).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 0090;
 X N.A.
 0369; PubMed-11025217;
 , Arias-de-la-Fuente C., Perez-Sanchez C., Parraga M.,
 dez L.A., del Mazo J., Rey-Campos J.;
 expression is activated during spermatogenesis and very
 rnyonic development.";
 7:157-160(2000).
 X N.A.
 ; TISSUE=Salivary gland;

RA MEDLINE-22389257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
 RA Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Prange C
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanche
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Transcriptional activator. Able to bind to two dif
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 fork-head domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a col
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 CC the European Bioinformatics Institute. There are no restrictio
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 CC entities requires a license agreement (See http://www.isb-sib.ch
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF253052; AAG30406.1; -;
 DR EMBL; BC040395; AAH40395.1; -;
 DR HSSP; O63245; 2HFH.
 DR TRANSFAC; T04170; -;
 DR MGD; MGI:1526805; Foxj2.
 DR InterPro; IPR001766; TF_Fork_head.
 DR Pfam; PF00250; Fork_head; 1.
 DR PRINTS; PR00053; FORKHEAD.
 DR ProDom; PD000425; TF_Fork_head; 1.
 DR SMART; SM00339; FH; 1.
 DR PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG.
 DR PROSITE; PS00658; FORK_HEAD_2; 1.
 DR PROSITE; PS00039; FORK_HEAD_3; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein; Activato
 FT DNA_BIND 66 143 FORK-HEAD.
 FT DOMAIN 266 269 POLY-SER.
 FT DOMAIN 290 296 POLY-GLN.
 FT DOMAIN 306 314 POLY-GLN.
 SQ SEQUENCE 565 AA; 61569 MW; 9178AFF3F9227AD4 CRC64;

 Query Match 1.7%; Score 9; DB 1; Length 565;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;

 QY 227 PPPQPPPP 235
 |||||
 Db 297 PPPQPPPP 305

 RESULT 39
 FXJ2 HUMAN
 ID FXJ2 HUMAN STANDARD; PRT; 574 AA.
 AC Q9P0K8; Q96PS9; Q9NSN5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Forkhead box protein J2 (Fork head homologous X).
 GN FOXJ2 OR FOXH.
 OS Homo sapiens (Human).

(Rel. 42, Last annotation update)
 rsor (Tropoelastin) (Fragment).
 jicus (Rat).
 :azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 :heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
)116;
 4 N.A., AND ALTERNATIVE SPLICING.
 :868; PubMed=1702999;
 Deak S.B., Stolle C.A., Boyd C.D.;
 y of rat tropoelastin mRNA revealed by cDNA cloning.";
 23:9677-9683(1990).
 781-864 FROM N.A.
 :868; PubMed=2971041;
 ierce R.A., Belsky S.A., Riley D.J., Boyd C.D.;
 astin is synthesized from a 3.5-kilobase mRNA.";
 n. 263:13504-13507(1988).
 264-533 AND 558-864 FROM N.A., AND ALTERNATIVE SPLICING.
 :859; PubMed=1572637;
 Alatawi A., Deak S.B., Boyd C.D.;
 the rat tropoelastin gene associated with alternative
 551-658(1992).
 : Major structural protein of tissues such as aorta and
 igament, which must expand rapidly and recover completely.
 The polymeric elastin chains are cross-linked together
 extensible 3D network.
 :AR LOCATION: Extracellular matrix of elastic fibers.
 (VE PRODUCTS:
 :ernative splicing; Named isoforms=8;
 :=Experimental confirmation may be lacking for some
 as;
 :99372-1; Sequence=Displayed;
 :99372-2; Sequence=VSP_004244;
 :99372-3; Sequence=VSP_004245;
 :99372-4; Sequence=VSP_004246;
 :99372-5; Sequence=VSP_004244, VSP_004245;
 :99372-6; Sequence=VSP_004245, VSP_004246;
 :99372-7; Sequence=VSP_004244, VSP_004246;
 :99372-8; Sequence=VSP_004244, VSP_004245, VSP_004246;
 crosslinks are made of deaminated Lys.
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 mail to license@isb-sib.ch).
 : AAA42269.1; -;
 : AAA42268.1; -;
 : AAA42271.1; -;
 : AAA42271.1; JOINED.
 : AAA42271.1; JOINED.
 : AAA42271.1; JOINED.
 : AAA42271.1; JOINED.
 : AAA42271.1; JOINED.
 : AAA42272.1; -;
 : AAA42272.1; JOINED.
 : AAA42272.1; JOINED.
 EART.

DR InterPro; IPR003979; tropoelastin.
 DR PRINTS; PRO1500; TROPOELASTIN.
 KW Structural protein; Connective tissue; Repeat; Signal;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT SIGNAL <1 21 BY SIMILARITY.
 FT CHAIN 22 864 ELASTIN.
 FT DISULFID 854 859 BY SIMILARITY.
 FT VARSPLIC 263 307 Missing (in isoform 2, isoform 5, i
 7 and isoform 8).
 FT VARSPLIC 308 308 /FTID=VSP 004244.
 FT Missing (in isoform 3, isoform 5, i
 6 and isoform 8).
 FT VARSPLIC 809 823 /FTID=VSP 004245.
 FT Missing (in isoform 4, isoform 6, i
 7 and isoform 8).
 FT /FTID=VSP 004246.
 SQ SEQUENCE 864 AA; 72786 MW; 456894BB09E79FD4 CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 864;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 117 GAPAAAAA 125
 DB 715 GAPAAAAA 723
 RESULT 42
 AL80 MOUSE STANDARD; PRT; 901 AA.
 ID A180 MOUSE Q61547;
 AC Q61548; Q61547;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Clathrin coat assembly protein AP180 (Clathrin coat associated p
 DE AP180) (91 kDa synaptosomal-associated protein) (Phosphoprotein
 DE 20).
 GN SNAP91.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RX MEDLINE=92300439; PubMed=1607933;
 RA Zhou S., Sousa R., Tannery N.H., Lafer E.M.;
 RT "Characterization of a novel synapse-specific protein. II. cDNA
 RT cloning and sequence analysis of the Fl-20 protein.";
 RL J. Neurosci. 12:2144-2155(1992).
 CC -! FUNCTION: Adaptins are components of the adaptor complexes w
 link clathrin to receptors in coated vesicles. Clathrin-asso
 protein complexes are believed to interact with the cytoplas
 tails of membrane proteins, leading to their selection and
 concentration. Binding of AP180 to clathrin triskelia induce
 their assembly into 60-70 nm coats.
 CC -! SUBCELLULAR LOCATION: Component of the coat surrounding the
 cytoplasmic face of coated vesicles in the plasma membrane.
 CC -! ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q61548-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=Q61548-2; Sequence=VSP 000172;
 CC -! TISSUE SPECIFICITY: Brain. Associated with the synapses.
 CC -! DEVELOPMENTAL STAGE: Developmentally regulated in a pattern
 coincident with active synaptogenesis and synaptic maturation
 CC -! DOMAIN: Possesses a three domain structure: the N-terminal 31
 residues harbor a clathrin binding site, an acidic middle do
 450 residues, interrupted by an Ala-rich segment, and the C-
 terminal domain (166 residues).
 CC -! PTM: Phosphorylated.
 CC -! SIMILARITY: Contains 1 epsin N-terminal homology (ENTH) doma

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 AAA37587.1; -;
 AAA37586.1; -;
 14825.
 12; Snap91.
 01026; ENTH.
 08943; PI_bind_N.
 : ENTH; 1.
 : ENTH; 1.
 142; ENTH; 1.
 Alternative splicing; Phosphorylation.
 4 145 ENTH.
 0 413 POLY-THR.
 5 539 POLY-ALA.
 7 550 POLY-ALA.
 9 664 POLY-SER.
 14 710 POLY-SER.
 5 719 Missing (in isoform Short).
 /FTid=VSP_000172.
 . AA; 91851 MW; 2498FBACEBDB8B1 CRC64;
 1.7%; Score 9; DB 1; Length 901;
 identity 100.0%; Pred. No. 20;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 TAAA 21
 |||||
 TAAA 555

STANDARD; PRT; 915 AA.

Rel. 35, Created)
 Rel. 35, Last sequence update)
 Rel. 43, Last annotation update)
 assembly protein AP180 (Clathrin coat associated protein
 synaptosomal-associated protein).

cus (Rat).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 16;

N.A. (ISOFORMS LONG AND SHORT).

42; PubMed=8440257;
 Schroeder S.; Plessmann U., Weber K., Ungewickell E.;
 mly protein AP180: Primary structure, domain
 and identification of a clathrin binding site.";
 "-675(1993).
 Adaptins are components of the adaptor complexes which
 rin to receptors in coated vesicles. Clathrin-associated
 mplexes are believed to interact with the cytoplasmic
 membrane proteins, leading to their selection and
 ion. Binding of AP180 to clathrin triskelion induces
 mly into 60-70 nm coats.
 AR LOCATION: Component of the coat surrounding the
 c face of coated vesicles in the plasma membrane.

PRODUCTS:
 nactive splicing; Named isoforms=2;

5140-1; Sequence=Displayed;

CC IsoId=Q05140-2; Sequence=VSP_000173;
 CC -1- DOMAIN: Possesses a three domain structure: the N-terminal 30
 CC residues harbor a clathrin binding site, an acidic middle dom
 CC 450 residues, interrupted by an Ala-rich segment, and the C-
 CC terminal domain (166 residues).
 CC -1- PTM: Phosphorylated (by similarity).
 CC -1- SIMILARITY: Contains 1 epsin N-terminal homology (ENTH) domai
 CC -----
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 DR EMBL; X68877; CAA48748.1; -;
 DR EMBL; X68878; CAA48749.1; -;
 DR PIR; S36326; S36326.
 DR PIR; S36327; S36327.
 DR InterPro; IPR001026; ENTH.
 DR Pfam; PF01417; ENTH; 1.
 DR SMART; SM00273; ENTH; 1.
 DR PROSITE; PS00942; ENTH; 1.
 KW Coated pits; Alternative splicing; Phosphorylation.
 FT DOMAIN 14 145 ENTH.
 FT DOMAIN 410 413 POLY-THR.
 FT DOMAIN 535 539 POLY-ALA.
 FT DOMAIN 547 550 POLY-ALA.
 FT DOMAIN 678 683 POLY-SER.
 FT DOMAIN 723 729 POLY-SER.
 FT VARSPLIC 614 632 Missing (in isoform Short).
 /FTid=VSP_000173.
 SQ SEQUENCE 915 AA; 93518 MW; 32EC1B38EC5DF8C0 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 915;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; G

QY 13 AAAATTAAA 21
 |||||
 Db 547 AAAATTAAA 555

RESULT 44

ID_MCR_HUMAN STANDARD; PRT; 984 AA.
 AC P08235; Q96KQ8; Q96KQ9;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Mineralocorticoid receptor (MR).
 GN NR3C2 OR MCR OR MCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
 RC TISSUE=Kidney;
 RX MEDLINE=87263386; PubMed=3037703;
 RA Arriaza J.L., Weinberger C., Cerelli G., Glaser T.M., Handelin B.L.
 RA Housman D.E., Evans R.M.;
 RT "Cloning of human mineralocorticoid receptor complementary DNA:
 RT structural and functional kinship with the glucocorticoid receptor;
 RL Science 237:268-275(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4), TISSUE SPECIFICITY,
 RP INTERACTIONS WITH NCOAL1, TIF1 AND NR1F1, AND VARIANTS VAL-180 AND
 RP VAL-241.
 RC TISSUE=Heart;
 RX MEDLINE=21410115; PubMed=11518808;

, Souque A., Viengchareun S., Poisson E., Lombes M.; MR splice variant is a ligand-independent transactivator of corticosteroid action." ; Mol. 15:1586-1598(2001).

145-984 FROM N.A., AND DISEASE. 1981; PubMed=9682404; Rodriguez-Soriano J., Vallo Boado A., Schifter S., Ling S.S., Lifton R.P.; The mineralocorticoid receptor gene cause autosomal adhypoadosteronism type 1." ; (9:279-281(1998).

LOCATION, AND PHOSPHORYLATION. 1536; PubMed=1655735; Makymowych A.B., Robertson N.M., Litwack G.; Location and characterization of the human mineralocorticoid 1. 266:18072-18081(1991).

IN OF ISOFORM 3. yte; 1549; PubMed=7495694; Luo C., Pratt J.H.; Location of a splice variant of the rat and human aldosterone receptor genes." ; Biochem. Mol. Biol. 55:159-162(1995).

ACTIVITY. 1347; PubMed=9141514; Farman N., Bonvalet J.-P., Lombes M.; Expression of alpha and beta messenger ribonucleic acid of the human mineralocorticoid receptor in normal and states." ; J. Clin. Endocrinol. Metab. 82:1345-1352(1997).

EX WITH HSP90; HSP70 AND FKBP4, AND DISSOCIATION UPON BINDING. 1330; PubMed=9332437; Derfoul A., Robertson N.M., Guerriero G., Lemarié T., Alnemri E.S., Litwack G.; The mineralocorticoid receptor is associated with heat shock protein 90 and the immunophilin FKBP-52." ; J. Biol. Chem. 272:1785-1791(1997).

OF CYS-808; CYS-849 AND CYS-942. 1467; PubMed=9724527; Hsieh D., Auzou G.; The C-terminal domain of the human mineralocorticoid receptor are crucial for its function." ; J. Biol. Chem. 273:12153-12159(1998).

OF ASN-770; GLN-776; ARG-817 AND THR-945. 548; PubMed=10760050; Hsieh D., Souque A., Rafestin-Oblin M.-E.; The C-terminal domain of the human mineralocorticoid receptor activation." ; J. Biol. Chem. 273:1250-1255(2000).

WITH NCOAL1, TIF1 AND NR1P1, AND MUTAGENESIS OF LEU-952; 954; PHE-956 AND PRO-957. 1588; PubMed=10935545; Hsieh D., Souque A., Wurtz J.-M., Moras D., et al.; The H11-H12 loop in stabilizing the active site of the human mineralocorticoid receptor." ; J. Biol. Chem. 275:14210-14216(2000).

LOCATION, AND INTERACTION WITH HSD11B2. 1362; PubMed=11350956; Arnold P., Frey F.J.; The C-terminal domain of the mineralocorticoid receptor is involved in the localization of the mineralocorticoid receptor in the nucleus." ; J. Biol. Chem. 275:28484-28492(2001).

12] VARIANTS VAL-180; THR-444; GLN-537 AND SER-554. RX MEDLINE=93118094; PubMed=10391210; RA Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A., Cooper R., Lipshutz R., Chakravarti A.; "Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis." ; Nat. Genet. 22:239-247(1999).

113] CHARACTERIZATION OF VARIANT PHA1 PRO-924. RX MEDLINE=20576523; PubMed=11134129; RA Tajima T., Kitagawa H., Yokoyama S., Tachibana K., Adachi M., Nakai Suwa S., Katoh S., Fujieda K.; "A novel missense mutation of mineralocorticoid receptor gene in Japanese family with a renal form of pseudohypoaldosteronism type 1." ; J. Clin. Endocrinol. Metab. 85:4690-4694(2000).

114] VARIANT EARLY ONSET HYPERTENSION LEU-810, AND MUTAGENESIS OF SER- MEDLINE=20342438; PubMed=10884226; RA Geller D.S., Farhi A., Pinkerton N., Fradley M., Moritz M., Spitzer A., Meinke G., Tsai F.T.F., Sigler P.B., Lifton R.P.; "Activating mineralocorticoid receptor mutation in hypertension exacerbated by pregnancy." ; Science 289:119-123(2000).

115] CHARACTERIZATION OF VARIANTS VAL-180 AND VAL-241. RX MEDLINE=22370905; PubMed=12483305; RA Arai K., Nakagami Y., Iketani M., Shimura Y., Amemiya S., Ohyama Shibasaki T.; "Functional polymorphisms in the mineralocorticoid receptor and amiloride-sensitive sodium channel genes in a patient with sporadic pseudohypoaldosteronism." ; Hum. Genet. 112:91-97(2003).

CC -!- FUNCTION: Receptor for both mineralocorticoids (MC) such as aldosterone and glucocorticoids (GC) such as corticosterone (CORT). Binds to mineralocorticoid response elements (MRE) and transactivates target genes. The effect of MC is to increase blood pressure and thus raise extracellular fluid volume and water transport and lower potassium levels.

CC -!- SUBUNIT: Heteromultimeric cytoplasmic complex with HSP90, HSP110, and FKBP4. In the absence of ligand, after ligand binding, it translocates to the nucleus and binds to DNA as a homodimer or a heterodimer with NR3C1. Binds the coactivator NCOA2 (By similarity). May interact with HSD11B2 in the absence of ligand. Binds the coactivators NCOA1, TIF1 and NR1P1.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear in the absence of ligand; nuclear after ligand-binding. When bound to HSD11B2, found associated with the endoplasmic reticulum membrane.

CC -!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=4; Comment=Additional isoforms seem to exist; Name=1; IsoId=P08235-1; Sequence=Displayed; Name=2; IsoId=P08235-2; Sequence=VSP_007358, VSP_007359; Note=Lacks steroid-binding activity and acts as ligand-independent transactivator; Name=3; IsoId=P08235-3; Sequence=VSP_007357; Name=4; Synonyms=Delta; IsoId=P08235-4; Sequence=VSP_007360; TISSUE SPECIFICITY: Ubiquitous. Highly expressed in distal tubules, convoluted tubules and cortical collecting duct in kidney, and in sweat glands. Detected at lower levels in cardiomyocytes, in epidermis and in colon enterocytes.

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

CC -!- PTM: Phosphorylated.

CC -!- DISEASE: Defects in NR3C2 are a cause of autosomal dominant pseudohypoaldosteronism type I (PHA1) [MIM:177735]. PHA1 is characterized by urinary salt wasting, resulting from target unresponsiveness to mineralocorticoids. There are 2 forms of the autosomal dominant form that is mild, and the recessive form

more severe and due to defects in any of the epithelial inner subunits. In autosomal dominant PHAI the target act is confined to kidney. Clinical expression can vary from asymptomatic to moderate. It may be severe at birth, but remit with age. Familial and sporadic cases have been reported.

Defects in NR3C2 are a cause of early onset hypertension (SH), with severe exacerbation in pregnancy. Inheritance is autosomal recessive. The disease is characterized by the onset of hypertension before the age of 20, and by suppression of aldosterone secretion.

NR3C2 belongs to the nuclear hormone receptor family. NR3

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1; AAC67405.1; --
2; AAC67406.1; --
3; AAC63513.1; --
4; AAC63513.1; JOINED.
5; AAC63513.1; JOINED.

1.7%; Score 9; DB 1; Length 984;
Identity 100.0%; Pred. No. 21;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

pppp 229
|||||
pppp 697

STANDARD; PRT; 987 AA.

1; 41, Created)
1; 41, Last sequence update)
1; 42, Last annotation update)
Translation initiation factor 3 subunit 10 (eIF-3 theta)
Translation initiation factor 3 large subunit (eIF3a)
H1420 OR F35E4.40.
Maliana (Mouse-ear cross).
Maliplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
brassicales; Brassicaceae; Arabidopsis.
12;

N.A.
umbia;
76; PubMed=11042177;
zerra P., Le H., Gallie D.R., Browning K.S.;
ion factor 3 subunit composition resembles mammalian
tor 3 and has a novel subunit.";
276:2122-2131 (2001).

N.A.
umbia;
88; PubMed=10617198;
Schueller C., Wamoutt R., Murphy G., Volckaert G.,
erhoeft A., Stiekema W., Entian K.-D., Terryn N.,
orge W., Brandt P., Grivell L.A., Rieger M.,
r M., de Simone V., Obermaier B., Mache R., Mueller M.,
eny M., Pulgdonesch P., Watson M., Schmidtheini T.,
ortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
el J., Zimmermann W., Wedler H., Ridley P.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E
RA Weitenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Roese M., Hauf J., Koetter P.,
RA Bernheiser S., Hempel S., Feldpausch M., Lamberth S., Van den Bael
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Maye
RA Pettitt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Blocker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Muelner-Auer S.,
RA Gabell C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedford P., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K
RA Parnell L., Dedhia N., Gao J., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Bernghoff A., Jones K., Drone K., Cotton M., Joshi
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RA thaliana.";
RA Nature 402:769-777(1999).
RL Nature 402:769-777(1999).
CC -1- FUNCTION: Binds to the 40S ribosome and promotes the binding
CC methionyl-tRNAi and mRNA.
CC -1- SUBUNIT: eIF-3 is composed of at least 12 different subunits.
CC -1- SIMILARITY: Contains 1 PCI domain.
CC -1- SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a coll
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CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF291711; AAC53635.1; --
CC EMBL; AL050399; CAB82147.1; --
CC EMBL; AL161531; CAB81243.1; --
CC FIR; T10562; T10562.
CC InterPro; IPR000717; PCI.
CC Pfam; PF01399; PCI; 1.
CC SMART; SM00088; PINT; 1.
KW Initiation factor; Protein biosynthesis.
FT DOMAIN 436 510 PCI.
SQ SEQUENCE 987 AA; 114298 MW; F38BA715209D55FB CRC64;

Query Match 1.7%; Score 9; DB 1; Length 987;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AAAAAAAAA 126
Db 881 AAAAAAAAA 889

STANDARD; PRT; 1065 AA.
 19; (Rel. 40, Created)
 (Rel. 40, Last sequence update)
 (Rel. 42, Last annotation update)
 21 Kinase, Iota (EC 2.7.1.107) (Diglyceride kinase) (DGK-
 inase Iota).
 (Human).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Primates; Catarrhini; Hominidae; Homo.
 506;
 4 N.A.
 7655; PubMed=9830018;
 ar E., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
 and characterization of a novel human diacylglycerol
 Iota";
 n. 273:32746-32752(1998).
 135-1065 FROM N.A., AND VARIANT PHE-153.
 3854; PubMed=10706894;
 Sullivan L.S., Ding L., Traer E., Prescott S.M.,
 Keman A., Humphries P., Daiger S.P.;
 of human diacylglycerol kinase Iota, DGKI, a homolog of
 39A, in inherited retinopathy mapping to 7q";
 6:6-9(2000).
 2 ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
 ycerol 3-phosphate.
 IAR LOCATION: Nuclear and cytoplasmic.
 FY: Belongs to the eukaryotic diacylglycerol kinase
 domain.
 FY: Contains 2 zinc-dependent phorbol-ester and DAG
 domains.
 FY: Contains 2 ANK repeats.
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 mail to license@isb-sib.ch).
 16; AAC62010.1; -
 19; AAF43006.1; -
 17; AAF43006.1; JOINED.
 18; AAF43006.1; JOINED.
 19; AAF43006.1; JOINED.
 20; AAF43006.1; JOINED.
 21; AAF43006.1; JOINED.
 22; AAF43006.1; JOINED.
 23; AAF43006.1; JOINED.
 24; AAF43006.1; JOINED.
 25; AAF43006.1; JOINED.
 26; AAF43006.1; JOINED.
 27; AAF43006.1; JOINED.
 28; AAF43006.1; JOINED.
 29; AAF43006.1; JOINED.
 30; AAF43006.1; JOINED.

DR EMBL; AF219931; AAF43006.1; JOINED.
 DR EMBL; AF219932; AAF43006.1; JOINED.
 DR EMBL; AF219933; AAF43006.1; JOINED.
 DR EMBL; AF219934; AAF43006.1; JOINED.
 DR EMBL; AF219935; AAF43006.1; JOINED.
 DR EMBL; AF219936; AAF43006.1; JOINED.
 DR EMBL; AF219937; AAF43006.1; JOINED.
 DR EMBL; AF219938; AAF43006.1; JOINED.
 DR Genew; HGNC:2855; DGKI.
 DR MIM; 604072; -
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0004143; F:diacylglycerol kinase activity; TAS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002219; DAG PE-bind.
 DR InterPro; IPR000756; DAGKa.
 DR Pfam; PF00023; ank; 2.
 DR Pfam; PF00609; DAGKa; 1.
 DR Pfam; PF00781; DAGK; 1.
 DR ProDom; PD002939; DAGKa; 1.
 DR ProDom; PD005043; DAGK; 1.
 DR SMART; SM00248; ANK; 2.
 DR SMART; SM00109; CI; 2.
 DR SMART; SM00045; DAGKa; 1.
 DR SMART; SM00046; DAGK; 1.
 DR PROSITE; PS00088; ANK REPEAT; 2.
 DR PROSITE; PS00297; ANK REP REGION; 1.
 DR PROSITE; PS00479; DAG PE BIND DOM 1; FALSE NEG.
 DR PROSITE; PS0081; DAG PE BIND DOM 2; FALSE NEG.
 DR Transferrase; Kinase; ANK repeat; Repeat; Nuclear protein;
 KW Multigene family; Polymorphism.
 FT DOMAIN 178 232 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 251 309 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 374 500 CATALYTIC-A (POTENTIAL).
 FT DOMAIN 526 683 CATALYTIC-B (POTENTIAL).
 FT REPEAT 958 990 ANK 1.
 FT REPEAT 997 1026 ANK 2.
 FT DOMAIN 20 31 POLY-ALA.
 FT DOMAIN 69 74 POLY-SER.
 FT DOMAIN 95 102 POLY-ALA.
 FT VARIANT 133 153 L -> F.
 FT /FTIG=VAR 010190.
 FT CONFLICT 160 160 A -> P (IN REF. 2).
 SQ SEQUENCE 1065 AA; 116996 MW; B84971AA7630A799 CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 118 APAAAAAA 126
 Db 22 APAAAAAA 30
 RESULT 47
 ID IFH1 YEAST STANDARD; PRT; 1085 AA.
 AC P39520;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IFH1 protein (RRP3 protein).
 GN IFH1 OR RRP3 OR YLR223C OR L8083.9.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 28383 / FL100;
 RX MEDLINE=95304839; PubMed=7785326;
 RA Chereil I., Thuriaux P.;

product interacts with a fork head protein in cerevisiae.";
[70(1995)].

N.A.
AB972;
PubMed=9169871;
Miller L., Riles L., Albermann K., Andre B., Ansoerge W.,
Kerner M., Delius H., Dubois E., Duesterhoeft A.,
Floeth M., Goffeau A., Hebling U., Heumann K.,
D., Hilbert H., Hilger F., Kleine K., Koetter P.,
essenguy F., Mewes H.-W., Miosga T., Moestl D.,
Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
Shrens B., Scholler P., Schwager C., Schwarz S.,
Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
Wermann F.K., Zollner A., Hani J., Hoheisel J.D.;
90(1997).
Controls the pre-rRNA processing machinery in
n with PHL1. Could convert PHL1 from a repressor
vator.

AR LOCATION: Nuclear (Probable).

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CAA82624.1; -;
AAB67412.1; -;
S5352.
1285; -;
IFHL.

; P:chromatin silencing at telomere; IMP.
; P:RNA processing; IGI.
in; Transcription regulation.
22 163 ASP/GLU-RICH (HIGHLY ACIDIC).
15 AA; 122491 MW; BEIC7DEF06213FE0 CRC64;

1.7%; Score 9; DB 1; Length 1085;
arity 100.0%; Pred.No.23;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

DED 337
11111
DED 141

STANDARD; PRT; 1137 AA.

rel. 17, Created)
rel. 17, Last sequence update)
rel. 42, Last annotation update)
repair protein Men3 (Divergent upstream protein) (DUP)
air protein 1) (MRP1).
r DUC1.
(Human).
:azoa; Chordata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;

N.A.
190; PubMed=2722860;
ada T.;
i characterization of cDNA clones derived from the
anscribed gene in the region upstream from the human

RT dihydrofolate reductase gene.";
RL J. Biol. Chem. 264:10057-10064(1989).
RN [2]
RX SEQUENCE FROM N.A., AND VARIANT ALA-1045.
RA MEDLINE=97098445; PubMed=8942985;
RA Acharya S., Wilson T., Gradia S., Kane M.F., Guerrette S.,
RA Marsischky G.I., Kolodner R., Fishel R.;
RT "hMSH2 forms specific mismatch-binding complexes with hMSH3 and
RT hMSH6.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13629-13634(1996).
CC -1- FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN
CC -1- DISEASE: Defects in MSH3 are a cause of susceptibility to
CC endometrial cancer [MIM:608089].
CC -1- SIMILARITY: Belongs to the DNA mismatch repair mutS family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL out
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CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).

EMBL; J04810; BAB47281.1; -;
EMBL; U61981; AAB6045.1; -;
PIR; A33507; A33507.
Genew; HGNC:7326; MSH3.
MIM; 608087; -;
MIM; 608089; -;

GO; GO:0006298; P:mismatch repair; TAS.
InterPro; IPR000432; MutS_C.
InterPro; IPR007860; MutS_I.
InterPro; IPR007696; MutS_III.
InterPro; IPR007695; MutS_N.
Pfam; PF01624; MutS_I_1.
Pfam; PF05188; MutS_II_1.
Pfam; PF05192; MutS_III_1.
Pfam; PF00488; MutS_V_1.
Pfam; PD001263; MutS_C_1.
ProDom; PD001263; MutS_C_1.
SMART; SM00534; MUTSAC; 1.
SMART; SM00533; MUTSD; 1.
PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
DNA repair; ATP-binding; DNA-binding; Polymorphism.
DOMAIN 51 62 POLY-ALA.
FT NP BIND 896 903 ATP (POTENTIAL).
FT VARIANT 709 709 F -> L (in dbSNP:1805354).
FT VARIANT 949 949 R -> Q (in dbSNP:184967).
FT VARIANT 1045 1045 /FTID=VAR_016161.
FT VARIANT 1054 1054 /FTID=VAR_016162.
FT VARIANT 1054 1054 /FTID=VAR_016163.
FT CONFLICT 57 65 MISSING (IN REF. 2).
FT CONFLICT 622 622 G -> E (IN REF. 2).
SQ SEQUENCE 1137 AA; 127383 MW; 704D1194E336848E CRC64;

Query Match 1.7%; Score 9; DB 1; Length 1137;
Best Local Similarity 100.0%; Pred.No.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G.

QY 120 AAAAAAAPP 128
Db 56 AAAAAAAPP 64

RESULT 49
NRDC HUMAN
ID NRDC HUMAN STANDARD; PRT; 1150 AA.
AC Q43847; O15241; O15242; Q96HB2; Q9NU57;
DT 15-DEC-1998 (Rel. 37, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

cursor (EC 3.4.24.61) (N-arginine dibasic convertase)
(see) (NRD-C).
(Human).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;
1 N.A. (ISOFORM 1).
123; PubMed=9479496;
Accarino M., Egeo A., Scartezzini P., Rappazzo G.,
vvanaggiato V., Simeone A., Arrigo G., Zuffardi O.,
Taramelli R.;
nvertase: a highly conserved metalloendopeptidase
specific sites during development and in adult
138-245(1998).
1 N.A. (ISOFORMS 1 AND 2).
1;
1057; PubMed=9581555;
Prat A., Joulie C., Cherif D., Day R., Cohen P.;
at testis express two mRNA species encoding variants of
se, a metalloendopeptidase of the insulinase family.";
127:773-779(1997).
1 N.A. (ISOFORM 1).
ita;
1257; PubMed=12477932;
L., Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Zeberg B., Suec K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
quellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
ton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
fadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
i., Touchman J.W., Green E.D., Dickson M.C.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schein J.E., Jones S.J.M., Marra M.A.;
and initial analysis of more than 15,000 full-length
use cDNA sequences";
Acad. Sci. U.S.A. 99:16899-16903(2002).
1-107 FROM N.A.
3757; PubMed=11042131;
Pierotti A.R.;
sion of the dibasic-pair cleaving enzyme NRD convertase
ibasic convertase) is differentially regulated in the
/ and Mat-Lu prostate cell lines.";
151:755-764(2000).
289-1150 FROM N.A.
EB-2000) to the EMBL/GenBank/DBJ databases.
: Cleaves peptide substrates on the N-terminus of arginine
in dibasic pairs.
: ACTIVITY: Hydrolysis of polypeptides, preferably at
f-Lys, and less commonly at Arg-|-Arg-Xaa, in which Xaa is
or Lys.
: Binds 1 zinc ion per subunit (By similarity).
IVE PRODUCTS:
ternative splicing; Named isoforms=2;
Synonyms=NRD1;
343847-1; Sequence=Displayed;
Synonyms=NRD2;

```

Isoid=043847-2; Sequence=VSP 007114;
 TISSUE SPECIFICITY: Primarily in adult heart, skeletal muscle
 testis and at much lower levels in other tissues.
 SIMILARITY: Belongs to peptidase family M16.
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 the European Bioinformatics Institute. There are no restriction
 use by non-profit institutions as long as its content is not
 modified and this statement is not removed. Usage by and for
 entities requires a license agreement (See <http://www.isb-sib.ch>
 or send an email to license@isb-sib.ch).

 EMBL; U64988; AAC39597.1; -;
 EMBL; X93209; CAA63698.1; -;
 EMBL; X93207; CAA63694.1; -;
 EMBL; BC008775; AAH08775.1; -;
 EMBL; AJ000350; CAA04025.1; -;
 EMBL; AL050343; CAB72328.1; -;
 Genew; HGNC:7395; NRDL.
 MIM; 602651; -;
 GO; GO:0004222; F:metalloendopeptidase activity; TAS.
 GO; GO:0007528; P:neuromuscular junction development; TAS.
 GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 InterPro; IPR001431; Peptidase_M16.
 InterPro; IPR007863; Peptidase_M16_C.
 Pfam; PF00675; Peptidase_M16; 1.
 Pfam; PF05193; Peptidase_M16_C; 2.
 PROSITE; PS00143; INSULINASE; 1.
 KW Hydroxylase; Metalloprotease; Zinc; Signal; Alternative splicing.
 SIGNAL 1 20 POTENTIAL.
 CHAIN 21 1150 NARDILYSIN.
 DOMAIN 142 200 ASP/GLU-RICH (HIGHLY ACIDIC).
 DOMAIN 144 153 POLY-GLU.
 FT METAL 232 232 ZINC (BY SIMILARITY).
 FT ACT_SITE 235 235 BY SIMILARITY.
 FT METAL 236 236 ZINC (BY SIMILARITY).
 FT METAL 313 313 ZINC (BY SIMILARITY).
 FT VARSP_LIC 209 209
 Q -> QQQSFLMSKLTDLRFNFKSTYSKMSSTL;
 IYGVVGAERSAPVQHLAQWAEQQGGTDTVL;
 isoform 2).
 /FTid=VSP 007114.
 EL -> DV (IN REF. 2).
 E -> EE (IN REF. 2).
 Q -> L (IN REF. 2).
 A -> G (IN REF. 1).
 V -> A (IN REF. 2).
 V -> A (IN REF. 1).
 T -> S (IN REF. 2).
 DCIIPTDIRAFTTTLNLLPYHKIVK -> SVSSP.
 SQHSTFSPFTIK (IN REF. 1).
 SQHSTFSPFTIK (IN REF. 1).
 MW; 3B46DAD898E038B CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 1150;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 QY 329 EEEEDDED 337
 Db 150 EEEEDDED 158
 RESULT 50
 IE18_PRVIF
 ID IE18_PRVIF STANDARD; PRT; 1461 AA.
 AC P11675;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Immediate-early protein IE180.
 GN IE.
 OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

ciniae; Varicellovirus.
123;
N.A.
207; PubMed=2546124;
ie sequence analysis of the immediate-early gene of
virus.";
Res. 17:4637-4646(1989).
1-1989) to the EMBL/GenBank/DBJ databases.
THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
NG TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
AL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
R LOCATION: Nucleus of infected cells.
g stretch of serine residues may be a major site of
ation.
: BELONGS TO THE ICP4/IE140/IE180 FAMILY.

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al to license@isb-sib.ch).

CAA33214.1; -;
DDEIF.
05205; Herpes_ICP4_C.
05206; Herpes_ICP4_N.
Herpes_ICP4_C; 1.
Herpes_ICP4_N; 1.
Transcription regulation: Trans-acting factor;
phosphorylation. Nuclear protein.
0 405 POLY-SER.
8 966 POLY-SER.
1 AA: 149833 MW; 7F31E7AB5403B208 CRC64;
1.7%; Score 9; DB 1; Length 1461;
rity 100.0%; Pred. No. 29;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 385
STANDARD; PRT; 2004 AA.
el. 36, Created)
el. 36, Last sequence update)
el. 42, Last annotation update)
cetyltransferase 3 (Runt-related transcription factor
n 2) (Monocytic leukemia zinc finger protein) (Zinc
.220).
P2 OR ZNF220 OR MOZ.
Human)
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;
N.A.
68; PubMed=8782817;
nton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,
.., Civin C.I., Distèche C., Dube I., Frischauf A.M.,
telman F., Volinia S., Watmore A.E., Housman D.E.;
tion t(8;16)(p11;p13) of acute myeloid leukaemia fuses
tyltransferase to the CREB-binding protein.";

RL Nat. Genet. 14:33-41(1996).
CC -I- FUNCTION: May represent a chromatin-associated acetyltransfer
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- DISEASE: Involved in acute myeloid leukemias through a chromo
CC translocation t(8;16)(p11;p13) involving MYST3 and CREBBP.
CC -I- SIMILARITY: Contains 2 PHD-type zinc fingers.
CC -I- SIMILARITY: Belongs to the MYST (SAS/MOZ) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL out
CC the European Bioinformatics Institute. There are no restriction
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (See <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; UA7742; AAC50662.1; -;
CC Genew; HGNC:13013; MYST3.
CC MIM; 601408; -;
CC GO; GO:0006323; P:DNA packaging; TAS.
CC InterPro; IPR005818; Histone H1/H5.
CC InterPro; IPR002717; MOZ SAS.
CC InterPro; IPR001965; Znf_PHD.
CC Pfam; PF01853; MOZ_SAS; 1.
CC Pfam; PF00628; PHD; 2.
CC SMART; SM00526; H15; 1.
CC SMART; SM00249; PHD; 2.
CC PROSITE; PS01359; ZF_PHD_1; 1.
CC PROSITE; PS50016; ZF_PHD_2; 2.
KW Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
KW Nuclear protein.
FT ZN FING 206 265 PHD-TYPE 1.
FT ZN FING 259 313 PHD-TYPE 2.
FT DOMAIN 371 379 POLY-SER.
FT ZN FING 538 560 C2HC-TYPE.
FT DOMAIN 788 801 POLY-GLU.
FT DOMAIN 989 995 POLY-GLU.
FT DOMAIN 1019 1026 POLY-ARG.
FT DOMAIN 1069 1078 POLY-GLU.
FT DOMAIN 1147 1150 POLY-LYS.
FT DOMAIN 1221 1242 GLU-RICH.
FT DOMAIN 1267 1302 GLU-RICH.
FT DOMAIN 1411 1414 POLY-SER.
FT DOMAIN 1593 1597 POLY-SER.
FT DOMAIN 1643 1704 GLN/PRO-RICH.
FT DOMAIN 1897 1977 MET-RICH.
FT SITE 1546 1547 BREAKPOINT FOR TRANSLOCATION TO FORM
FT MOZ-CBP.
SQ SEQUENCE 2004 AA; 225054 MW; 9FFBAC3792854BA CRC64;
Query Match 1.7%; Score 9; DB 1; Length 2004;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; G
QY 225 QPPPPQPPQ 233
Db 1660 QPPPPQPPQ 1668
RESULT 52
NC06_HUMAN
ID NC06_HUMAN STANDARD; PRT; 2063 AA.
AC Q14686; Q9NTZ9; Q9UH74; Q9UK86;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nuclear receptor coactivator 6 (Amplified in breast cancer-3 prote
DE (Cancer-amplified transcriptional coactivator ASC-2) (Activating
DE signal cointegrator-2) (ASC-2) (Peroxisome proliferator-activated
DE receptor-interacting protein) (PPAR-interacting protein) (PRIP)
DE (Nuclear receptor-activating protein, 250 kDa) (Nuclear receptor
DE coactivator RAP250) (NRC RAP250) (Thyroid hormone receptor-binding
DE protein).

OR RAP250 OR TRBP OR KIAA0181.
(Human).
tazoo; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;
[N.A., AND INTERACTION WITH CREBBP; NCOA1; GTF2A; TBP;
ARA AND THRA.
574; PubMed=10567404;
Zick S.L., Choi J.-E., Bubendorf L., Guan X.-Y.,
Gallionieri O.P., Kononen J., Trent J.M., Azorsa D.,
Heong J.H., Lee Y.C., Meltzer P.S., Lee J.W.;
ector ASC-2, as a cancer-amplified transcriptional
essential for ligand-dependent transactivation by nuclear
vivo".
l. 274:34283-34293 (1999).
[N.A., HOMODIMERIZATION, AND INTERACTION WITH CREBBP;
IR3C1; RARA; VDR AND THRA.
329; PubMed=10866662;
Samuels H.H.;
of nuclear receptor coregulators that integrates nuclear
aling through CBP".
ol. 20:5048-5063 (2000).
[N.A., AND INTERACTION WITH PPARA; PPARG; ESR1; ESR2 AND
3;
724; PubMed=10681503;
onson P., Palto-Huikko M., Treuter E., Gustafsson J.-A.;
Characterization of RAP250, a nuclear receptor
;
n. 275:5308-5317 (2000).
[N.A., PHOSPHORYLATION BY PRKDC, AND INTERACTION WITH
300 AND CRSP3.
ocytes;
3976; PubMed=10823961;
na G.R., Chin W.W.;
none receptor-binding protein, an LXXLL motif-containing
ctions as a general coactivator".
Acad. Sci. U.S.A. 97:6212-6217 (2000).
[N.A.
narrow;
1124; PubMed=8724849;
eki N., Iihikawa K.-I., Tanaka A., Nomura N.;
of the coding sequences of unidentified human genes. V.
quences of 40 new genes (KIAA0161-KIAA0200) deduced by
cDNA clones from human cell line KG-1".
7-24 (1996).
M N.A.
749; PubMed=11780052;
Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
avrides G., Almeida J.P., Babage A.K., Bagguley C.L.,
arlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
rill W.D., Butler A.P., Carder C., Carter N.P.,
Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
bley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coville G.J., Deadman R., Dhani P.D., Dunn M.,
G., Frankland J.A., Fraser A., French L., Garner P.,
Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
unt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
mberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
arker A., Patel R., Pearce T.A.V., Peck A.I.,
J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
oss M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe J.
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whithead S.L., Whittaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2(
RL Nature 414:865-871 (2001).
RN [7]
RN INTERACTION WITH NCOA6IP.
RX MEDLINE=21417756; PubMed=11517327;
RA Zhu Y.-J., Qi C., Cao W.-Q., Yeldandi A.V., Rao M.S., Reddy J.K.
RT "Cloning and characterization of PIMT, a protein with a
methyltransferase domain, which interacts with and enhances nuclei
receptor coactivator PRIP function".
RT Proc. Natl. Acad. Sci. U.S.A. 98:10380-10385 (2001).
RN [8]
RN INTERACTION WITH RBM14.
RX MEDLINE=21423995; PubMed=11443112;
RA Iwasaki T., Chin W.W., Ko L.;
RT "Identification and characterization of RRM-containing coactivat
activator (CoAA) as TRBP-interacting protein, and its splice var
as a coactivator modulator (CoAM)".
RL J. Biol. Chem. 276:33375-33383 (2001).
RN [9]
RN INTERACTION WITH HRMTL1.
RX MEDLINE=22151129; PubMed=12039952;
RA Qi C., Chang J., Zhu Y., Yeldandi A.V., Rao S.M., Zhu Y.-J.;
RT "Identification of protein arginine methyltransferase 2 as a
coactivator for estrogen receptor alpha".
RL J. Biol. Chem. 277:28624-28630 (2002).
RN [10]
RN INTERACTION WITH MLL3 AND THE ASCOM COMPLEX.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=22371496; PubMed=12482968;
RA Goo Y.-H., Sohn Y.C., Kim D.-H., Kim S.-W., Kang M.-J., Jung D.-
RA Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,
Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee
Lee J.W.;
RT "Activating signal cointegrator 2 belongs to a novel steady-stat
complex that contains a subset of trithorax group proteins".
Mol. Cell. Biol. 23:140-149 (2003).
RN [11]
RN MUTAGENESIS OF 883-THR-GLU-894, AND PHOSPHORYLATION.
RX MEDLINE=21635582; PubMed=11773444;
RA Ko L., Cardona G.R., Iwasaki T., Bramlett K.S., Burris T.P.,
Chin W.W.;
RT "Ser-884 adjacent to the LXXLL motif of coactivator TRBP defines
selectivity for ERS and TRs".
RL Mol. Endocrinol. 16:128-140 (2002).
CC -I- FUNCTION: Nuclear receptor coactivator that directly binds n
receptors and stimulates the transcriptional activities in a
hormone-dependent fashion. Coactivates expression in an agon
and AP2-dependent manner. Involved in the coactivation of
different nuclear receptors, such as for steroids (GR and ER
retinoids (RARs and RXRs), thyroid hormone (TRs), vitamin D3
and prostanoids (PPARs). Probably functions as a general
coactivator, rather than just a nuclear receptor coactivator
also be involved in the coactivation of the NF-kappa-B pathw
May coactivate expression via a remodeling of chromatin and
interaction with histone acetyltransferase proteins.
CC -I- SUBUNIT: Monomer and homodimer. Interacts with RNPC2 (By
similarity). Interacts in vitro with the basal transcription
factors GTF2A and TBP, suggesting an autonomous transactivat
function. Interacts with NCOA1, CRSP3, RBM14, the histone
acetyltransferases EP300 and CREBBP, and with the
methyltransferases NCOA6IP and HRMTL1/PRMT2. Belongs to the
ASC-2/NCOA6 complex (ASCOM), which contains ASC-2/NCOA6, the
retinoblastoma-binding protein RBQ-3/RBP5, alpha- and beta
tubulins, the trithorax group proteins MLL2 and MLL3, and
ASH2/ASCL2.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain,

testis and ovary; weakly expressed in lung, thymus and
 istine.
 contains two Leu-Xaa-Leu-Leu (LXXLL) motifs. Only
 essential for the association with nuclear receptors,
 cent Ser-884 displays selectivity for nuclear receptors.
 horylated by PRKDC.
 horylation on Ser-884 leads to a strong decrease in
 ESR1 and ESR2.
 XOUS: Frequently amplified or overexpressed in colon,
 lung cancers.
 ref.1 (AA16403) sequence differs from that shown due to
 ft in position 88.

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 ail to license@isb-sib.ch).

;; AA13595.1; -
 ;; AA16403.1; ALT_FRAME.
 ;; AA178480.1; -
 ;; AA178003.1; -
 ;; AA171829.1; -
 ;; AA11498.2; ALT_INIT.
 ;; CAB92721.1; -
 ;; 9336; NCOA6.

;; C:nucleus; IDA.
 ;; C:transcription factor complex; TAS.
 ;; F:chromatin binding; ISS.
 ;; F:estrogen receptor binding; TAS.
 ;; F:retinoid X receptor binding; TAS.
 ;; F:thyroid hormone receptor binding; IDA.
 ;; F:transcription co-activator activity; IDA.
 ;; F:transcriptional activator activity; TAS.
 ;; F:brain development; ISS.
 ;; P:embryonic development (sensu Mammalia); ISS.
 ;; P:heart development; ISS.
 ;; P:myeloid blood cell differentiation; IDA.

1.7%; Score 9; DB 1; Length 2063;
 ivity 100.0%; Pred.No.39;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;

PPPP 229
 |||||
 PPPP 1018

STANDARD; PRT; 2067 AA.

;;
 rel. 41, Created)
 rel. 41, Last sequence update)
 rel. 42, Last annotation update)
 or coactivator 6 (Amplified in breast cancer-3 protein)
 fied transcriptional coactivator ASC-2) (Activating
 rator-2) (ASC-2) (Peroxisome proliferator-activated
 racting protein) (PPAR-interacting protein) (Nuclear
 ating protein, 250 kDa) (Nuclear receptor coactivator
 (Thyroid hormone receptor binding protein).
 OR RAP250 OR PRIP OR TRBP.
 (Mouse).

taxoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 990;

N.A. (ISOFORMS 1 AND 2), AND INTERACTION WITH
 RARA; RXRA; ESR1; ESR2 AND THR3.

RC TISSUE=liver;
 RX MEDLINE=20250907; PubMed=10788465;
 RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
 RA Reddy J.K.,
 RT "Isolation and characterization of peroxisome proliferator-activa
 RT receptor (PPAR) interacting protein (PRIP) as a coactivator for
 RL PPAR.";
 RL J. Biol. Chem. 275:13510-13516(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Breast;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.F., Schuler G.D
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 786-1142 FROM N.A. (ISOFORM 1), INTERACTION WITH PPAR
 RP PARG; ESR1; ESR2; THRA AND THR3, AND MUTAGENESIS OF LEU-831 AND
 RP LEU-894.
 RC TISSUE=Embryo;
 RX MEDLINE=20148724; PubMed=10681503;
 RA Cairra F., Antonson P., Pelto-Huikko M., Treuter E., Gustafsson J.
 RT "Cloning and characterization of RAP250, a nuclear receptor
 RT coactivator.";
 RL J. Biol. Chem. 275:5308-5317(2000).
 RN [4]
 RP INTERACTION WITH RNPC2.
 RX MEDLINE=21638469; PubMed=11704680;
 RA Jung D.-J., Na S.-Y., Na D.S., Lee J.W.;
 RT "Molecular cloning and characterization of CAPER, a novel coactiv
 RT of activating protein-1 and estrogen receptors.";
 RL J. Biol. Chem. 277:1229-1234(2002).
 CC -1- FUNCTION: Nuclear receptor coactivator that directly binds nu
 CC receptors and stimulates the transcriptional activities in a
 CC hormone-dependent fashion. Coactivates expression in an agoni
 CC and AP2-dependent manner. Involved in the coactivation of
 CC different nuclear receptors, such as for steroids (GR and ERs
 CC retinoids (RARs and RXRs), thyroid hormone (TRs), vitamin D3
 CC and prostanooids (PPARs). Probably functions as a general
 CC coactivator, rather than just a nuclear receptor coactivator.
 CC also be involved in the coactivation of the NF-kappa-B pathwa
 CC May coactivate expression via a remodeling of chromatin and i
 CC interaction with histone acetyltransferase proteins. Involved
 CC placental, cardiac, hepatic and embryonic development.
 CC -1- SUBUNIT: Monomer and homodimer. Interacts in vitro with the b
 CC transcription factors GTF2A and TBP, suggesting an autonomous
 CC transactivation function. Interacts with NCOA1, CREBBP, RBM14,
 CC histone acetyltransferase proteins EP300 and CREBBP, and with
 CC methyltransferase proteins NCOA6IP and HMT111 (By similarity
 CC interacts with RNPC2. Belongs to the ASC-2/NCOA6 complex (ASC
 CC which contains ASC-2/NCOA6, the retinoblastoma-binding protei
 CC RBQ-3/ RBBP5, alpha- and beta-tubulins, the trithorax group
 CC proteins MLL2 and MLL3, and ASH2/ASCL2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

Best Local Similarity 100.0%; Pred. No. 39; Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 221 PQQQPPPP 229
DB 1014 PQQQPPPP 1022

RESULT 54
MLL4 HUMAN
ID MLL4 HUMAN STANDARD; PRT: 2715 AA.
AC Q9UNW6: O15022; Q95836; Q96IP2; Q96IP3; Q9UK25; Q9Y668; Q9Y669;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myeloid/lymphoid or mixed-lineage leukemia protein 4 (Trithorax homolog 2).
GN MLL4 OR TRX2 OR HRX2 OR MLL2 OR KIAA0304.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Angrand P.O., Valvatne H., Jeanmougin F., Adamson A., van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O., Lamerdin J., Chambon P., Lossos R., Stewart A., Asland R.; "Mammalian trithorax- and ASH1-like proteins: putative chromatin regulators which contain PHD fingers and SET domains."; Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K., Garcia E., Kyle A., Ramirez M., Stillwagen S., Ganes J., Dangana Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O., Carrano A.V.; "Sequence analysis of a 1 Mb region in human 19q13.1."; Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 111-2715 FROM N.A. (ISOFORM 1).
RC TISSUE=Leukocyte, and Testis;
RX MEDLINE=20105772; PubMed=10637508;
RA Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P., Wiedemann L.M., Aparicio S., Caldas C.; "MLL2, the second human homolog of the Drosophila trithorax gene to 19q13.1 and is amplified in solid tumor cell lines."; Oncogene 18:7975-7984(1999).
RN [4]
RP SEQUENCE OF 816-2715 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Skin;
RX MEDLINE=97349994; PubMed=9205841;
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 4:141-150(1997).
RN [5]
RP SEQUENCE OF 1918-2715 FROM N.A.
RC TISSUE=Brain, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. Villalón D.K., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanche

9UL19-1; Sequence=Displayed;
9UL19-2; Sequence=VSP 003410;
ites as a dominant negative repressor;
ECIFICITY: Widely expressed. High expression in testis
expression in small intestine.
NTAL STAGE: Expressed at E9 in placenta and at weaker
uterus. High expression in neural tube and in CNS
at development. High expression in sensory ganglia and
som E11. In the alimentary tract and olfactory epithelium
y, from E11 and E13 respectively, and then expression
i at later stages of development. Moderate expression in
n E13, while it decreases during postnatal life. Strong
on in thymus from E15 onwards, and in spleen from E17 and
arly postnatal life. Then, the expression decreases.
Contains two Leu-Xaa-Xaa-Leu-Leu (LXXLL) motifs. Only
is essential for the association with nuclear receptors.
phorylated (By similarity).
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mail to licenses@isb-sib.ch).
36; RAFP35860.1; -;
33; AAF31113.1; -;
39; AAF35973.1; -;
3915; NCOA6.
34; C:nucleus; IDA.
57; C:transcription factor complex; IDA.
32; F:chromatin binding; IDA.
31; F:estrogen receptor binding; ISS.
35; F:retinoid X receptor binding; ISS.
56; F:thyroid hormone receptor binding; ISS.
53; F:transcription co-activator activity; ISS.
53; F:transcriptional activator activity; IDA.
20; P:brain development; IMP.
21; P:embryonic development (sensu Mammalia); IMP.
37; P:heart development; IMP.
39; P:myeloid blood cell differentiation; ISS.
57; P:transcription initiation from Pol II promoter; IDA.
a regulation; Activator; Nuclear protein; Repeat;
splicing.
1 1060 CREBBP-BINDING REGION (BY SIMILARITY).
1 932 TBP/GTF2A-BINDING REGION (BY SIMILARITY).
1 1314 NCOA1-BINDING REGION (BY SIMILARITY).
777 931 NCOA6IP-BINDING REGION (BY SIMILARITY).
544 2067 EP300/CRSP3-BINDING REGION (BY SIMILARITY).
227 1044 GLN-RICH.
376 381 POLY-PRO.
917 922 POLY-LYS.
543 1592 SER-RICH.
891 895 LXXLL MOTIF 1.
495 1499 LXXLL MOTIF 2.
458 2067 Missing (in isoform 2).
/FTID=VSP_003410.
891 894 LVNL->AVNA: ABOLISHES INTERACTION WITH NUCLEAR RECEPTORS.
39 39 G -> S (IN REF. 2).
109 109 W -> R (IN REF. 2).
194 194 M -> I (IN REF. 2).
290 290 Q -> QQ (IN REF. 2).
014 1014 P -> L (IN REF. 3).
141 1142 SE -> RS (IN REF. 3).
067 AA; 219663 MW; C855F877167AD48 CRC64;
1.7%; Score 9; DB 1; Length 2067;

dan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Touchman J.W., Green E.D., Dickson M.C.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Hein J.E., Jones S.J.M., Marra M.A.,
Initial analysis of more than 15,000 full-length
cDNA sequences.",
Sci. U.S.A. 99:16999-16903(2002).

ICE FROM N.A. (ISOFORMS 1 AND 2).
arrow, and Placenta;
83; PubMed=10409430;
Diaz M.O.;
mammalian member of the trx/MLL family of genes.";
192(1999).

Possibly acts as a transcriptional regulatory factor.
AR LOCATION: Nuclear (By similarity).

FE PRODUCTS:

native splicing; Named isoforms=2;

/nonys=long;

/UNN6-1; Sequence=Displayed;

/nonys=truncated;

/UNN6-2; Sequence=VSP_006668, VSP_006669;

SPECIFICITY: Widely expressed. Highest levels in testis.

in brain, bone marrow, heart, muscle, kidney, pancreas,

ymus, prostate, ovary, intestine, colon, peripheral

chocytes, and placenta.

often amplified in pancreatic carcinomas.

Belongs to the TRX/MLL family.

Contains 1 bromodomain.

Contains 3 PHD-type zinc fingers.

Contains 1 CXXC-type zinc finger.

Contains 1 post-SET domain.

This protein was first named MLL2 by Ref.3 and Ref.6.

aponds to another protein located on chromosome 12 (see

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il to license@isb-sib.ch).

1; CAB45385.1; -;

1; -; NOT ANNOTATED_CDS.

1; BAA20763.2; -;

1; AAD56420.1; -;

1; AAD17932.1; -;

1; AAD26113.1; -;

1; AAH09337.1; -;

1; AAH07353.1; -;

1; AAD26112.1; -;

1; Cnucleus; NAS.

1; F:transcription factor activity; NAS.

1; F:zinc ion binding; NAS.

1; P:chromatin-mediated maintenance of transcrip. . .; NAS.

03889; Fvrich.C.

03888; Fvrich.N.

03616; PostSET.

01214; SET.

02857; Znf_CXXC.

01965; Znf_PHD.

PHD; 3.

SET; 1.

zf_CXXC; 1.

FYRC; 1.

FYRN; 1.

PHD; 4.

PostSET; 1.

DR SMART; SM00317; SET; 1.
DR PROSITE; PS00868; POST SET; 1.
DR PROSITE; PS0280; SET; 1.
DR PROSITE; PS01359; ZF_PHD_1; 3.
DR PROSITE; PS00016; ZF_PHD_2; 3.
KW DNA-binding; Bromodomain; Nuclear protein; Zinc-finger; Metal-bin
KW Transcription regulation; Alternative splicing; Repeat.
FT DNA_BIND 37 44 A.T HOOK (BY SIMILARITY).
FT DNA_BIND 110 117 A.T HOOK (BY SIMILARITY).
FT DNA_BIND 357 365 A.T HOOK (BY SIMILARITY).
FT ZN_FING 959 1005 CXXC-TYPE.
FT ZN_FING 1201 1252 PHD-TYPE 1.
FT ZN_FING 1249 1303 PHD-TYPE 2.
FT ZN_FING 1335 1396 PHD-TYPE 3.
FT DOMAIN 1449 1471 BROMODOMAIN (DIVERGENT).
FT DOMAIN 2574 2695 SET.
FT DOMAIN 2699 2715 POST-SET.
FT DOMAIN 26 37 POLY-GLY.
FT DOMAIN 248 255 POLY-PRO.
FT DOMAIN 362 398 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 402 771 PRO-RICH.
FT DOMAIN 808 812 POLY-GLN.
FT DOMAIN 1963 1970 POLY-PRO.
FT DOMAIN 2251 2259 POLY-PRO.
FT VARSPLIC 532 582 VSARSRVKTPRRFMDEPPKPKVEVSPVLRPPPI
FT VQEPAPVPS -> PLSQSLLEMTQLSLGQWA
FT ACLESLPMSPLLRPCPLTGLQL (in isoform
FT /FTid=VSP_006668.
FT Missing (in isoform 2).
FT /FTid=VSP_006669.
FT K -> E (IN REF. 6).
FT S -> Y (IN REF. 6).
FT E -> Q (IN REF. 6).
FT H -> Y (IN REF. 6).
FT D -> N (IN REF. 6).
FT PLA -> GTR (IN REF. 5; AAH09337).
FT DEE -> ARG (IN REF. 5; AAH07353).
FT D -> H (IN REF. 6).
SQ SEQUENCE 2715 AA; 293511 MW; C0615B981BBE7BF CRC64;

Query Match 1.7%; Score 9; DB 1; Length 2715;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 9; Conservative 0; Mismatches 0; Indels 0; G

Qy 131 PAPPPPPAP 139

Db 623 PAPPPPPAP 631

RESULT 55

DY1B CHLRE

ID DY1B CHLRE STANDARD; PRT; 4513 AA.

AC Q9MBF8; Q9ZPC2;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Dynein 1-beta heavy chain, flagellar inner arm 11 complex (1-beta

DE DHC) (Dynein 1, subspecies f).

GN DHC10 OR IDA2.

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.

OX NCBI_TaxID=3055;

RN [1]

RP SEQUENCE FROM N.A., CHARACTERIZATION, MUTAGENESIS, AND EXPRESSION

RC STRAIN=219T.

RX MEDLINE=20346958; PubMed=10888669;

RA Perrone C.A., Myser S.H., Bower R., O'Toole E.T., Porter M.E.;

RT "Insights into the structural organization of the 11 inner arm dy

RL from a domain analysis of the 1 beta dynein heavy chain.";

RL Mol. Biol. Cell 11:2297-2313(2000).

RN [2]

RP SEQUENCE OF 1820-1901 FROM N.A.

015; PubMed=10069812;
Bower R., Knott J.A., Byrd P., Dentler W.L.;
dynein heavy chain 1b is required for flagellar assembly
nas.";
11 10:693-712(1999).
X ELECTRON MICROSCOPY.
722; PubMed=2957507;
W., Gebhart B., Mermall V., Mitchell D.R., Heuser J.E.;
e liquid chromatography fractionation of Chlamydomonas
ts and characterization of inner-arm dynein subunits.";
194:481-494(1987).
IPTON AND LOCALIZATION.
628; PubMed=2137128;
amanis Z., Smith B.F., Sale W.S.;
ct inner dynein arms in Chlamydomonas flagella: molecular
nd location in the axoneme.";
110:379-389(1990).
F I1 DYNEIN COMPLEX FOR PHOTOTAXIS.
457; PubMed=9008712;
tcher S.K.;
ation of an inner dynein arm complex in Chlamydomonas
s altered in phototactic mutant strains.";
136:177-191(1997).
Force generating protein of eukaryotic cilia and
roduces force towards the minus ends of microtubules.
s ATPase activity; the force-producing power stroke is
o occur on release of APP. Required for assembly of the
arm complex and its targeting to the appropriate axoneme
Also required for phototaxis. Mutants swim slowly with
waveforms, and are unable to phototax.
The I1 inner arm complex (also known as the f dynein
is a two-headed isoform composed of two heavy chains (1-
1-beta), three intermediate chains and three light
1 occupies a specific position proximal to the first
oke and repeats every 96 nm along the length of the
AR LOCATION: Flagellar.
f; BY deflagellation.
dynein heavy chains probably consist of an N-terminal stem
nds cargo and interacts with other dynein components),
ead or motor domain. The motor contains six tandemly-
A domains in the head, which form a ring. A stalk-like
; formed by two of the coiled coil domains) protrudes
AA 4 and AAA 5 and terminates in a microtubule-binding
eventh domain may also contribute to this ring; it is not
ther the N-terminus or the C-terminus forms this extra
here are four well-conserved and two non-conserved ATPase
e per AAA domain. Probably only one of these (within AAA
ly hydrolyzes ATP, the others may serve a regulatory
construct encoding the first 989 amino acids but lacking
domain is able to assemble I1 complexes and target them
correct location on the axoneme, partially restores
and fully rescue phototaxis.
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3; CAB99316.1; --
4; CAB99316.1; JOINED.
5; CAB99316.1; JOINED.
9; CAB39160.1; --
003593; AAA_ATPase.

DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy_1.
DR SMART; SM00362; AAA; 3.
KW Motor protein; Dynein; Flagellum; Microtubule; ATP-binding; Repes
KW Coiled coil.
FT DOMAIN 1 1806 STEM (BY SIMILARITY).
FT DOMAIN 1807 2028 AAA 1 (BY SIMILARITY).
FT DOMAIN 2089 2350 AAA 2 (BY SIMILARITY).
FT DOMAIN 2458 2706 AAA 3 (BY SIMILARITY).
FT DOMAIN 2808 3059 AAA 4 (BY SIMILARITY).
FT DOMAIN 3107 3384 STALK (BY SIMILARITY).
FT DOMAIN 3443 3674 AAA 5 (BY SIMILARITY).
FT DOMAIN 3890 4109 AAA 6 (BY SIMILARITY).
FT DOMAIN 192 223 COILED COIL (POTENTIAL).
FT DOMAIN 1544 1577 COILED COIL (POTENTIAL).
FT DOMAIN 1704 1727 COILED COIL (POTENTIAL).
FT DOMAIN 3107 3193 COILED COIL (POTENTIAL).
FT DOMAIN 3301 3384 COILED COIL (POTENTIAL).
FT DOMAIN 3499 3519 COILED COIL (POTENTIAL).
FT NP_BIND 1845 1852 ATP (POTENTIAL).
FT NP_BIND 2127 2134 ATP (POTENTIAL).
FT NP_BIND 2497 2504 ATP (POTENTIAL).
FT NP_BIND 2848 2855 ATP (POTENTIAL).
SQ SEQUENCE 4513 AA; 510655 MW; F2A3E10767FD6719 CRC64;
Query Match 1.7%; Score 9; DB 1; Length 4513;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
QY 120 AAAAAAAP 128
DB 2374 AAAAAAAP 2382
RESULT 56
ANP3_PSEAM
ID ANP3_PSEAM STANDARD; PRT; 37 AA.
AC P02733;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antifreeze peptide 3.
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
OS americanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE.
RX MEDLINE=78060969; PubMed=588591;
RA Devries A.L., Lin Y.;
RT "Structure of a peptide antifreeze and mechanism of adsorption to
RT ice.";
RL Biochim. Biophys. Acta 495:388-392(1977).
CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
CC -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE I AFP ARE
CC ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.
DR PIR; A03192; FDFL3W.
DR InterPro; IPR000104; Antifreeze_1.
DR PRINTS; PR00308; ANTIFREEZE1.
KW Antifreeze protein; Repeat; Multigene family.
SQ SEQUENCE 37 AA; 3144 MW; 46AA951A962DECA9 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 37;
Best Local Similarity 100.0%; Pred.No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
DB 29 AAAAAATA 36

AA; 7215 MW; 8562E1D2B44117BC CRC64;
 1.5%; Score 8; DB 1; Length 85;
 arity 100.0%; Pred. No. 18;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATA 158
 ||||
 AATA 35

STANDARD; PRT; 91 AA.
 (Rel. 08, Created)
 (Rel. 32, Last sequence update)
 (Rel. 40, Last annotation update)
 otein IIA7 precursor (AFP)
 lectes americanus (Winter flounder) (Pleuronectes
 azoia; Chordata; Craniata; Vertebrata; Euteleostomi;
 i; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 a; Acanthopterygii; Percomorpha; Pleuronectiformes;
 lei; Pleuronectidae; Pseudopleuronectes.
 155;

1 N.A.
 1993; PubMed=6548752;
 in Y., Price J., Devries A.L., Powers D., Huang R.C.C.;
 der antifreeze proteins: a multigene family.";
 1. 259:14960-14965(1984).
 Antifreeze proteins lower the blood freezing point.
 Y: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
 RICH, AMPHIPHILIC AND ALPHA-HELICAL.

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AAA49465.1; -.
 A22592.
 000104; Antifreeze 1.
 08; ANTIFREEZE1.
 otein; Repeat; Multigene family; Signal.
 1 21 POTENTIAL.
 22 39 REMOVED BY A DIPEPTIDYLPEPTIDASE
 (PROBABLE).
 40 91 ANTIFREEZE PROTEIN IIA7.
 AA; 8326 MW; DIFC542FD865012C CRC64;
 1.5%; Score 8; DB 1; Length 91;
 arity 100.0%; Pred. No. 19;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

AAATA 158
 ||||
 AATA 52

STANDARD; PRT; 91 AA.
 (Rel. 20, Created)
 (Rel. 20, Last sequence update)
 (Rel. 40, Last annotation update)
 otein precursor (AFP)
 lectes americanus (Winter flounder) (Pleuronectes

OS americanus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Pleuronectidae; Pseudopleuronectes.
 OX NCBI_TaxID=8285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90384854; PubMed=2402466;
 RA Gauthier S., Wu Y., Davies P.L.;
 RT "Nucleotide sequence of a variant antifreeze protein gene.";
 RL Nucleic Acids Res. 18:5303-5303(1990).
 CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point
 CC -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
 CC ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.

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CC EMBL; X53718; CAA37754.1; -.
 DR InterPro; IPR000104; Antifreeze_1.
 DR PRINTS; PRO0308; ANTIFREEZE1.
 KW Antifreeze protein; Repeat; Multigene family; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 39 REMOVED BY A DIPEPTIDYLPEPTIDASE
 (PROBABLE).
 FT CHAIN 40 91 ANTIFREEZE PROTEIN.
 FT SEQUENCE 91 AA; 8354 MW; DIFC5439A902012C CRC64;
 SQ

Query Match 1.5%; Score 8; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 151 AAAAAATA 158
 |||||
 Db 45 AAAAAATA 52

RESULT 61
 ANP LIMFE STANDARD; PRT; 97 AA.
 ID ANP LIMFE STANDARD; PRT; 97 AA.
 AC P09031;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE Antifreeze protein precursor (AFP).
 OS Limanda ferruginea (Yellowtail flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Pleuronectidae; Limanda.
 OX NCBI_TaxID=8258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88029483; PubMed=3665937;
 RA Scott G.K., Davies P.L., Shears M.A., Fletcher G.L.;
 RT "Structural variations in the alanine-rich antifreeze proteins of
 RT pleuronectinae.";
 RL Eur. J. Biochem. 168:629-633(1987).
 CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.
 CC -!- SIMILARITY: BELONGS TO THE TYPE-I AFP FAMILY. TYPE 1 AFP ARE
 CC ALANINE-RICH, AMPHIPHILIC AND ALPHA-HELICAL.

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all to license@isb-sib.ch).

CAA29655.1; --

00104; Antifreeze_1.

8; ANTIFREEZE1.

tein; Repeat; Signal.

1 23

4 48

9 97

AA; 8865 MW; 62AD582DF8E459B6 CRC64;

1.5%; Score 8; DB 1; Length 97;

identity 100.0%; Pred.No. 20;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 126

|||

AAA 46

STANDARD; PRT; 99 AA.

tel. 36, Created)

tel. 36, Last sequence update)

tel. 42, Last annotation update)

n 2 (BC-NCP2).

ifer (Death's head cockroach).

azoa; Arthropoda; Hexapoda; Insecta; Pterygota;

opterodea; Dictyoptera; Blattaria; Blaberoidea;

aberus.

2;

caeca;

97; PubMed=9065121;

othmann A., Skou L., Andersen S.O., Roepstorff P.,

teins from the giant cockroach, Blaberus craniifer.;

1. Mol. Biol. 27:109-120(1997).

tein; Cuticle; Repeat; Pyrrolidone carboxylic acid.

1 1

5 42

6 31

7 92

AA; 9867 MW; 690142670EA91BB CRC64;

1.5%; Score 8; DB 1; Length 99;

identity 100.0%; Pred.No. 20;

conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAP 127

|||

AAP 43

STANDARD; PRT; 99 AA.

tel. 11, Created)

tel. 11, Last sequence update)

tel. 39, Last annotation update)

protein L12P ('A' type).

vannielii.

rchaeota; Methanococci; Methanococcales;

ae; Methanococcus.

7;

RN SEQUENCE FROM N.A.
RP MEDLINE=88198213; PubMed=2834382;
RA Strobel O., Koepke A.K.E., Kamp R.M., Boeck A., Wittmann-Liebold I;
RT "Primary structure of the archaeobacterial Methanococcus vannielii
ribosomal protein L12. Amino acid sequence determination, ";
RT oligonucleotide hybridization, and sequencing of the gene.;"
RL J. Biol. Chem. 263:6538-6546(1988).
CC -!- FUNCTION: Seems to be the binding site for several of the fac
involved in protein synthesis and appears to be essential for
accurate translation (By similarity).
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
CC
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entities requires a license agreement (See <http://www.isb-sib.ch/>;
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CC
CC EMBL; J03187; AAA72191.1; --
DR PIR; B28152; R6MXL2.
DR InterPro; IPR001813; Ribosomal_SOS.
DR Pfam; PF0428; 608_ribosomal; 1.
KW Ribosomal protein.
SQ SEQUENCE 99 AA; 9818 MW; 94E91B61C201BED2 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 99;
Best Local Similarity 100.0%; Pred.No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G;

QY 138 APVAAAAP 145
Db |||||
60 APVAAAAP 67

RESULT 64

HSP3 RAT

ID HSP3 RAT STANDARD; PRT; 104 AA.

AC Q64256;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Sperm protamine P3.

GN PRM3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96341725; PubMed=8720108;

RA Schlueter G., Celik A.B., Obata R., Schlicker M., Hofferbert S.,

RA Schlung A., Adham I.M., Engel W.;

RT "Sequence analysis of the conserved protamine gene cluster shows t

it contains a fourth expressed gene.;"

RL Mol. Reprod. Dev. 43:1-6(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96103469; PubMed=8521723;

RA Schlueter G., Engel W.;

RT "The rat Prm3 gene is an intronless member of the protamine gene

cluster and is expressed in haploid male germ cells.;"

RL Cytogetet. Cell Genet. 71:352-355(1995).

CC -!- FUNCTION: Protamines substitute for histones in the chromatin

sperm during the haploid phase of spermatogenesis. They compac

CC sperm DNA into a highly condensed, stable and inactive comple

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- TISSUE SPECIFICITY: Testis.

CC
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CAA87063.1; -
 AAB35760.1; -
 protein; Nucleosome core; Spermatogenesis; DNA-binding;
 condensation; Nucleolar protein.
 45 69 ASP/GLU-RICH (HIGHLY ACIDIC).
 77 80 POLY-LEU
 14 AA; 11450 MW; 0EF1BFA0CEFC9CA CRC64;

1.5%; Score 8; DB 1; Length 104;
 identity 100.0%; Pred.No. 21;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 EDDDE 336
 ||||
 EDDDE 63

STANDARD; PRT; 105 AA.

Rel. 19, Created)
 Rel. 20, Last sequence update)
 Rel. 43, Last annotation update)
 bosomal protein P2.

discoideum (Slime mold).
 ctenozoa; Dictyosteliida; Dictyostelium.
 689;

1 N.A., AND PARTIAL SEQUENCE.

1921; PubMed=1840653;
 uncl E., Coloma A.;
 sequence of a cDNA encoding acidic ribosomal
 P2 in Dictyostelium discoideum.;
 Res. 19:1341-1341(1991).
 Plays an important role in the elongation step of
 synthesis.
 P1 and P2 exist as dimers at the large ribosomal subunit.
 phosphorylated.
 Y; Belongs to the L12P family of ribosomal proteins.

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CAA39655.1; -
 R6DOP2.
 R0001822; X56192.
 R001813; Ribosomal 60S.
 60s_ribosomal; I.
 tein; Phosphorylation.
 0
 15 AA; 10378 MW; 519FAB6679A5B840 CRC64;

1.5%; Score 8; DB 1; Length 105;
 identity 100.0%; Pred.No. 21;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 125
 ||||
 AAAAA 82

RESULT 66

RL12_ARCFU
 ID RL12_ARCFU STANDARD; PRT; 106 AA.
 AC O28780;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 50S ribosomal protein L12P.
 GN RPL12P OR AF1492
 OS Archaeoglobus fulgidus.
 CC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 CC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.
 Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.
 Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glöckle A., Zhi
 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback
 Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Venter J.C.;
 RA "The complete genome sequence of the hyperthermophilic, sulphate
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -!- FUNCTION: Seems to be the binding site for several of the fa
 involved in protein synthesis and appears to be essential fo
 accurate translation (By similarity).
 CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE000999; AAB89748.1; -
 DR PIR; C69436; C69436.
 DR TIGR; AF1492;
 DR InterPro; IPR001813; Ribosomal 60S.
 DR Pfam; PF00428; 60s_ribosomal; I.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 106 AA; 11037 MW; 4895667825663B1 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred.No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 118 APAAAAAA 125
 |||||
 Db 66 APAAAAAA 73

RESULT 67

RLA1_CAEEL
 ID RLA1_CAEEL STANDARD; PRT; 111 AA.
 AC P91913; Q9GRS9;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60S acidic ribosomal protein P1.
 GN RPA-1 OR Y37E3.7
 OS Caenorhabditis elegans.

azoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; peloderinae; Caenorhabditis.

39;

N.A.

1 N2;

Brodie J.;

3-1997) to the EMBL/GenBank/DBJ databases.

N.A.

1 N2;

R.; Doeber A.;

2-2000) to the EMBL/GenBank/DBJ databases.

2-2001) to the EMBL/GenBank/DBJ databases.

Plays an important role in the elongation step of

P1 and P2 exist as dimers at the large ribosomal subunit.

1: Belongs to the L12P family of ribosomal proteins.

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AA048625.1; -

1; AAK27864.1; -

1; CE26658.

001813; Ribosomal 60S.

001859; Ribosomal P2.

1: 60S ribosomal; 1.

06; RIBOSOMALP2.

ein.

12 42 Y -> N (IN REF. 1).

1; AA; 11283 MW; 6DB5B65BACFC04A6 CRC64;

1.5%; Score 8; DB 1; Length 111;

urity 100.0%; Pred. No. 22;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

AAA 125

|||

AAA 79

STANDARD; PRT; 112 AA.

1; 08, Created)

rel. 33, Last sequence update)

rel. 43, Last annotation update)

osomal protein P1 (RP21C) (Acidic ribosomal protein

C OR RPA2 OR RP21C OR CG4087.

anogaster (Fruit fly).

azoa; Arthropoda; Hexapoda; Insecta; Pterygota;

pterygota; Diptera; Brachycera; Muscomorpha;

rosophilidae; Drosophila.

17;

N.A.

110; PubMed=3122177;

1;

iced amino acid sequence of Drosophila rp21C, another

omal protein."

Res. 15:10064-10064(1987).

SEQUENCE FROM N.A.

RP MEDLINE=93273819; PubMed=8501137;

RX Olson P.F., Salo T., Garrison K., Fessler J.H.;

RA "Drosophila acidic ribosomal protein rpA2: sequence and

RT characterization."

RL J. Cell. Biochem. 51:353-359 (1993).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely; TISSUE=Head;

RX MEDLINE=22426066; PubMed=12537569;

RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan

RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan

RA Rubin G.M., Celnik S.E.;

RT "A Drosophila full-length cDNA resource."

RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

CC -1- FUNCTION: Plays an important role in the elongation step of

CC protein synthesis.

CC -1- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal sub

CC -1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.

CC -----

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CC -----

DR EMBL; Y00504; CAA68557.1; -

DR EMBL; S62170; AAB26902.1; -

DR EMBL; AE003589; AAF51499.1; -

[illegible]

eria; Cetartiodactyla; Suina; Suidae; Sus.
3, 9913, 10141;
N.A.

95; PubMed-2315322;
eeler M.B., Leiter A.B.;
ucture of the precursor and tissue distribution of the
ad. Sci. U.S.A. 87:2299-2303(1990).

56.
ne;
89; PubMed-8618828;
ernvall H., Mutt V., Sillard R.;
ve processing pathways for a preprohormone: a bioactive
in.";
ad. Sci. U.S.A. 92:11985-11989(1995).

-56.
34; PubMed-5465996;
s J.B., Magnusson S.;
porine secretin. The amino acid sequence.";
m. 15:513-519(1970).

-59 AND 92-131.
67; PubMed-2395872;
oernvall H., Mutt V.;
prosecretin: isolation of a secretin precursor from
ine.";
ad. Sci. U.S.A. 87:6781-6785(1990).

0-131.
20; PubMed-5978238;
Ondetti M.A., Levine S.D., Narayanan V.L.,
Sheehan J.T., Williams N.J., Sabo E.F.;
a heptacosapeptide amide with the hormonal activity of
1757-1758(1966).

-56.
02; PubMed-7250377;
Joernvall H., Mutt V.;
amino acid sequence of bovine secretin.";
:71-74(1981).

-56.
ellus;
63; PubMed-2340294;
uvin A., Gourlet P., Gossen D., de Neef P., Rathe J.,
Vandermeers-Piret M.-C., Vandermeers A., Christophe J.;
and amino acid sequence of vasoactive intestinal
de histidine isoleucineamide (1-27) and secretin from
stine of guinea pig.";
ys. Acta 1038:355-359(1990).

MR OF SECRETIN.
42; PubMed-2831051;
lges M., Bruenger A., Gronenborn A.M.;
l of the backbone conformation of secretin by restrained
mics on the basis of interproton distance data.";
m. 171:479-484(1988).

MR OF SECRETIN.
117; PubMed-2883029;
1; Bovermann G., Clore G.M.;
ly of the solution conformation of secretin. Resonance
secondary structure.";

RL FEBS Lett. 215:88-94(1987).
CC -!- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic ju;
CC and secretion of NaHCO(3)-rich bile and inhibits HCl producti;
CC the stomach.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PHARMACEUTICAL: Available under the name Secretin-Perring (Fe;
CC Pharmaceuticals).
CC -!- SIMILARITY: Belongs to the glucagon family.
CC
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CC
CC EMBL; M31496; AAA31121.1; -.
DR PIR; B35094; SEPG.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF0123; hormone2; 1.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation;
KW Cleavage on pair of basic residues; Signal; Pharmaceutical.
FT NON TER 1 1
FT SIGNAL <1 18
FT PEPTIDE 30 56
FT MOD_RES 56 56
SQ SEQUENCE 131 AA; 14277 MW; 1A24BDDA600E4E34 CRC64;
SECRETIN.
AMIDATION (G-57 PROVIDE AMIDE GROUP)
Query Match 1.5%; Score 8; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G;
QY 109 PAPPAPR 116
DB 22 PAPPAPR 29
|||||
RESULT 72
RS16_BRUME STANDARD; PRT; 134 AA.
ID RS16_BRUME AC Q8YJ59;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S16.
GN RPSP OR BMEI0227 OR BR1824.
OS Brucella melitensis, and
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459, 29461;
RN [1]
SEQUENCE FROM N.A.
RP SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Muej C., Lo
Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsma
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
RN [2]
SEQUENCE FROM N.A.
RP SPECIES=B.suis; STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.I
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 Tettelin H., Gill S.R., White O., Salzberg S.L.,
 Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 suis genome reveals fundamental similarities between
 ant pathogens and symbionts";
 Cad. Sci. U.S.A. 99:13148-13153(2002).
 Y: Belongs to the S16P family of ribosomal proteins.
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 ail to license@isb-sib.ch).

 5; AAL51409.1; -;
 3; RAN30719.1; -;
 AF3280.

 85; -; 1.
 .000307; Ribosomal S16.
 : Ribosomal S16; 1.
 791; Ribosomal_S16; 1.
 R000002; S16; 1.
 732; RIBOSOMAL_S16; FALSE_NEG.
 tein; Complete proteome.
 4 AA; 14529 MW; 5A716087E496C172 CRC64;

 1.5%; Score 8; DB 1; Length 134;
 arity 100.0%; Pred.No. 26;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

 AAAP 127
 |||||
 AAAP 127

 STANDARD; PRT; 136 AA.

 Rel. 30, Created)
 Rel. 30, Last sequence update)
 Rel. 42, Last annotation update)
 ition particle 14 kDa protein (SRP14) (18 kDa ALU RNA
 in).
 (Human).
 : Chordata; Craniata; Vertebrata; Euteleostomi;
 : Heria; Primates; Catarrhini; Hominidae; Homo.
 : 06;

 1 N.A.
 : 854; PubMed-7542942;
 : Mallaz M., Jeffers H., Strub K.;
 : subunit of the signal recognition particle (SRP) is
 : re than 20-fold excess over SRP in primate cells and
 : ily free but also in complex with small cytoplasmic Alu
 : all 6:471-484(1995).

 1 N.A.
 : 852; PubMed-8196634;
 : Nelson B., Bilyeu T., Hsu K., Darlington G.J.,
 : RNA-binding protein whose expression is associated with
 : of small cytoplasmic Alu RNA.";
 : ol. 14:3949-3959(1994).
 : : Signal-recognition-particle assembly has a crucial role
 : : ing secretory proteins to the rough endoplasmic reticulum
 : . SRP together with SRP14 and the Alu portion of the SRP
 : stitutes the elongation arrest domain of SRP. The complex

CC of SRP9 and SRP14 is required for SRP RNA binding.
 CC -!- SUBUNIT: Signal recognition particle consists of a 7S RNA mo
 CC of 300 nucleotides and six protein subunits: SRP72, SRP68, SR
 CC SRP19, SRP14 and SRP9.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the SRP14 family.

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 CC the European Bioinformatics Institute. There are no restriction
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 CC modified and this statement is not removed. Usage by and for
 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X73459; CAA51838.1; -;
 CC EMBL; U07857; AAA59066.1; -;
 CC PIR; A56082; A56062.
 CC PIR; S34196; S34196.
 CC FDB; I880; 08-NOV-00.
 CC DR SWISS-2DPAGE; P37108; HUMAN.
 CC DR Genew; HGNC:11299; SRP14.
 CC MIM; 600708; -;
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005786; C:signal recognition particle; TAS.
 CC GO; GO:0008312; F:7S RNA binding; TAS.
 CC GO; GO:0006613; P:cotranslational membrane targeting; TAS.
 CC InterPro; IPR003210; SRP14.
 CC InterPro; IPR009018; SRP9/14.
 CC Pfam; PF02290; SRP14; 1.
 CC Probdom; PD009170; SRP14; 1.
 CC Signal recognition particle; RNA-binding; 3D-structure.
 CC DOMAIN 108 136
 CC CONFLICT 124 124 A -> P (IN REF. 2).
 CC SEQUENCE 136 AA; 14544 MW; 2B5B2D1D77BA5E8E CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred.No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; (

QY 120 AAAAARAP 127

Db 110 AAAAARAP 117

RESULT 74

HEX9 ADE07

ID HEX9 ADE07 STANDARD; PRT; 138 AA.

AC P03283;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Hexon-associated protein (Protein IX).

GN PIX

OS Human adenovirus type 7, and

OS Human adenovirus type 3.

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenoviri

OX NCBI TaxID=10519, 45659;

RP [1] TaxID=10519, 45659;

RP SEQUENCE FROM N.A.

RC SPECIES=Human adenovirus type 7; STRAIN=Gomen;

RX MEDLINE=81261948; PubMed=6266923;

RA Dijkema R., Maat J., Dekker B.M.M., van Ormondt H., Boyer H.W.;

RT "The gene for polypeptide IX of human adenovirus type 7.";

RL Gene 13:375-385(1981).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=Human adenovirus type 3;

RX MEDLINE=81261949; PubMed=7262560;

RA Engler J.A.;

RT "The nucleotide sequence of the polypeptide IX gene of human

RT adenovirus type 3.";

RL Gene 13:387-394(1981).

11:33:41 2004

us-09-976-740-43.olig.rsp

ivum (Wheat).
ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
Triticum.
365;
1 N.A., AND REVISION TO 66.
in Pastore; TISSUE=Endosperm;
618; PubMed=10727084;
rtini L., Tucci M., Caporale C., Leonardi L.,
Bressan R.A., Veronese P., Buonocore V.;
id characterisation of wheat cDNA clones encoding PR4
301-307(1999).
22-146, AND VARIANT ASP-109.
in Pastore; TISSUE=Kernel;
2073; PubMed=8251057;
porale C., Poerio E., Facchiano A., Buonocore V.;
id sequence of a protein from wheat kernel closely
related to the wheat protein PR4.
12:379-386(1993).
ENCE, AND 3D-STRUCTURE MODELING.
in Pastore;
7016; PubMed=10398366;
Caruso C., Facchiano A., Nobile M., Leonardi L.,
Colonna G., Buonocore V.;
modelled structure of wheatw1 by controlled proteolysis
analysis of unfractionated digestion mixtures.";
192-204(1999).
CTIVITY.
5702; PubMed=8836588;
porale C., Chilosi G., Vacca F., Bertini L., Magro P.,
Buonocore V.;
and antifungal properties of a pathogenesis-related
wheat kernel.";
15:35-44(1996).
Shows antifungal activity towards B.cinerea and towards
specific pathogenic fungi F.culmorum and F.graminearum
1 and 2).
Monomer.
RY: Belongs to the barwin family.
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98; CAA06856.1; -.
T06485.
7-JUL-99.
R001153; Barwin.
R009009; Barwin_like.
7; Barwin, 1.
602; BARWIN.
4535; Barwin, 1.
0771; BARWIN_1; 1.
0772; BARWIN_2; 1.
e; Fungicide, Pyrolidone carboxylic acid; Signal;
1 21
22 146 WHEATWIN1.
22 22 PYRROLIDONE CARBOXYLIC ACID.
22 146 WIN.
52 84 BY SIMILARITY.
73 107 BY SIMILARITY.
87 144 BY SIMILARITY.

FT VARIANT 109 109 N -> D.
SQ SEQUENCE 146 AA; 15634 MW; F23B79E93CC2D7AA CRC64;
Query Match 1.5%; Score 8; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAAATA 158
Db 14 AAAAAATA 21
RESULT 78
WHW2 WHEAT
ID WHW2 WHEAT STANDARD; PRT; 148 AA.
AC O6433;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wheatwin2 precursor (Pathogenesis-related protein 4b).
GN PR4B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poide
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. San Pastore; TISSUE=Endosperm;
RX MEDLINE=20189618; PubMed=10727084;
RA Caruso C., Bertini L., Tucci M., Caporale C., Leonardi L.,
RA Saccardo F., Bressan R.A., Veronese P., Buonocore V.;
RT "Isolation and characterisation of wheat cDNA clones encoding PR
RT proteins.";
RL DNA Seq. 10:301-307(1999).
RN [2]
RP SEQUENCE OF 24-148, AND ANTIFUNGAL ACTIVITY.
RC STRAIN=cv. San Pastore; TISSUE=Kernel;
RX MEDLINE=96435702; PubMed=8838588;
RA Caruso C., Caporale C., Chilosi G., Vacca F., Bertini L., Magro
RA Poerio E., Buonocore V.;
RT "Structural and antifungal properties of a pathogenesis-related
RT protein from wheat kernel.";
RL J. Protein Chem. 15:35-44(1996).
CC -!- FUNCTION: Shows antifungal activity towards B.cinerea and to
CC the wheat-specific pathogenic fungi F.culmorum and F.gramine
CC (groups 1 and 2).
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the barwin family.
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CC the European Bioinformatics Institute. There are no restrictio
CC use by non-profit institutions as long as its content is i
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ006099; CAA06857.1; -.
CC PIR; T06486; T06486.
CC HSP; P28814; LBW4.
CC InterPro; IPR001153; Barwin.
CC InterPro; IPR009009; Barwin_like.
CC Pfam; PF00967; Barwin, 1.
CC PRINTS; PR00602; BARWIN.
CC ProDom; PD004535; Barwin, 1.
CC PROSITE; PS00771; BARWIN_1; 1.
CC PROSITE; PS00772; BARWIN_2; 1.
CC Plant defense; Fungicide; Pyrolidone carboxylic acid; Signal.
KW SIGNAL 1 23
FT CHAIN 24 148 WHEATWIN2.
FT MOD RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
FT DOMAIN 24 148 WIN.

14 86 BY SIMILARITY.
15 109 BY SIMILARITY.
16 146 BY SIMILARITY.
17 111 N -> D (IN REF. 2).
18 AA; 15867 MW; 3D4EA32E085B8C1 CRC64;
19 1.5%; Score 8; DB 1; Length 148;
20 identity 100.0%; Pred. No. 28;
21 conservative 0; Mismatches 0; Indels 0; Gaps 0;
22
23 DATA 158
24 |||||
25 DATA 23
26
27 STANDARD; PRT; 149 AA.
28
29 rel. 31, Created)
30 rel. 31, Last sequence update)
31 rel. 42, Last annotation update)
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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S16.
GN RPS16 OR CC3652.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19689 / Cbl5;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whit
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
CC
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CC
CC EMBL; AE006023; AAK25614.1; -
DR PIR; B87702; B87702.
DR HSSP; P80379; LEWM.
DR TIGR; CC3652;
DR HAMAP; MF 00385; -; 1.
DR InterPro; IPR000307; Ribosomal_S16.
DR Pfam; PF00886; Ribosomal_S16; 1.
DR ProDom; PD003791; Ribosomal_S16; 1.
DR TIGRFAMs; TIGR00002; S16; 1-
DR PROSITE; PS00732; RIBOSOMAL_S16; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 165 AA; 17605 MW; ED46FC2798C5BE1C CRC64;
Query Match 1.5%; Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 120 AAAAAAAP 127
Db 135 AAAAAAAP 142
|||||
RESULT 81
OM19 BRUME
ID - OM19 BRUME STANDARD; PRT; 177 AA.
AC Q44663; Q44699;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer membrane lipoprotein omp19 precursor (Minor outer membrane
DE protein omp19) (19-kDa OMP) (18 kDa immunoreactive antigen).
GN OMP19 OR BME10135 OR BR1930.
OS Brucella melitensis,
OS Brucella suis, and
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459, 29461, 235;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.abortus; STRAIN=544 / Biovar 1;

Complete proteome; Palmitate.	1	20	PROBABLE.
FT SIGNAL	21	177	OUTER MEMBRANE LIPOPROTEIN OMP19.
FT CHAIN	21	177	N-palmitoyl cysteine (Probable).
FT LIPID	21	21	S-diacylglycerol cysteine (Probable).
FT LIPID	21	21	SR -> IG (IN STRAIN 2308).
FT VARIANT	176	177	
FT SEQUENCE	177 AA;	17604 MW;	8038D5ABD87019E2 CRC64;
Query Match	1.5%;	Score 8;	DB 1; Length 177;
Best Local Similarity	100.0%;	Pred. No. 33;	
Matches	8;	Conservative	0; Mismatches 0; Indels 0;
QY	133 PPPPPAPV 140		
DbB	34 PPPPPAPV 41		
RESULT 82			
REMS_CHICK			
ID	REMS_CHICK	STANDARD;	PRT; 200 AA.
AC	Q9W6I1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DDT	16-OCT-2001 (Rel. 40, Last sequence update)		
DDT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	RNA-binding protein with multiple splicing homolog (RBP-MS) (HEA: RRM Expressed Sequence) (Hermes).		
DE	RRPMS OR HERMES.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasian		
OC	Gallus.		
OC	NCBI_TaxID=9031;		
CC	[1]		
CC	SEQUENCE FROM N.A.		
CC	TISSUE=Heart;		
CC	MEDLINE=99157599; PubMed=10096065;		
CC	Gerber W.V., Yatskevych T.A., Antin P.B., Correia K.M., Conlon J		
CC	Krieg P.A.;		
CC	"The RNA-binding protein gene, hermes, is expressed at high level		
CC	the developing heart.";		
CC	Mech. Dev. 80:77-86(1999).		
CC	-!- FUNCTION: May bind RNA.		
CC	-!- TISSUE SPECIFICITY: Expressed in developing heart.		
CC	-!- DEVELOPMENTAL STAGE: mRNA already detected at stage 7-8 in tl		
CC	cardiogenic mesoderm, and become almost undetectable in the		
CC	curvature of the ventricular region whereas remaining high in		
CC	developing atrial regions.		
CC	-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; AF129933; AAD30273.1; -.		
DR	InterPro; IPR000504; RNA_rec_mot.		
DR	Pfam; PF00076; rrm; 1.		
DR	SMART; SM00360; RRM; 1.		
DR	PROSITE; PS0102; RRM; 1.		
DR	PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.		
DR	RNA-binding.		
FW	DOMAIN 22 99 RNA-BINDING (RRM).		
FT	DOMAIN 169 176 POLY-ALA.		
FT	SEQUENCE 200 AA; 21856 MW; 4093B3C780B8C1DF CRC64;		
QY			
Query Match	1.5%;	Score 8;	DB 1; Length 200;
Best Local Similarity	100.0%;	Pred. No. 36;	
Matches	8;	Conservative	0; Mismatches 0; Indels 0;
QY	119 PAAAAAAA 126		

||||
AAAA 175

STANDARD; PRT; 205 AA.

(rel. 29, Last sequence update)
(rel. 43, Last annotation update)
Reaction center subunit II, chloroplast precursor
20 kDa subunit (PSI-D).

(Barley).
Chlorophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
Triticum.

N.A.
Tissue: TISSUE=Seedling;
296; PubMed=8278501;

Sequencing of a full-length cDNA clone encoding the
photosystem I from barley.
101:335-336(1993).

1-82; 118-133; 156-195 AND 203-205.

Protein;
Hoej P.B., Svendsen I., Moeller B.L.;
acid sequence of two nuclear-encoded photosystem I
from barley.
Acta 933:501-505(1988).

PSAD can form complexes with ferredoxin and ferredoxin-
thylakoid docking protein.
PSAD may

LOCATION: Chloroplast thylakoid membrane, stromal

By light.
Belongs to the psad family.

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European Bioinformatics Institute. There are no restrictions
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derivative of the original. This statement is not removed. Usage
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AAAA18567.1; -.

02247.

03685; Psad.

Psad; 1.

Photosystem I; Chloroplast; Transit peptide;

ubane.

1 43 CHLOROPLAST.

14 205 PHOTOSYSTEM I REACTION CENTER SUBUNIT II.

30 80 G -> GG (IN REF. 2).

32 82 T -> G (IN REF. 2).

38 118 R -> P (IN REF. 2).

41 191 S -> F (IN REF. 2).

5 AA; 21933 MW; 5B6A2CAD81D5E029 CRC64;

1-58; Score 8; DB 1; Length 205;

Identity 100.0%; Pred. No. 37;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPA 189

||||

APPA 57

RESULT 84

YNP2 CAEEL STANDARD; PRT; 205 AA.

AC P34535;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical protein T05G5.2 in chromosome III.

GN T05G5.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=94150718; PubMed=79063398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kireten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Staden R.

RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

RA Wohldman P.

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of

RT elegans."

RL Nature 368:32-38(1994).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL out

CC the European Bioinformatics Institute. There are no restriction

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CC modified and this statement is not removed. Usage by and for c

CC entities requires a license agreement (See <http://www.isb-sib.ch/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z27079; CAA81583.1; -.

DR PIR; S41002; S41002.

DR WormPep; T05G5.2; CE00314.

DR InterPro; IPR001092; HLH_basic.

DR Pfam; PF00010; HLH; 1.

DR SMART; SM00353; HLH; 1.

DR PROSITE; PS00888; HLH; 1.

KW Hypothetical protein; Nuclear protein.

FT DOMAIN 38 89 HELIX-LOOP-HELIX MOTIF (BY SIMILARIT

SQ SEQUENCE 205 AA; 22691 MW; 577E59E04268FA1C CRC64;

Query Match 1.5%; Score 8; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 132 APPPPAP 139

Db 176 APPPPAP 183

RESULT 85

HS27 CANFA

ID HS27 CANFA STANDARD; PRT; 209 AA.

AC P42929;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Heat shock 27 kDa protein (HSP 27).

GN HSPB1 OR HSP27.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

heria; Carnivora; Fissipedia; Canidae; Canis.
15;
[N.A.
smooth muscle;
379; PubMed=7665102;
Gerthoffer W.T., Hickey E., Weber L.A.;
sequencing of a cDNA encoding the canine HSP27 protein.";
306(1995).
INVOLVED IN STRESS RESISTANCE AND ACTIN ORGANIZATION.
Y: Belongs to the small heat shock protein (HSP20)
-----
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-----
AA087172.1; -
JC4244. Crystallin_alpha.
001436; Hsp20.
002068; Hsp20.
008978; HSP20_chap.
; HSP20; 1.
99; ACRYSTALIN.
031; HSP20; 1.
phosphorylation.
15 15 PHOSPHORYLATION (BY PKC AND PKA)
86 86 (BY SIMILARITY).
PHOSPHORYLATION (BY PKC AND PKA)
09 AA; 22939 MW; 7E59F696D8C7F1BD CRC64;
1.5%; Score 8; DB 1; Length 209;
arity 100.0%; Pred. No. 38;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 73
STANDARD; PRT; 211 AA.
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
group protein 1-like 10 (HMG-1110).
(Human).
razo; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;
A.N.A.
7165; PubMed=10591208;
nt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
ink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
Bailey J., Barlow K.F., Bates K.N., Beasly O.P.,
lakey S.E., Bridgeman A.M., Buck D., Burgess J.,
Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
obley V.E., Cole C.G., Collier R.E., Connor R.,
rby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
ockree C., Doddsworth S.J., Durbin R.M., Ellington A.G.,
ey J.M., Fleming K., French L., Garner A.A.,
z., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
all-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
ones M.C., Kershaw J., Kimberley A.M., King A.,

```

```

RA Laird G.K., Langford C.P., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.
RA Phillips S.H., Plumb R.W., Ramsay H., Ransey Y., Rogers L., Ross
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Stuston J.E., Swann R.M.,
RA Vaudin M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming I
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimi:
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan I
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., So:
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Letreille P., Layman D., Ozersky P., Rohlfing
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransoni I., Tapia I., Bruder
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box domains.
CC
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CC
CC EMBL; Z95115; CAB62951.1; -.
CC HSP; P07156; INHN.
CC Genew; HGNC:4994; HMG1L10.
CC InterPro; IPR000135; Highmoblty_12.
CC InterPro; IPR000910; HMG_12_box.
CC Pfam; PF00505; HMG_box; 2.
CC PRINTS; PR00886; HIGHMOBLTY12.
CC SMART; SM00398; HMG; 2.
CC PROSITE; PS00353; HMG_BOX_1; 1.
CC PROSITE; PS0118; HMG_BOX_2; 2.
CC Nuclear protein; Chromosomal HMG BOX 1.
CC DNA_BIND 9 79
CC FT DNA_BIND 95 163 HMG_BOX_2.
CC FT DOMAIN 186 211 ASP/GLU-RICH (ACIDIC).
CC SQ SEQUENCE 211 AA; 24218 MW; 2A53BA2AE6DF7CD CRC64;
Query Match 1.5%; Score 8; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 336 EDEDEDD 343
Db 203 EDEDEDD 210
RESULT 87
RSE CORGL STANDARD; PRT; 211 AA.
ID -RSE_CORGL

```

rel. 41, Created)
 rel. 41, Last sequence update)
 rel. 41, Last annotation update)
 protein S5.
 10.
 m glutamicum (Brevibacterium flavum).
 mbacteria; Actinobacteridae; Actinomycetales;
 eae; Corynebacteriaceae; Corynebacterium.
 8;
 N.A.
 3032 / DSM 20300 / NCIB 10025;
 omic sequence of Corynebacterium glutamicum ATCC 13032.;
 f-2002) to the EMBL/GenBank/DBJ databases.
 With S4 and S12 plays an important role in translational
 (By similarity).
 Located at the back of the 30S subunit body where it
 s the conformation of the head with respect to the body
 arity).
 part of the 30S ribosomal subunit. Contacts proteins S4
 / similarity).
 ie N-terminal domain interacts with the head of the 30S
 the C-terminal domain interacts with the body and
 protein S4. The interaction surface between S4 and S5 is
 in control of translational fidelity.
 f: Contains 1 S5 DRDM domain.
 f: Belongs to the S5P family of ribosomal proteins.

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 5; BAB97933.1; -.
 07; -. 1.
 000851; Ribosomal_S5.
 005712; Ribosomal_S5_b/o.
 005324; Ribosomal_S5_C.
 ; Ribosomal_S5; 1.
 ; Ribosomal_S5_C; 1.
 201021; rpsE_bact; 1.
 585; RIBOSOMAL_S5; 1.
 381; S5_DRDM; 1.
 -ein; RNA-binding; rRNA-binding; Complete proteome.
 14 107 S5_DRDM.
 1 AA; 22670 MW; D9816AE5550A3D3A CRC64;

 1.5%; Score 8; DB 1; Length 211;
 arity 100.0%; Pred. No. 38;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 ARPV 249
 |||||
 ARPV 147

 STANDARD; PRT; 214 AA.
 Rel. 15, Created)
 Rel. 15, Last sequence update)
 Rel. 42, Last annotation update)
 ribonucleoprotein associated protein B (snRNP-B) (Sm
 m-B) (Smb) (SM11) (Fragment).
 icus (Rat).
 tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rat
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9009348; PubMed=2532363;
 RA Li S., Klein E.S., Russo A.F., Simmons D.M., Rosenfeld M.G.;
 RT "Isolation of cDNA clones encoding small nuclear ribonucleopartic
 RT associated proteins with different tissue specificities.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9778-9782(1989).
 CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May ha
 CC functional role in the pre-mRNA splicing or in snRNP structur
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: HEART, AND LESS IN BRAIN, PITUITARY, & LI
 CC -!- SIMILARITY: BELONGS TO THE snRNP SMB/SMN FAMILY.
 CC -----
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 CC the European Bioinformatics Institute. There are no restriction
 CC use by non-profit institutions as long as its content is in
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M29295; AAA2159.1; -.
 DR PIR; B34503; B34503.
 DR HSP; P14678; ID3B.
 DR InterPro; IPR001163; snRNP_Sm.
 DR Pfam; PF01423; LSM; 1.
 DR SMART; SM00651; Sm; 1.
 KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
 FT NON TER 1 1
 FT DOMAIN 158 211 REPEAT-RICH REGION.
 FT REPEAT 158 164
 FT REPEAT 174 179
 FT REPEAT 199 204
 FT REPEAT 205 211
 FT SEQUENCE 214 AA; 21594 MW; 3FC57DE1BF68E603 CRC64;
 SQ

 Query Match 1.5%; Score 8; DB 1; Length 214;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 OY 151 AAAAAATA 158
 |||||
 DB 135 AAAAAATA 142

 RESULT 89
 HANI_HUMAN
 ID HANI_HUMAN STANDARD; PRT; 215 AA.
 AC O96004;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Heart- and neural crest derivatives-expressed protein 1
 DE (Extraembryonic tissues, heart, autonomic nervous system and neuro
 DE crest derivatives-expressed protein 1) (eHAND).
 GN HAND1 OR EHAND.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99132638; PubMed=9931445;
 RA Knoefler M., Meinhardt G., Vasicek R., Husslein P., Egarter C.;
 RT "Molecular cloning of the human Hand1 gene/cDNA and its tissue-
 RT restricted expression in cytotrophoblastic cells and heart.";
 RL Gene 224:77-86(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

18257; PubMed=12477932;
 L.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 J.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Lton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 W., Touchman J.W., Green E.D., Dickson M.C.,
 C., Grimwood J., Schmutz J., Myers R.M.,
 Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 Schein J.E., Jones S.J.M., Matra M.A.;
 and initial analysis of more than 15,000 full-length
 use cDNA sequences.";
 Acad. Sci. U.S.A. 99:16899-16903 (2002).
 : Plays an essential role in early trophoblast
 tiation and in cardiac morphogenesis. In the adult, could
 red for ongoing expression of cardiac-specific genes.
 e DNA sequence 5'-NRTCTG-3' (noncanonical E-box) (By
 ty).
 Efficient DNA binding requires dimerization with another
 tein. Forms homodimers and heterodimers with TCF3 gene
 E12 and E47, HAND2 and HEY1, HEY2 and HEYL (hairly-related
 ption factors) (By similarity).
 PECIFICITY: Heart.
 TY: Contains 1 basic helix-loop-helix (bHLH) domain.

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 12; AAD19283.1; -
 56; AAD19280.1; -
 90; AAD21190.1; -
 1373; -
 1807; HAND1.

 00; F:transcription factor activity; TAS.
 07; P:heart development; TAS.
 56; P:transcription from Pol II promoter; TAS.
 2001092; HLH_basic.
 0; HLH; 1.
 53; HLH; 1.
 0888; HLH; 1.
 (protein; transcription regulation; DNA-binding;
 sin.
 9 17 POLY-HIS.
 64 71 POLY-ALA.
 94 106 BASIC DOMAIN.
 07 150 HELIX-LOOP-HELIX MOTIF.
 5 AA; 23627 MW; 7ED98EA081A8D6BA CRC64;
 1.5%; Score 8; DB 1; Length 215;
 arity 100.0%; Pred. No. 38;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AATA 158
 |||||
 AATA 71

RSMB_MOUSE STANDARD; PRT; 231 AA.
 P27048;
 01-AUG-1992 (Rel. 23, Created)
 01-AUG-1992 (Rel. 23, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Small nuclear ribonucleoprotein associated protein B (snRNP-B)
 protein B) (Sm-B) (Smb).
 GN SNRPB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92290275; PubMed=1376292;
 RX Griffith A., deJonge E., Huang S., Ohosone Y., Craft J.E.;
 RT "The murine gene encoding the highly conserved Sm B protein cont
 a nonfunctional alternative 3' splice site.";
 RL Gene 114:193-201 (1992).
 CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May b
 functional role in the pre-mRNA splicing or in snRNP structu
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.

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 entities requires a license agreement (See <http://www.isb-sib.ch>
 or send an email to license@isb-sib.ch).

 EMBL; M58761; AAA40119.1; -
 DR PIR; I53659; I53659.
 DR HSSP; P14678; ID3B.
 DR MGD; MGI:98342; Snrpb.
 DR InterPro; IPR001163; snRNP_Sm.
 DR Pfam; PF01423; LSM; 1.
 DR SMART; SM00651; Sm; 1.
 DR KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
 FT DOMAIN 175 228 REPEAT-RICH REGION.
 FT REPEAT 175 181
 FT REPEAT 191 196
 FT REPEAT 216 221
 FT REPEAT 222 228
 SQ SEQUENCE 231 AA; 23656 MW; 5CB0BE7E20B93D4A CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 231;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 151 AAAAAATA 158
 |||||
 Db 152 AAAAAATA 159

 RESULT 91
 UCRI_NEUCR
 ID UCRI_NEUCR STANDARD; PRT; 231 AA.
 AC P07056;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondri
 precursor (EC 1.10.2.2) (Rieske iron-sulfur protein) (RISP).
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203899; PubMed=2986972;
 Harnisch U., Weiss H., Sebald W.;

structure of the iron-sulfur subunit of ubiquinol-reductase from Neurospora, determined by cDNA and gene

em. 149:95-99(1985).

Component of the ubiquinol-cytochrome c reductase complex III or cytochrome b-c1 complex), which is a

ry chain that generates an electrochemical potential

o ATP synthesis.

ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2

chrome c.

Binds 1 2Fe-2S iron sulfur cluster per subunit (By

Y).

Fungal bc1 complex contains 10 subunits; 3 respiratory

2 core proteins and 5 low-molecular weight proteins.

AR LOCATION: Mitochondrial inner membrane.

EOUS: The Rieske protein is a high potential 2Fe-2S

Y: Belongs to the Rieske family.

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ail to license@isb-sib.ch).

DE (Sm protein B') (Sm-B') (Smb') (snRNP-B').

GN SNRNP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasian

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20027344; PubMed=10556313;

RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves

RA McCarrey J.R., Nicholls R.D.;

RT "Concerted regulation and molecular evolution of the duplicated

RT SNRNP-B' and SNRNP loci.";

RL Nucleic Acids Res. 27:4577-4584(1999).

CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May ha

CC functional role in the pre-mRNA splicing or in snRNP structu

CC similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.

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CC between the Swiss Institute of Bioinformatics and the EMBL out

CC the European Bioinformatics Institute. There are no restriction

CC use by non-profit institutions as long as its content is ir

CC modified and this statement is not removed. Usage by and for c

CC entities requires a license agreement (See <http://www.isb-sib.ch/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF134830; AAD54495.1; -.

DR HSP; P14678; 1D3B.

DR InterPro; IPR001163; snRNP_Sm.

DR Pfam; PF01423; LSM; 1.

DR SMART; SM00651; Sm; 1.

DR SMART; SM00651; Sm; 1.

KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.

FT DOMAIN 175 236

FT REPEAT 175 181

FT REPEAT 191 196

FT REPEAT 216 221

FT REPEAT 222 228

FT REPEAT 230 236

SQ SEQUENCE 240 AA; 24588 MW; 2988181A0F54D581 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 240;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 151 AAAAAATA 158

Db 152 AAAAAATA 159

RESULT 93

RSMB_ERIEU STANDARD; PRT; 240 AA.

AC Q9TU67; Q9TU64;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Small nuclear ribonucleoprotein associated protein B' (snRNP-B')

DE (Sm protein B') (Sm-B') (Smb') (snRNP-B').

GN SNRNP.

OS Brinaceus europaeus (Western European hedgehog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceae; Erinace

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20027344; PubMed=10556313;

RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves J.

RA McCarrey J.R., Nicholls R.D.;

RT "Concerted regulation and molecular evolution of the duplicated

RT SNRNP-B' and SNRNP loci.";

is Res. 27:4577-4584 (1999).
 is Associated with sn-RNP U1, U2, U4/U6 and U5. May have a
 al role in the pre-mRNA splicing or in snRNP structure (By
 cy).
 IAR LOCATION: Nuclear.
 TY: BELONGS TO THE snRNP SMB/SMN FAMILY.

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 mail to license@isb-sib.ch).

 126; AAD54481.1; -;
 129; AAD54484.1; -;
 ; 1D3B.
 3; LSM; 1.
 51; Sm; 1.
 ein; Ribonucleoprotein; RNA-binding; Repeat.
 REPEAT-RICH REGION.
 175 236
 175 181
 191 196
 216 221
 222 228
 230 236
 40 AA; 24592 MW; F2E1D5E1A61A170 CRC64;
 1.5%; Score 8; DB 1; Length 240;
 larity 100.0%; Pred. No. 42;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAATA 158
 |||||
 AAATA 159

 STANDARD; PRT; 240 AA.
 90; Q9U1S5;
 (Rel. 14, Created)
 (Rel. 20, Last sequence update)
 (Rel. 42, Last annotation update)
 r ribonucleoprotein associated proteins B and B' (snRNP-B)
 B/B') (Sm-B/Sm-B') (SMB/SMB').
 PB1 OR COD.
 (Human).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 theria; Primates; Catarrhini; Hominidae; Homo.
 506;
 N.A. (ISOFORMS B AND B').
 9988; PubMed:2531083;
 Winkel I., Zijlstra-Baalbergen J., Smeenk R.,
 a snRNP proteins B and B' differ only in their carboxy-
 .";
 53-3860 (1989).
 N.A.
 id carcinoma;
 0326; PubMed:2522186;
 McAllister G., Ohosone Y., Hardin J.A., Lerner M.R.;
 a of snRNP-associated Sm-autoantigens: human N, rat N and
 ;
 Res. 17:1733-1743 (1989).
 McAllister G., Ohosone Y., Hardin J.A., Lerner M.R.;
 Res. 17:6777-6777 (1989).

RN SEQUENCE FROM N.A.
 RP Gray T.A., Martone D.L., Schaldach M.A., McCarrey J.R., Nicholl;
 RA "Concerted regulation and molecular evolution of the duplicated
 RT and snRNP loci";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RP MEDLINE=11780052;
 RX DELoukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.;
 RA Jones M., Stavrides G., Almeida J.P., Sabbage A.K., Bagguely C.;
 BA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee (,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johns
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawl
 RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell (,
 RA Marsh V.L., Martin S.L., McConachie L.J., Mclay K., McMurray A.
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims
 RA Suce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.B.
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams
 RA Wilming I., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 2
 RL Nature 414:865-871 (2001).
 RN [6]
 RN SEQUENCE OF 8-240 FROM N.A.
 RX MEDLINE=90308305; PubMed=1694885;
 RA Elkon K.B., Hines J.J., Chu J.-L., Parnassa A.;
 RT "Epitope mapping of recombinant Hela SMB and B' peptides obtaine
 RL the polymerase chain reaction.";
 J. Immunol. 145:636-643 (1990).
 RN [7]
 RN SEQUENCE OF 209-240 FROM N.A.
 RX MEDLINE=91153665; PubMed=1825643;
 RA Chu J.-L., Elkon K.B.;
 RT "The small nuclear ribonucleoproteins, SMB and B', are products
 RL single gene.";
 Gene 97:311-312 (1991).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99148270; PubMed=10025403;
 RA Kambach C., Walke S., Young R., Avis J.M., de la Fortelle E.,
 RA Raker V.A., Luhrmann R., Li J., Negai K.;
 RT "Crystal structures of two Sm protein complexes and their implic
 RL for the assembly of the spliceosomal snRNPs.";
 Cell 96:375-387 (1999).
 CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May h
 CC functional role in the pre-mRNA splicing or in snRNP structu
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=SM-B';
 CC IsoID=P14678-1; Sequence=Displayed;
 CC Name=SM-B;
 CC IsoID=P14678-2; Sequence=VSP_005914;
 CC -!- DISEASE: Patients with the autoimmune disease systemic lupus
 CC erythematosus (SLE) have autoantibodies directed against som
 CC the individual snRNP polypeptides. The most common autoantig
 CC called Sm. B/b' bear Sm epitopes.
 CC -!- SIMILARITY: BELONGS TO THE snRNP SMB/SMN FAMILY.
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to error

1 prediction.

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CAB57867.1; -;
 CAB57868.1; -;
 CAA33902.1; -;
 5; AAD54488.1; ALT SEQ.
 2; AAD54488.1; JOINED.
 3; AAD54488.1; JOINED.
 4; AAD54488.1; JOINED.
 0; CAB46715.1; -;
 0; CAB46714.1; -;
 AAA36578.1; -;
 AAA36579.1; -;
 CAA37170.1; -;
 CAA37171.1; -;
 S09377.
 -DEC-99.
 1153; SNRNP.
 -;
 -;
 2; C:small nuclear ribonucleoprotein complex; TAS.
 1; C:spliceosome complex; TAS.
 1; P:mRNA splicing; TAS.
 001163; snRNP_Sm.
 1; Sm; 1.
 1; LSM; 1.
 in; Ribonucleoprotein; RNA-binding; Repeat;
 s erythematous; Alternative splicing; 3D-structure.
 75 236 REPEAT-RICH REGION.
 75 181
 91 196
 16 221
 22 228
 30 236
 30 240
 PPPQMRPPRP -> LL (in isoform SM-B).
 /FTid=VSP_005914.
 3 4
 6 10
 11 14
 16 21
 22 23
 26 34
 36 37
 40 51
 56 57
 51 72
 74 76
 77 84
) AA; 24610 MW; F2E1D5E11A601170 CRC64;
 1.5%; Score 8; DB 1; Length 240;
 irity 100.0%; Pred. No. 42;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AATA 158
 |||||
 AATA 159
 STANDARD; PRT; 240 AA.
 (rel. 40, Created)
 (rel. 40, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
 Small nuclear ribonucleoprotein associated protein B' (snRNP-B')
 (Sm protein B') (Sm-B') (SMB') (snRNP-B')
 SNRNP.
 OS Monodelphis domestica (Short-tailed grey opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
 NCBI_TaxID=13616;
 (1)_TaxID=13616;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20027344; PubMed=10556313;
 RA Gray T.A., Smithwick M.J., Schaldach M.A., Martone D.L., Graves
 RA McCarrey J.R., Nicholls R.D.,
 RT "Concerted regulation and molecular evolution of the duplicated
 SNRNP/B and SNRNP loci";
 RL Nucleic Acids Res. 27:4577-4584(1999).
 CC -!- FUNCTION: Associated with sn-RNP U1, U2, U4/U6 and U5. May ha
 CC functional role in the pre-mRNA splicing or in snRNP structu
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE SNRNP SMB/SMN FAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF134827; AAD54482.1; -;
 DR HSSP; P14678; 1D3B.
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam; PF01423; LSM; 1.
 DR SMART; SM00651; Sm; 1.
 KW Nuclear protein; Ribonucleoprotein; RNA-binding; Repeat.
 FT DOMAIN 175 236 REPEAT-RICH REGION.
 FT REPEAT 175 181
 FT REPEAT 191 196
 FT REPEAT 216 221
 FT REPEAT 222 228
 FT REPEAT 230 236
 SQ SEQUENCE 240 AA; 24542 MW; 2498CFABE943C828 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 240;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 Qy 151 AAAAAATA 158
 |||||
 Db 152 AAAAAATA 159
 |||||
 RESULT 96
 YPBE_BACSU
 ID YPBE_BACSU STANDARD; PRT; 240 AA.
 AC P50731;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein ypbe.
 GN YPBE OR BSU23000.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / Marburg;
 RX MEDLINE=96349105; PubMed=8760912;
 RA Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
 RA Serron P.;
 RT "Sequence analysis of the Bacillus subtilis chromosome region bet
 RT the serA and kds loci cloned in a yeast artificial chromosome.";

R1	R2	R3	R4	R5	R6	R7	R8	R9	R10	R11	R12	R13	R14	R15	R16	R17	R18	R19	R20	R21	R22	R23	R24	R25	R26	R27	R28	R29	R30	R31	R32	R33	R34	R35	R36	R37	R38	R39	R40	R41	R42	R43	R44	R45	R46	R47	R48	R49	R50	R51	R52	R53	R54	R55	R56	R57	R58	R59	R60	R61	R62	R63	R64	R65	R66	R67	R68	R69	R70	R71	R72	R73	R74	R75	R76	R77	R78	R79	R80	R81	R82	R83	R84	R85	R86	R87	R88	R89	R90	R91	R92	R93	R94	R95	R96	R97	R98	R99	R100	R101	R102	R103	R104	R105	R106	R107	R108	R109	R110	R111	R112	R113	R114	R115	R116	R117	R118	R119	R120	R121	R122	R123	R124	R125	R126	R127	R128	R129	R130	R131	R132	R133	R134	R135	R136	R137	R138	R139	R140	R141	R142	R143	R144	R145	R146	R147	R148	R149	R150	R151	R152	R153	R154	R155	R156	R157	R158	R159	R160	R161	R162	R163	R164	R165	R166	R167	R168	R169	R170	R171	R172	R173	R174	R175	R176	R177	R178	R179	R180	R181	R182	R183	R184	R185	R186	R187	R188	R189	R190	R191	R192	R193	R194	R195	R196	R197	R198	R199	R200	R201	R202	R203	R204	R205	R206	R207	R208	R209	R210	R211	R212	R213	R214	R215	R216	R217	R218	R219	R220	R221	R222	R223	R224	R225	R226	R227	R228	R229	R230	R231	R232	R233	R234	R235	R236	R237	R238	R239	R240	R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300	R301	R302	R303	R304	R305	R306	R307	R308	R309	R310	R311	R312	R313	R314	R315	R316	R317	R318	R319	R320	R321	R322	R323	R324	R325	R326	R327	R328	R329	R330	R331	R332	R333	R334	R335	R336	R337	R338	R339	R340	R341	R342	R343	R344	R345	R346	R347	R348	R349	R350	R351	R352	R353	R354	R355	R356	R357	R358	R359	R360	R361	R362	R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385	R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408	R409	R410	R411	R412	R413	R414	R415	R416	R417	R418	R419	R420	R421	R422	R423	R424	R425	R426	R427	R428	R429	R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452	R453	R454	R455	R456	R457	R458	R459	R460	R461	R462	R463	R464	R465	R466	R467	R468	R469	R470	R471	R472	R473	R474	R475	R476	R477	R478	R479	R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502	R503	R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R5
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142: 2005-2016 (1996).

M N A.

4033; PubMed=9384377;
asawara N., Moszer I., Albertini A.M., Alloni G.,
Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
odani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
Erington J., Fabre C., Ferrali E., Foulger D.,
jita M., Fujita Y., Fuma S., Gallizi E.J., Galleron N.,
laer P., Goffeau A., Gollightly E.J., Grandi G.,
Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hollappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
ramata D., Kasahara Y., Klaers-Blanchard M., Klein C.,
Koester P., Konigstein G., Krogh S., Kumano M.,
apidus A., Lardinols S., Lauber J., Lazarevic V.,
vine A., Liu H., Masuda S., Maue J.C., Medigue C.,
ellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
hl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Pujic B., Purnelle B., Rapoport G., Rey M., Reynolds S.,
ivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
nlan E., Schleich S., Schroeter R., Scoffone F.,
Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
Racconi E., Takagi T., Takahashi H., Takemaru K.,
Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
chiyama S., Vandenbol M., Vannier F., Vassarotti A.,
mbat R., Wedler E., Wedler H., Weitzenegger T.,
Mpat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
foshikawa H.P., Zumbstein E., Yoshikawa H., Danchin A.;
= Genome sequence of the Gram-positive bacterium *Bacillus*
19-256(1997).

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mail to license@isb-sib.ch).

: AAC83949.1; -;
: CAB14216.1; -;
H69932.
311431; ypbE.
002482; LysM.
; LysM; 1.
17; LysM; 1.
protein; Transmembrane; Complete proteome.
57 77 POTENTIAL.
10 AA; 27288 MW; 39E29660E0F9BF3 CRC64;
1.5%; Score 8; DB 1; Length 240;
arity 100.0%; Pred. No. 42;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
IASSS 25
|||||
IASSS 167
STANDARD; PRT; 243 AA.
(Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 33, Last annotation update)
protein AUX28.

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N.A.
732; PubMed=11234002;
Gleimer K., Parkhill J., James K.D., Thomson N.R.,
Honoré N., Garnier T., Churcher C., Harris D.,
Asham D., Brown D., Chillingworth T., Connor R.,
Devlin K., Dutoy S., Feltwell T., Fraser A., Hamlin N.,
Ornaby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Iver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Eger K., Simon S., Simmonds M., Skelton J., Squares R.,
Tevens K., Taylor K., Whitehead S., Woodward J.R.,
decay in the leprosy bacillus.";
07-1011(2001).
TS N-TERMINUS, WHICH CONTAINS THE PROLINE-RICH REPEATS,
IMMUNOREACTIVE.
Y: STRONG, TO M. TUBERCULOSIS PRA HOMOLOG.
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ail to license@isb-sib.ch).
CAA46515.1; -;
AA63035.1; -;
5; CAC31911.1; -;
441497.
35; -;
at; Complete proteome.
16 85
4 X 10 AA TANDEM REPEATS OF [PV]-G-G-S-
Y-P-P-P-P-P.
16 55
1-1.
36 65
1-2.
56 75
1-3.
76 85
1-4 (APPROXIMATE).
11 156
2 X 23 AA APPROXIMATE REPEATS.
11 123
2-1.
14 156
2-2.
1 212
QL -> HV (IN REF. 1).
AA; 26295 MW; 28565587EL570DA CRC64;
1.58; Score 8; DB 1; Length 249;
urity 100.0%; Pred.No. 43;
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ppp 136
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ppp 19
STANDARD; PRT; 251 AA.
el. 16, Created)
el. 16, Last sequence update)
el. 43, Last annotation update)
NA polymerase III 31 kDa polypeptide (EC 2.7.7.6) (C31).
OR ACP2 OR YNL151C OR N1769.
cerevisiae (Baker's yeast).
gi; Ascomycota; Saccharomycotina; Saccharomycetes;
iles; Saccharomycetaceae; Saccharomyces.
2;
N.A., AND PARTIAL SEQUENCE.
90; PubMed=2201900;
a M., Beltrame M., Cassar E., Sentenac A., Thuriaux P.,
e of Saccharomyces cerevisiae encodes a subunit of RNA
III) with an acidic tail.";

Mol. Cell. Biol. 10:4737-4743(1990).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBG1091 / DKY1;
RX MEDLINE=88216604; PubMed=2835668;
RA Haggren W., Kolodrubetz D.;
RT "The Saccharomyces cerevisiae ACP2 gene encodes an essential
HMGI-like protein.";
RL Mol. Cell. Biol. 8:1282-1289(1988).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / F1679;
RX MEDLINE=96287653; PubMed=8686380;
RA Nasr F., Becam A.-M., Herbert C.J.;
RT "The sequence of 36.8 kb from the left arm of chromosome XIV reve
24 complete open reading frames: 18 correspond to new genes, one
which encodes a protein similar to the human myotonic dystrophy
kinase.";
RL Yeast 12:169-175(1996).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcri
of DNA into RNA using the four ribonucleoside triphosphates a
substrates. C31 is involved in the formation of the initiatc
complex.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
(RNA) (N).
CC -!- SUBUNIT: RNA polymerase III consists of about 15 different
subunits.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: The acidic domain is essential for its funcic
-!- MISCELLANEOUS: Three distinct zinc-containing RNA polymerases a
found in eukaryotic nuclei: polymerase I for the ribosomal RN
precursor, polymerase II for the mRNA precursor, and polymera
III for 5S and tRNA genes.
CC -!- SIMILARITY: TO HMGI PROTEINS.

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or send an email to license@isb-sib.ch).

EMBL; X51498; CAA35866.1; -;
EMBL; M20315; AAA34390.1; -;
EMBL; X92517; CAA63288.1; -;
EMBL; Z71427; CAA96038.1; -;
PIR; A36465; RMBY3C.
GermOnline; 143157; -;
DR SGD; S0005095; RPC31.
KW Transferase; DNA-directed RNA polymerase; Transcription;
KW Nuclear protein; DNA-binding.
FT DOMAIN 202 248 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 12 12 G -> R (IN REF. 2).
FT CONFLICT 205 205 D -> H (IN REF. 2).
SQ SEQUENCE 251 AA; 27724 MW; 33A7D8EAE47793E1 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 251;
Best Local Similarity 100.0%; Pred.No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 336 EDEDEDD 343
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Db 215 EDEDEDD 222
RESULT 100
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AC Q10863;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

protein Rv1995/MT2051/Wb2018.
2051 OR MTCY39.24C OR MB2018.
n tuberculosis, and
n bovis.
inobacteria; Actinobacteridae; Actinomycetales;
ineae; Mycobacteriaceae; Mycobacterium.
773, 1765;
4 N.A.
erculosis; STRAIN=H37Rv;
5987; PubMed=9634230;
rosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Eiglmier K., Gas S., Barry C.E. III, Tekle A.F.,
Asham D., Brown D., Chillingworth I., Connor R.,
evlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
borne J., Quail M.A., Rajandream M.A., Rogers J.,
eger K., Skelton S., Squares S., Squares R.,
Taylor K., Whitehead S., Barrell B.G.;
the biology of Mycobacterium tuberculosis from the
me sequence.";
37-544 (1998).
4 N.A.
erculosis; STRAIN=CDC 1551 / Oshkosh;
5494; PubMed=12218036;
D., Alland D., Eisen J.A., Carpenter L., White O.,
DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
tterback T., Weidman J., Khouri H., Gill J., Mikula A.,
cobs W.R. Jr., Venter J.C., Fraser C.M.;
a comparison of Mycobacterium tuberculosis clinical and
rains.";
184:5479-5490 (2002).
4 N.A.
is; STRAIN=AF2122/97;
1107; PubMed=12788972;
Eiglmier K., Camus J.-C., Medina N., Mansoor H.,
hey S., Grondin S., Lacroix C., Monsemp C., Simon S.,
kin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
a genome sequence of Mycobacterium bovis";
Acad. Sci. U.S.A. 100:7877-7882 (2003).
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CAA98391.1; -;
57; AAK46328.1; -;
11; CAD96871.1; -;
A70758.
Rv1995; -;
2005544; HHE.
i; HHE; 2.
rotein; Complete proteome.
5 AA; 28072 MW; 31513556B9A7740 CRC64;
arity 1.5%; Score 8; DB 1; Length 255;
100.0%; Pred. No. 44;
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CAAAA 22
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CAAAA 166
Query Match 1.5%; Score 8; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 45;
RESULT 101
GSHI MOUSE
ID -GSHI MOUSE STANDARD; PRT; 261 AA.
AC P31315;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein GSH-1.
DE Homeobox protein GSH-1.
GN GSH1 OR GSH-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=NIH Swiss;
RX MEDLINE=96172995; PubMed=8589431;
RA Valerius M.T., Li H., Stock J.L., Weinstein M., Kaur S., Singh G
Potter S.S.;
RA "Gsh-1: a novel murine homeobox gene expressed in the central ne
RT system.";
RT Dev. Dyn. 203:337-351 (1995).
RN [2]
RP SEQUENCE FROM N.A. AND FUNCTION.
RX MEDLINE=96181350; PubMed=8631293;
RA Li H., Zeitler P.S., Valerius M.T., Small K., Potter S.S.;
RT "Gsh-1, an orphan Hox gene, is required for normal pituitary
RT development.";
RL EMBO J. 15:714-724 (1996).
RN [3]
RP SEQUENCE OF 146-205 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes";
RT Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710 (1991).
CC -!- FUNCTION: Probable transcription factor that binds to the DN
CC the GHRH gene. Plays an important role in pituitary developm
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U21224; AAA96814.1; -;
CC PIR; S63604; S63604.
CC HSP; P14653; I872.
CC TRANSFAC; T05100; -;
CC MGD; MGI:95842; Gsh1.
CC InterPro; IPR001356; HTH lambdarepressor.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; Hox; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
CC Transcription regulation; Activator; Homeobox; DNA-binding;
KW Nuclear protein; Developmental protein.
FT DNA_BIND 146 205 HOMEBOX.
FT DOMAIN 110 117 POLY-ALA.
SQ SEQUENCE 261 AA; 27727 MW; BA9D6B94359E4FF3 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 45;

nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAA 126
|||
AAA 116
STANDARD; PRT; 264 AA.
Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 42, Last annotation update)
in GSH-1.
(Human).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarhini; Hominidae; Homo.
6;
N.A.
'23; PubMed=11731616;
asaki Y., Morishita M., Nomura A., Yamamori E.,
ai M., Ozaki N., Kambe F., Seo H., Oiso Y., Saito H.;
ein Gsh-1-dependent regulation of the rat GHRH gene
l. 15:2149-2156(2001).
N.A.
-2000) to the EMBL/GenBank/DBJ databases.
Probable transcription factor that binds to the DNA
'-GC(TA)(AC)ATTA(GA)-3'. Activates the transcription of
ene. Plays an important role in pituitary development.
R LOCATION: Nuclear (By similarity)
'R: Belongs to the Antp homeobox family.
' : Contains 1 homeobox domain.
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wiss Institute of Bioinformatics and the EMBL outstation -
Bioinformatics Institute. There are no restrictions on its
profit institutions as long as its content is in no way
his statement is not removed. Usage by and for commercial
res a license agreement (see <http://www.isb-sib.ch/announce/>
all to license@sib-sib.ch).
; BAB78692.1; -
; BAB78693.1; -
; CAC12721.1; -
1B72.
'374; GSH1.
'01356; Homeobox.
'00047; HTH lambdarepressr.
homeobox; 1.
'4; HOMEBOX.
'1; HTHREPRESSR.
'10; Homeobox; 1.
'27; HOMEBOX 1; 1.
'71; HOMEBOX 2; 1.
n; Developmental protein.
'7 206 HOMEBOX.
'1 118 POLY-ALA.
'3 223 POLY-GLY.
'AA; 27882 MW; 25F4C4336E270C00 CRC64;
urity 1.5%; Score 8; DB 1; Length 264;
urity 100.0%; Pred. No. 46;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAA 126

Db 110 PAAAAAAA 117
|||||
RESULT 103
HXA9_MOUSE
ID HXA9_MOUSE STANDARD; PRT; 271 AA.
AC P09631; O70154; O70155;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-A9 (Hox-1.7).
GN HOXA9 OR HOXA-9 OR HOX-1.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (HOXA-9 AND HOXA-9T).
RC STRAIN=ICR, and C57BL/6;
RX MEDLINE=98192518; PubMed=9524228;
RA Fujimoto S., Araki K., Chisaka O., Araki M., Takagi K., Yamamura
RT "Analysis of the murine Hoxa-9 cDNA: an alternatively spliced
transcript encodes a truncated protein lacking the homeodomain."
RL Gene 209:77-85(1998).
RN [2]
SEQUENCE FROM N.A. (ISOFORM HOXA-9).
RP STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
SEQUENCE OF 180-271 FROM N.A. (HOXA-9).
RP MEDLINE=88065527; PubMed=2891029;
RA Rubin M.R., King W., Toth L.E., Sawczuk I.S., Levine M.S.,
RA D'Eustachio P., Nguyen-Huu M.C.;
RT "Murine Hox-1.7 homeo-box gene: cloning, chromosomal location, an
expression."
RL Mol. Cell. Biol. 7:3836-3841(1987).
RN [4]
REVISIONS.
RP Rubin M.R., King W., Toth L.E., Sawczuk I.S., Levine M.S.,
RA D'Eustachio P., Nguyen-Huu M.C.;
RL Mol. Cell. Biol. 8:5593-5593(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=HoxA-9;
CC IsoId=P09631-1; Sequence=Displayed;
CC Name=HoxA-9T;
CC IsoId=P09631-2; Sequence=VSP_002382, VSP_002383;
CC -!- TISSUE SPECIFICITY: Expressed in high level in the embryonic ;

5; P:development; TAS.
 001356; Homeobox.
 006711; Hox9 act.
 000047; HTH lambrepressr.
 ; homeobox; 1.
 ; Hox9 act; 1.
 24; HOMEBOX.
 11; HTHREPRESSR.
 110; Homeobox; 1.
 ; Hox; 1.
 27; HOMEBOX 1; 1.
 71; HOMEBOX 2; 1.
 -binding; Developmental protein; Nuclear protein;
 regulation; Chromosomal translocation; Proto-oncogene.
 06 265 HOMEBOX.
 54 64 G -> V (IN REF. 1).
 57 67 W -> R (IN REF. 2).
 30 80 MISSING (IN REF. 1).
 13 243 L -> F (IN REF. 1).
 ; AA; 30172 MW; 823A1A22BB07A881 CRC64;
 1.5%; Score 8; DB 1; Length 272;
 identity 100.0%; Pred. No. 47;
 conservative 0; Mismatches 0; Gaps 0;
 VAP 145
 VAP 103
 STANDARD; PRT; 279 AA.
 (el. 27, Created)
 (el. 27, Last sequence update)
 (el. 41, Last annotation update)
 ; protein 1.
 ; W OR J0755.
 cerevisiae (Baker's yeast).
 ; Ascomycota; Saccharomycotina; Saccharomycetes;
 ; Saccharomycetaceae; Saccharomycetes.
 2;
 N.A.
 76; PubMed=9290207;
 ; Konopka J.B., Sternglanz R.;
 se-specific genes from *Saccharomyces cerevisiae*.";
 1042(1997).
 N.A.
 FY1679;
 75; PubMed=8948101;
 Kordes B., Pujol A., Jauniaux J.-C.;
 analysis of a 40.2 kb fragment of yeast chromosome X
 n reading frames including URA2 (5' end), TRK1, PBS2,
 RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes,
 delta elements and a Ty4 transposon.";
 1474(1996).
 Derepression of silent mating type loci when
 sed.
 ; TO S.POMBE CIAI.

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 ioinformatics Institute. There are no restrictions on its
 rofit institutions as long as its content is in no way
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 il to license@isb-sib.ch).

 AAC37512.1; -.

DR EMBL; Z49390; CAA89410.1; -.
 DR PIR; S30766; S30766.
 DR GerOnline; 141727; -.
 DR SGD; S0003651; ASF1.
 DR GO; GO:0005678; Chromatin assembly complex; IDA.
 DR GO; GO:0008630; P:DNA damage response, signal transduction re..
 DR InterPro; IPR006818; Anti-silence.
 DR Pfam; PF04729; Anti-silence; 1.
 FT DOMAIN 170 242 ASP/GLU-RICH (HIGHLY ACIDIC).
 SQ SEQUENCE 279 AA; 31603 MW; 186E76075C0B1644 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 279;
 Best local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 330 EEEEDDED 337
 Db 178 EEEEDDED 185
 RESULT 106
 CEBE RAT
 ID_CEBE RAT STANDARD; PRT; 281 AA.
 AC P56261;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CCAAT/enhancer binding protein epsilon (C/EBP epsilon) (C/EBP-rel
 DE protein 1).
 GN CEBPE OR CRP1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98256268; PubMed=9593684;
 RA Williams S.C., Du Y., Schwartz R.C., Weiler S.R., Ortiz M.,
 RA Keller J.R., Johnson P.F.;
 RT "C/EBPepsilon is a myeloid-specific activator of cytokine, chemok
 and macrophage-colony-stimulating factor receptor genes.";
 RL J. Biol. Chem. 273:13493-13501(1998).
 RN [2]
 RP SEQUENCE OF 31-281 FROM N.A.
 RX MEDLINE=91357471; PubMed=1884998;
 RA Williams S.C., Cantwell C.A., Johnson P.F.;
 RT "A family of C/EBP-related proteins capable of forming covalently
 linked leucine zipper dimers in vitro.";
 RL Genes Dev. 5:1553-1567(1991).
 CC -!- FUNCTION: C/EBP ARE DNA-BINDING PROTEINS THAT RECOGNIZE TWO
 DIFFERENT MOTIFS: THE CCAAT HOMOLOGY COMMON TO MANY PROMOTERS
 THE ENHANCED CORE HOMOLOGY COMMON TO MANY ENHANCERS (BY
 SIMILARITY).
 CC -!- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMER;
 WITH C/EBP DELTA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the bZIP family. C/EBP subfamily.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 EMBL; AF034716; AAC24455.1; -.
 DR InterPro; IPR004827; TF_bZIP.
 DR Pfam; PF00170; bZIP; 1.
 DR SMART; SM00338; BRLZ; 1.
 DR PROSITE; PS50217; bZIP; 1.
 DR PROSITE; PS00036; bZIP_BASIC; Activator; DNA-binding; Nuclear protein.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein.

208 228 BASIC MOTIF.
239 267 LEUCINE-ZIPPER.
81 AA; 30589 MW; 68B16455C034E250 CRC64;
1.5%; Score 8; DB 1; Length 281;
larity 100.0%; Pred. No. 48;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAP 145
|||||
AAAAAP 178

STANDARD; PRT; 294 AA.
(Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 39, Last annotation update)
n (NPM) (Nucleolar phosphoprotein B23) (Numatrin)
rotein NO38).

s (Chicken).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

031;
M N.A.
6792; PubMed=2320420;
Nigg E.A.;
ces of chicken nucleolin/C23 and NO38/B23, two major
oteins.";
s Res. 18:1286-1286(1990).

F SEQUENCE.
4215; PubMed=2114180;
Krek W.; Nigg E.A.;
nd developmental expression of chicken nucleolin and
nate expression of two abundant non-ribosomal nucleolin
phys. Acta 1049:126-133(1990).
: Associated with nucleolar ribonucleoprotein structures
single-stranded nucleic acids. It may function in the
and/or transport of ribosome.
LAR LOCATION: Nuclear. Generally nucleolar, but is
ated to the nucleolus in case of serum starvation or
t with anticancer drugs (By similarity).
phorylated.
RY: Belongs to the nucleoplasmin family.
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mail to license@isb-sib.ch).

; CAA35061.1; --
DNCHFW.
R004301; Nucleoplasmin.
6; Nucleoplasmin; 1.
ein; Phosphorylation; RNA-binding.
1 11 MET-RICH.
122 133 ASP/GLU-RICH (ACIDIC).
153 158 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
161 186 ASP/GLU-RICH (HIGHLY ACIDIC).
190 196 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
94 AA; 32632 MW; B1FF89B5F2322DED CRC64;
1.5%; Score 8; DB 1; Length 294;

Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 332 EDDDEDED 339
Db 164 EDDDEDED 171

RESULT 108
PP3D HUMAN
ID PP3D_HUMAN STANDARD; PRT; 299 AA.
AC 095685;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 1, regulatory subunit 3D (Protein phosphatase
DE regulatory subunit 6) (Protein phosphatase 1 binding subunit R6)
GN PP1R3D OR PP1R6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ASSOCIATION WITH GLYCOGEN, AND INTERACTION W
RP PP1CC.
RC TISSUE=Brain;
RX MEDLINE=98074939; PubMed=9414128;
RA Armstrong C.G., Browne G.J., Cohen P., Cohen P.T.W.;
RT "PP1R6, a novel member of the family of glycogen-targeting sub
RT of protein phosphatase 1.";
RL FEBS Lett. 418:210-214(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.I
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Giffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johns
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlc
RA Lehesaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J
RA Marsh V.D., Martin S.D., McConnachie L.J., McKay K., McMurray A.
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.
RA Swann R.M., Symancore N., Taylor R., Tee L., Thomas D.W., Thorpe
RA Tracsey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Protein phosphatase 1 regulatory subunit is consid
CC as a glycogen-targeting subunit. PP1 is essential for cell
CC division, and participates in the regulation of glycogen
CC metabolism, muscle contractility and protein synthesis.
CC -!- SUBUNIT: Interacts with PP1CC catalytic subunit of PP1, and
CC associates with glycogen.
CC -!- TISSUE SPECIFICITY: Expressed in all tissue tested. High
CC expression in skeletal muscle and heart.
CC -!- DOMAIN: CBM 21 domain is known to be involved in the localiz
CC to glycogen and is characteristic of some regulatory subunit
CC phosphatase complexes.
CC -!- SIMILARITY: Contains 1 CBM_21 domain.

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EMBL; X54212; CAA38124.1; -;
EMBL; X07987; CAA30797.1; -;
PIR; S03172; S03172.
MaizeDB; 30000; -;
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
DOMAIN 182 188 POLY-ALA.
DOMAIN 286 294 POLY-ALA.
CONFLICT 269 269 D -> N (IN REF. 2).
SEQUENCE 303 AA; 32428 MW; 24003521CEP91790 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 299;

Best Local Similarity 100.0%; Pred. No. 51;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CPAP 133
|||||
CPAP 57

STANDARD; PRT; 303 AA.

Rel. 11, Created

Rel. 27, Last sequence update

Rel. 43, Last annotation update

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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EMBL; X54212; CAA38124.1; -;
EMBL; X07987; CAA30797.1; -;
PIR; S03172; S03172.
MaizeDB; 30000; -;
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
DOMAIN 182 188 POLY-ALA.
DOMAIN 286 294 POLY-ALA.
CONFLICT 269 269 D -> N (IN REF. 2).
SEQUENCE 303 AA; 32428 MW; 24003521CEP91790 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 303;

Best Local Similarity 100.0%; Pred. No. 51;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CPAP 133
|||||
CPAP 57

STANDARD; PRT; 304 AA.

Rel. 11, Created

Rel. 27, Last sequence update

Rel. 43, Last annotation update

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

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protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

protein (EC 3.2.2.22) (Opague-6 protein) (rRNA N-

```

-----
/ AAA33454.1; -.
00; -.
2001574; RIP.
1; RIP; 1.
396; SHIGARICIN.
3275; SHIGA-RICIN; 1.
2; Protein synthesis inhibitor; Hydrolase; Toxin;
nily.
208 208 BY SIMILARITY.
183 189 POLY-ALA.
287 295 POLY-ALA.
04 AA; 33514 MW; 978789A2DD2BBF3C CRC64;
1.5%; Score 8; DB 1; Length 304;
arity 100.0%; Pred. No. 51;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AATA 158
|||||
AATA 294
STANDARD; PRT; 311 AA.
(Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
lein CDX-2 (Caudal-type homeobox protein 2).
;.
(Mouse).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0090;
A N.A.
;
086; PubMed=7910823;
xler T., Kazenwadel J.;
the murine homeobox gene cdx-2. Expression in embryonic
intestinal epithelium."
a. 269:15229-15237(1994).
A N.A.
intestine;
1263; PubMed=7935448;
L., Taylor J., Traber P.G.;
in protein related to caudal regulates intestine-specific
tion."
ol. 14:7340-7351(1994).
04-229 FROM N.A.
1633; PubMed=1671571;
Kazenwadel J.;
re expression in the intestinal epithelium of adult
a. 266:3246-3251(1991).
CON OF SER-60.
3654; PubMed=11729123;
oudreau F., Taylor J.K., Moffett J., Suh E.R.,
tion of the serine 60 residue within the Cdx2 activation
es its transactivation capacity."
logy 121:1437-1450(2001).
; Involved in the transcriptional regulation of multiple
pressed in the intestinal epithelium. Important in broad
functions from early differentiation to maintenance of
stinal epithelial lining of both the small and large
a.
LAR LOCATION: Nuclear.

```

```

CC CC -!- TISSUE SPECIFICITY: Intestine; expressed specifically in gut
CC CC epithelium where it is not restricted to a particular cell
CC CC lineage. Abundant expression is seen in the proximal colon w
CC CC slightly lower levels in distal colon. Expression in the pro
CC CC colon is not restricted either to a particular cell lineage
CC CC stage of differentiation while in the distal colon it is mor
CC CC abundant in the differentiated cells towards the top of the
CC CC -!- PTM: Phosphorylation of Ser-60 mediates the transactivation
CC CC capacity.
CC CC -!- SIMILARITY: Belongs to the Caudal homeobox family.
CC CC -!- SIMILARITY: Contains 1 homeobox domain.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a col
CC CC between the Swiss Institute of Bioinformatics and the EMBL ou
CC CC the European Bioinformatics Institute. There are no restrictio
CC CC use by non-profit institutions as long as its content is i
CC CC modified and this statement is not removed. Usage by and for
CC CC entities requires a license agreement (See http://www.isb-sib.ch
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; U00454; AAA19645.1; -.
CC CC EMBL; S74520; AAB32251.1; -.
CC CC PIR; A53808; A53808.
CC CC HSP; P02835; 1FTZ.
CC CC TRANSFAC; T02002; -.
CC CC MGD; MGI:88361; Cdx2.
CC CC GO; GO:007389; P:pattern specification; IMP.
CC CC InterPro; IPR006820; Caudal act.
CC CC InterPro; IPR001356; Homeobox.
CC CC InterPro; IPR000047; HTH_lambrepresr.
CC CC Pfam; PF04731; Caudal_act; 1.
CC CC Pfam; PF00046; homeobox; 1.
CC CC PRINTS; PR00024; HOMEBOX.
CC CC PRINTS; PR00031; HTHREPRESSR.
CC CC ProDom; PD000010; Homeobox; 1.
CC CC SMART; SM00389; HOX; 1.
CC CC PROSITE; PS00027; HOMEBOX 1; 1.
CC CC PROSITE; PS00071; HOMEBOX 2; 1.
CC CC KW Transcription regulation; Activator; Developmental protein; Home
CC CC DNA-binding; Nuclear protein; Phosphorylation.
CC CC FT DNA_BIND 185 244 HOMEBOX.
CC CC FT DOMAIN 46 53 POLY-ALA.
CC CC FT DOMAIN 85 92 POLY-ALA.
CC CC FT DOMAIN 247 257 POLY-GLN.
CC CC FT MOD_RES 60 60 PHOSPHORYLATION.
CC CC FT CONFLICT 69 69 Y -> H [IN REF. 2].
CC CC SQ SEQUENCE 311 AA; 33476 MW; 71FFC4C263462FF3 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 311;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 151 AAAAATA 158
DB 46 AAAAATA 53
|||||
RESULT 112
HEM3_PSEPK STANDARD; PRT; 313 AA.
AC Q88RE5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilar
DE synthase) (HMS) (Pre-uroporphyrinogen synthase).
GN HEMC OR PP0186.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RN SEQUENCE FROM N.A.

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262 262 A -> T (IN REF. 1 AND 2).
17 AA; 34186 MW; 8C85F4C2B235EACA CRC64;

1.5%; Score 8; DB 1; Length 317;
larity 100.0%; Pred. No. 53;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTAA 20
|||||
ATTAA 288

STANDARD; PRT; 320 AA.
(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
line (TTP) (TIS11A protein) (TIS11) (Zinc finger protein
11A.
ficus (Rat).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;

% N.A.
0517; PubMed=1511903;
shama M., Chung S.Y., Guroff G.;
a rat TIS11 cDNA, an immediate early gene induced by
rs and phorbol esters.";
-291(1992).
: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
E INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.
LAR LOCATION: Nuclear.
TY: Contains 2 C3H1-type zinc fingers.

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-----
; CAA44970.1; -.
JC1255.
R000571; Znf CCCH.
2; zf-CCCH; 2.
36; Znf_C3H1; 2.
sin; Repeat; Metal-binding; Zinc-finger; DNA-binding;
ion.
64 68 P-P-P-P-G.
191 195 P-P-P-P-G.
212 216 P-P-P-P-G.
102 121 C3H1-TYPE 1.
140 159 C3H1-TYPE 2.
221 221 PHOSPHORYLATION (BY MAPK) (BY
SIMILARITY).
20 AA; 33653 MW; CFC597E3C7B5CA76 CRC64;

1.5%; Score 8; DB 1; Length 320;
larity 100.0%; Pred. No. 54;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PPAPP 221
|||||
PPAPP 307

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KHSE_XANCP
ID KHSE_XANCP STANDARD; PRT; 322 AA.
AC Q8P9Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homoserine kinase (EC 2.7.1.39) (HK).
GN THRB OR XCC1801.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.F.
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with dif
RT host specificities.";
RL Nature 417:459-463(2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
CC homoserine.
CC -!- PATHWAY: Threonine biosynthesis from aspartate; fourth step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the GHMP kinase family. Homoserine ki
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a col
CC between the Swiss Institute of Bioinformatics and the EMBL ou
CC the European Bioinformatics Institute. There are no restrictio
CC use by non-profit institutions as long as its content is i
CC modified and this statement is not removed. Usage by and for
CC entities requires a license agreement (See http://www.isb-sib.ch
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE012282; AAM41090.1; -.
CC HAMAP; MF_00384; -.
CC InterPro; IPR006204; GHMP_kinase.
CC InterPro; IPR006203; GHMP_kinase_ATP.
CC InterPro; IPR000870; Homoser_Kin.
CC Pfam; PF00288; GHMP_kinases_1.
CC PRINTS; PR00958; HOMSERKINASE.
CC PROSITE; PS00627; GHMP_KINASES_ATP; FALSE NEG.
KW Threonine biosynthesis; Transferase; Kinase; ATP-binding;
FT Complete proteome.
FT NP BIND 106 116 ATP (POTENTIAL).
SQ SEQUENCE 322 AA; 32924 MW; C3F64B273D3CC70F CRC64;

Query Match 1.5%; Score 8; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 120 AAAAAAAP 127
|||||
DB 286 AAAAAAAP 293

```

RESULT 116
OLG2_HUMAN

STANDARD; PRT; 323 AA.
 rel. 39, Created)
 rel. 41, Last sequence update)
 rel. 43, Last annotation update)
 re transcription factor 2 (Basic helix-loop-helix protein
 corein kinase C-binding protein RACK17) (Protein kinase C
 in 2).
 31 OR PRKCBP2 OR RACK17.
 (Human).
 :azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 :eria; Primates; Catarrhini; Homnidae; Homo.
 6;
 N.A.
 ampus;
 unaga C., Kiyohara Y., Konishi H., Kikkawa U.;
 se C-binding protein.";
 3-1996) to the EMBL/GenBank/DBJ databases.
 N.A.
 564; PubMed=10737801;
 -Sait S.N., Escalon E.A., Carroll A.J., de Jong P.J.,
 Aplan P.D.;
 (q11.2;q22) chromosomal translocation associated with
 lymphoblastic leukemia activates the BHLHB1 gene.";
 ad. Sci. U.S.A. 97:3497-3502(2000).
 Required for oligodendrocyte and motor neuron
 ion in the spinal cord (By similarity).
 AR LOCATION: Nuclear (Potential).
 Involved in a form of T-cell acute lymphoblastic leukemia
 through a chromosomal translocation t(14;21)(q11.2;q22)
 olves OLIG2 and T-cell receptor alpha chain (TCRA) genes.
 t: Contains 1 basic helix-loop-helix (bHLH) domain.
 OT entry is copyright. It is produced through a collaboration
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 profit institutions as long as its content is in no way
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 res a license agreement (See <http://www.isb-sib.ch/announce/>
 ail to license@isb-sib.ch).
 AAC72247.1; ALT INIT.
); AAF61215.1; ALT_INIT.
 98; OLIG2.
 01092; HLH_basic.
 HLH; 1.
 88; HLH; 1.
 regulation; DNA-binding; Nuclear protein;
 Chromosomal translocation.
 9 120 BASIC DOMAIN.
 1 162 HELIX-LOOP-HELIX MOTIF.
 7 88 POLY-SER.
 6 212 POLY-ALA.
 5 237 POLY-ALA.
 6 270 POLY-ALA.
 3 280 POLY-GLY.
 AA; 32384 MW; OEC9223961062509 CRC64;
 1.5%; Score 8; DB 1; Length 323;
 ivity 100.0%; Pred.No. 54;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAA 126
 |||
 AAAA 231

OLIG2 MOUSE STANDARD; PRT; 323 AA.
 O9B06; O9JKN4;
 28-FEB-2003 (Rel. 41, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Oligodendrocyte transcription factor 2.
 GN OLIG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=20544962; PubMed=11091082;
 RA Takebayashi H., Yoshida S., Sugimori M., Kosako H., Kominami R.,
 RA Nakafuku M., Nabeshima Y.;
 RT "Dynamic expression of basic helix-loop-helix Olig family members
 RT implication of Olig2 in neuron and oligodendrocyte differentiatio
 RT identification of a new member, Olig3.";
 RL Mech. Dev. 99:143-148(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20182808; PubMed=10719889;
 RX Zhou Q., Wang S., Anderson D.J.;
 RA "Identification of a novel family of oligodendrocyte lineage-spec
 RT basic helix-loop-helix transcription factors.";
 RL Neuron 25:331-343(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hoieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
 RA Vallalou D.K., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez
 RA Fahy J., Whitman J., Young A.C., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.;
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Required for oligodendrocyte and motor neuron
 CC specification in the spinal cord.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Specifically expressed in zones of
 CC neuroepithelium from which oligodendrocyte precursors emerge,
 CC well as in the precursors themselves.
 CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB038697; BAB18907.1; -
 DR EMBL; AF232929; AAF61722.1; -
 DR EMBL; BC051967; AAF51967.1; -
 DR MGD; MGI:1355331; OLIG2.
 DR GO; GO:0042055; P:neuroanal lineage restriction; IMP.

3001092; HLH_basic.
 33; HLH; 1.
 3888; HLH; 1.
 a regulation; DNA-binding; Nuclear protein.
 109 120 BASIC DOMAIN.
 121 162 HELIX-LOOP-HELIX MOTIF.
 77 88 POLY-SER.
 206 212 POLY-ALA.
 225 237 POLY-ALA.
 266 270 POLY-ALA.
 273 284 POLY-GLY.
 198 198 L -> I (IN REF. 2).
 205 205 P -> PRRGAP (IN REF. 2).
 23 AA; 32406 MW; 598AE76CB512D716 CRC64;
 1.5%; Score 8; DB 1; Length 323;
 larity 100.0%; Pred. No. 54;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AAAAA 126
 |||||
 AAAAA 231
 STANDARD; PRT; 335 AA.
 (Rel. 29, Created)
 (Rel. 36, Last sequence update)
 (Rel. 42, Last annotation update)
 :ein Hox-D13 (Hox-41).
 (41.
 (Human).
 :kzooa; Chordata; Craniata; Vertebrata; Euteleostomi;
 :heria; Primates; Catarrhini; Hominidae; Homo.
 106;
 1 N.A.
 1671; PubMed=8614804;
 Mundlos S., Upton J., Olsen B.R.;
 th and branching patterns in synpolydactyly caused by
 HOXD13.";
 48-551(1996).
 1 N.A.
 K., Kita K., Miwa H., Kamada N., Ohki M.;
 q31;p15) translocation in acute myeloid leukemia fuses
 origin gene to HOXD13 homeobox gene.";
 (P-1999) to the EMBL/GenBank/DBJ databases.
 68-333 FROM N.A.
 849; PubMed=1675198;
 Morelli F., Acampora D., Migliaccio E., Simeone A.,
 a homeobox gene homologous to the even-skipped
 gene, is localized at the 5' end of HOX4 locus on
 3-50(1991).
 LA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-ALA-49 INS.
 300; PubMed=8817328;
 Stoklov I., Yilmaz E., Sayli B.S., Sarfarazi M.;
 ctur of HOXD13 gene; a nine polyalanine duplication
 ydactyly in two unrelated families.";
 et. 5:945-952(1996).
 CYS-308 AND LEU-314, AND VARIANT BDD CYS-308.
 987; PubMed=12649808;
 an S.H., Oldridge M., Trembath R.C., Roche P.,
 Giele H., Wilkie A.O.;
 ations in the homeodomain of HOXD13 are associated with

brachydactyly types D and E.";
 Am. J. Hum. Genet. 72:984-997(2003).
 -!- FUNCTION: Sequence-specific transcription factor which is pa
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axi
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- DISEASE: Defects in HOXD13 are the cause of synpolydactyly ([MIM:186000]; also known as syndactyly type II. SPD is a lim malformation that shows a characteristic manifestation in bo hands and feet. This condition is inherited as an autosomal dominant trait with reduced penetrance.
 -!- DISEASE: Defects in HOXD13 are the cause of brachydactyly ty (BDD) [MIM:113200]. BDD is characterized by short and broad terminal phalanges of the thumbs and big toes. Inheritance i autosomal dominant.
 -!- DISEASE: Defects in HOXD13 are the cause of brachydactyly ty (BDE) [MIM:113300]. BDE is characterized by shortening of th fingers mainly in the metacarpals and metatarsals. Inheritan autosomal dominant.
 -!- SIMILARITY: Belongs to the Abd-B homeobox family.

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 EMBL; AF005220; AAC51635.1; -
 EMBL; AF005219; AAC51635.1; JOINED.
 EMBL; AB032481; BAA95352.1; -
 PIR; B39065; B39065.
 HSP; P14653; 1B72.
 TRANSFAC; T03335; -
 Genew; HGNC:5136; HOXD13.
 MIM; 142989; -
 MIM; 113200; -
 MIM; 113300; -
 MIM; 186000; -
 GO; GO:0003677; P:DNA binding; TAS.
 GO; GO:0007275; P:development; TAS.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; TA
 GO; GO:0001501; P:skeletal development; TAS.
 GO; GO:0006366; P:transcription from Pol II promoter; TAS.
 InterPro; IPR001356; Homeobox.
 Pfam; PF00046; homeobox; 1.
 ProDom; PD000010; Homeobox; 1.
 SMART; SM00389; HOX; 1.
 PROSITE; PS00027; HOMEBOX_1; 1.
 PROSITE; PS50071; HOMEBOX_2; 1.
 Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 Transcription regulation; Disease mutation.
 FT DOMAIN 17 22 POLY-SER.
 FT DOMAIN 24 28 POLY-ALA.
 FT DOMAIN 49 63 POLY-ALA.
 FT DOMAIN 77 84 POLY-SER.
 FT DOMAIN 105 110 POLY-ALA.
 FT DNA_BIND 268 327 HOMEBOX.
 FT VARIANT 49 49 A -> AAAAAAAAAA (in SPD).
 FT FTID=VAR_003818.
 FT S -> C (in BDE and BDD).
 FT FTID=VAR_015952.
 FT I -> L (in BDE).
 FT FTID=VAR_015953.
 SQ SEQUENCE 335 AA; 35210 MW; 0558D7B29F9B6E3E CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 121 AAAAAAPP 128
 |||||

AAPP 112

STANDARD; PRT; 337 AA.

5; Rel. 30, Created)

Rel. 30, Last sequence update)

Rel. 43, Last annotation update)

gamma receptor beta chain precursor (Interferon-gamma

transducer-1) (AF-1) (Interferon-gamma transducer-1).

371.

(Human).

tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

heria; Primates; Catarrhini; Hominidae; Homo.

06;

N.A.

ibroblast;

380; PubMed=8124716;

lly R.J., Kosenko S., Mariano T.M., Cook J.R.,

uel S.L., Schwartz B., Miki T., Pestka S.;

on and sequence of an accessory factor required for

the human interferon gamma receptor.";

02(1994).

N.A.

257; PubMed=12477932;

L., Feingold E.A., Grouse L.H., Derge J.G.,

Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

quellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,

Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

ton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

adan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Touchman J.W., Green E.D., Dickson M.C.,

Grimwood J., Schmutz J., Myers R.M.,

S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

Schein J.E., Jones S.J.M., Marra M.A.;

nd initial analysis of more than 15,000 full-length

se cDNA sequences.";

cad. Sci. U.S.A. 99:16899-16903 (2002).

-24 FROM N.A.

142; PubMed=8910544;

asperger C., Dembic Z., Pestka S.;

e of the gene for the second chain of the human

gamma receptor.";

271:28947-28952(1996).

Part of the receptor for interferon gamma. Required for

anaduction. This accessory factor is an integral part of

gamma signal transduction pathway and is likely to

with GAF, JAK1, and/or JAK2.

AR LOCARION: Type I membrane protein.

Y: Belongs to the type II cytokine family of receptors.

Y: Contains 2 fibronectin type III domains.

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DR EMBL; U05875; AAA16955.1; -.
 DR EMBL; U05877; AAA16956.1; -.
 DR EMBL; BC003624; AAH03624.1; -.
 DR EMBL; U68755; AAC52066.1; -.
 DR PIR; I38500; I38500.
 DR Genew; HGNC:5440; IFNGR2.
 DR MIN; 147569; -.
 DR MIN; 209950; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0003800; F:antiviral response protein activity; TAS.
 DR GO; GO:0004906; F:interferon-gamma receptor activity; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu.
 DR GO; GO:0009619; P:resistance to pathogenic bacteria; TAS.
 DR GO; GO:0009615; P:response to viruses; TAS.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN
 FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 64 64 R -> Q.
 FT SEQUENCE 337 AA; 37834 MW; 18C61B10AD90E509 CRC64;
 /FTID=VAR_002718.
 Query March 1.5%; Score 8; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G

QY 121 AAAAAAPP 128
 |||||
 DB 17 AAAAAAPP 24

RESULT 120
 LIMA_PSEAE
 ID LIMA_PSEAE STANDARD; PRT; 340 AA.
 AC Q01725; P95420; Q04591;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lipase modulator (lipase helper protein).
 GN LIPIB OR LIPIB OR PA2863.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TE3285;
 RX MEDLINE=92337414; PubMed=1632642;
 RA Chihara-Siomi M., Yoshikawa K., Oshima-Hirayama N., Yamamoto K.,
 RA Sogabe Y., Nakatani T., Nishioka T., Oda J.;
 RT "Purification, molecular cloning, and expression of lipase from
 RT Pseudomonas aeruginosa".
 RL Arch. Biochem. Biophys. 296:505-513 (1992).
 RP [2]
 RP REVISIONS.
 RC STRAIN=TE3285;
 RA Shibata H.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.

31156; PubMed=982856;
 Hirano A., Aisaka K.;
 ns of Ser for Asn-163, and Pro for Leu-264 are important
 ation of lipase from *Pseudomonas aeruginosa*.";
 120:915-921(1996).
 M N.A.
 15692 / PA01;
 1478; PubMed=1512563;
 , Hoesche C., Strunk C., Winkler U.K.;
 enetics of the extracellular lipase of *Pseudomonas*
 AO1.";
 obiol. 138:1325-1335(1992).
 ;
 AY-1994) to the EMBL/GenBank/DBJ databases.
 M N.A.
 15692 / PA01;
 7337; PubMed=10984043;
 Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 alier M.H., Hancock R.E.W., Iori S., Olson M.V.;
 aome sequence of *Pseudomonas aeruginosa* PA01, an
 c pathogen.";
 59-964(2000).
 : SEEMS TO BE ACTING IN THE FOLDING OF THE EXTRACELLULAR
 URING ITS PASSAGE THROUGH THE PERIPLASM (BY SIMILARITY).
 LAR LOCATION: Inner membrane-anchored (By similarity).
 TY: Belongs to the lipase chaperone family.

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 52; BAA23129.1; -;
 ; BAA03136.1; -;
 ; CAA44998.1; ALT INIT.
 12; AAG06251.1; ALT_INIT.
 S25769.
 R004961; Lipase chap.
 0; Lipase chap. 1.
 ation; Chaperone, Transmembrane; Periplasmic;
 ne; Complete proteome.
 4 24 POTENTIAL.
 210 210 A -> T (IN STRAINS TE3285 AND ATCC
 31156).
 301 301 T -> A (IN STRAINS TE3285 AND ATCC
 31156).
 41 42 DR -> VH (IN REF. 6).
 40 AA; 37686 MW; 55217FCDF8F8FC251 CRC64;
 1.5%; Score 8; DB 1; Length 340;
 larity 100.0%; Pred. No. 56;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PAASA 312
 |||||
 PAASA 49

 STANDARD; PRT; 341 AA.

AC QOUKPE;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Muscblind-like protein (Triplet-expansion RNA-binding protein)
 GN MEN1L OR MEN1 OR EXP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Castagnola P., Monticone M., Borsani G., Bassi M.T., Tonachini I
 RT "cDNA cloning of mouse muscblind.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Binds to CUG triplet repeat expansion dsRNA (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 4 C3H1-type zinc fingers.

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 or send an email to license@isb-sib.ch).

 CC EMBL; AF231110; AAF72159.1; -;
 CC MGD; MGI:1928482; Mbn1l.
 DR GO; GO:0005737; Cytoplasm; ISS.
 DR GO; GO:0005634; Cnucleus; ISS.
 DR GO; GO:0003725; P:double-stranded RNA binding; ISS.
 DR GO; GO:0001701; P:embryonic development (sensu Mammalia); IEP.
 DR GO; GO:0030326; P:limb morphogenesis; IEP.
 DR GO; GO:0007517; P:muscle development; IEP.
 DR GO; GO:0045445; P:myoblast differentiation; IDA.
 DR GO; GO:0007399; P:neurogenesis; IEP.
 DR InterPro; IPR000571; Znf_CCHC.
 DR SMART; SM00356; Znf_C3H1; 4.
 DR Pfam; PF00642; zf-CCCH; 4.
 KW Zinc-finger; Repeat; Nuclear protein; RNA-binding.
 FT ZN_FING 14 40 C3H1-TYPE 1.
 FT ZN_FING 47 72 C3H1-TYPE 2.
 FT ZN_FING 178 205 C3H1-TYPE 3.
 FT ZN_FING 215 239 C3H1-TYPE 4.
 SQ SEQUENCE 341 AA; 36975 MW; 8E008DB5C7EF8AB9 CRC64;

 Query Match 1.5%; Score 8; DB 1; Length 341;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 QY 119 PAAAAAAA 126
 Db 165 PAAAAAAA 172
 |||||
 |||||
 RESULT 122
 RLAO METAC
 ID RLAO METAC STANDARD; PRT; 347 AA.
 AC QBT80;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acidic ribosomal protein P0 homolog (L10E).
 GN RPLP0 OR MA4276.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;

```

760; PubMed=11932238;
Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
Lor J., Stange-Thomann N., DeArellano K., Johnson R.,
Ewan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Rober R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Unayam L.A., White O., White R.H., de Macario E.C.,
Farrell K.F., Jing H., Macario A.J.L., Paulsen I.,
Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Birren B.;
of Methanocaldococcus acetivorans reveals extensive metabolic
ical diversity";
2:532-542(2002);
Ribosomal protein P0 is the functional equivalent of
rotein L10.
Y: Belongs to the L10P family of ribosomal proteins.
-----
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ail to license@isb-sib.ch).
-----
8; AAM07620.1; -.
80; -. 1.
001813; Ribosomal 60S.
001790; Ribosomal L10.
; 60s ribosomal; 1.
; Ribosomal L10; 1.
tein; Complete proteome.
7 AA; 37167 MW; 3595EBDEB28821F CRC64;
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1.5%; Score 8; DB 1; Length 347;
arity 100.0%; Pred. No. 57;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AASP 127
|||||
AASP 315
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STANDARD; PRT; 353 AA.
Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 42, Last annotation update)
sin Nkx-2.4 (Homeobox protein NKX2.4) (Homeobox protein
2D.
(Human).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
6;
N.A.
749; PubMed=11780052;
Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Arides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Clow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
Ill W.D., Butler A.P., Carder C., Carter N.P.,
Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Ley V.E., Collier R.E., Connor R.E., Corby N.R.,
ville G.J., Deadman R., Dhani P.D., Dunn M.,
Frankland J.A., Fraser A., French L., Garner P.,
Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
urley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

```

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RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johns
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlo
RA Lehuvsialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Be
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 2(
RL Nature 414:865-871(2001).
RN (2)
RP SEQUENCE OF 1-289 FROM N.A.
RX MEDLINE=20279852; PubMed=10818213;
Wang C.-C., Brodnicki T., Copeland N.G., Jenkins N.A., Harvey R.I
RT "Conserved linkage of NK-2 homeobox gene pairs Nkx2-2/2-4 and
RT Nkx2-1/2-9 in mammals.";
RL Mamm. Genome 11:466-468(2000).
CC -!- FUNCTION: Probable transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the NK-2 homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
-----
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-----
EMBL; AL158013; -. NOT ANNOTATED_CDS.
EMBL; AF202037; AAG35617.1; -.
HSSP; P23441; 1FTT.
Genew; HGNC:7837; NKX2-4.
MIM; 607808;
InterPro; IPR001356; Homeobox.
Pfam; PF000046; Homeobox; 1.
PRINTS; PR00024; HOMEBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEBOX_1; 1.
PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein; Developmental protein.
FT DNA_BIND 189 248 HOMEBOX.
FT DOMAIN 44 47 POLY-ALA.
FT DOMAIN 76 91 POLY-ALA.
FT DOMAIN 181 187 POLY-ALA.
FT DOMAIN 264 272 POLY-PRO.
SQ SEQUENCE 353 AA; 36011 MW; B6780C4E4020BED6 CRC64;
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Query Match 1.5%; Score 8; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
Qy 120 AAAAAAAP 127
Db 181 AAAAAAAP 188
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RESULT 124
ATH1_HUMAN STANDARD; PRT; 354 AA.
AC Q92858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Atonal protein homolog 1 (Helix-loop-helix protein HATH-1).

```

RP SEQUENCE FROM N.A. (ISOFORMS MS3 AND CM1), FUNCTION, AND DEVELOP
RC STRAIN.
RX STRAIN=Oregon-R;
RA MEDLINE=89077532; PubMed=344435;
RA Bell L.R., Maine E.M., Schedl P., Cline T.W.;
RT "Sex-lethal, a Drosophila sex determination switch gene, exhibit
RT specific RNA splicing and sequence similarity to RNA binding
RT proteins.";
RL Cell 55:1037-1046(1988).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS MS3; MS11 AND MS16), FUNCTION, AND
RP DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX MEDLINE=91260708; PubMed=1710769;
RA Samuels M.E., Schedl P., Cline T.W.;
RT "The complex set of late transcripts from the Drosophila sex
RT determination gene sex-lethal encodes multiple related
RT polypeptides.";
RL Mol. Cell. Biol. 11:3584-3602(1991).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananietis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.
RA Arlil J.F., Agayani A., An H.-J., Andrews-pfannkuch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brockstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandr
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deucher A., Deng Z., Mays A.D., Dew I., Dietz S.M.
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Du
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischma
RA Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostis N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston K., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarat C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskay R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S.Q.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]

RP REVISIONS, AND ALTERNATIVE SPLICING.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";

3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [N.A. (ISOFORM MS16).
 ey; TISSUE=Embryo;
 Brokstein P., Hong L., Agbayani A., Carlson J.W.,
 avez C., Dorsett V., Drensek D., Farfan D., Friese E.,
 Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
 lungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
 uanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
 B-2003) to the EMBL/GenBank/DBJ databases.
 -26 FROM N.A. (ISOFORM 1), AND FUNCTION.
 272; PubMed=1547493;
 line T.W., Schedl P.;
 sex determination signal of Drosophila acts at the level
 ion.";
 43(1992).
 -41 FROM N.A. (ISOFORM FEMALE-SPECIFIC).
 600; PubMed=8978052;
 ., Sakamoto H., Navarro-Sabate A., Sakashita E.,
 Segarra C., Sanchez L.;
 f the gene Sex-lethal: a comparative analysis of
 lanogaster and Drosophila subobscura.";
 1653-1664(1996).
 ION.
 158; PubMed=1454517;
 Inoue K., Higuchi I., Ono Y., Shimura Y.;
 rosophiha Sex-lethal pre-mRNA splicing by its own female-
 act.";
 Res. 20:5533-5540(1992).
 NMR OF 199-294.
 815; PubMed=7524663;
 ar R., Rio D.C., Memmer D.E.;
 signments and solution structure of the second
 dmain of sex-lethal determined by multidimensional
 magnetic resonance.";
 33:13775-13786(1994).
 NMR OF 122-209.
 155; PubMed=9299339;
 Y., Sakamoto H., Kigawa T., Takio K., Shimura Y.,
 stic arrangement of aromatic amino acid residues in the
 ture of the amino-terminal RNA-binding domain of
 (-lethal.";
 272:82-94(1997).
 Sex determination switch protein which controls sexual
 it by sex-specific splicing. Regulates dosage
 on in females by suppressing hyperactivation of X-linked
 pression of the embryo-specific isoform is under the
 ; primary sex-determining signal, which depends on the
 ; Chromosomes relative to autosomes (X:A ratio).
 occurs in 2X:2A cells, but not in X:2A cells. The X:A
 is to be signaled by the relative concentration of the X-
 uscription factors SIS-A and SIS-B. As a result, the
 ific product is expressed early only in female embryos
 ies female-adult specific splicing, in the male where it
 pressed, the default splicing gives rise to a truncated
 nal protein. The female-specific isoform specifies the
 if its own transcript, thereby initiating a positive
 itory feedback loop leading to female development
 he female-specific isoform controls the sex-specific
 of transformer (TRA); acts as a translational repressor
 specific lethal-2 (MSL-2) and prevents male-less (MLE),
 MSL-3 proteins from associating with the female X
 .
 E PRODUCTS:
 rnative splicing; Named isoforms=5;

CC Comment=Additional isoforms seem to exist;
 CC Name=MS3; Synonyms=A, CF1;
 CC IsoId=P19339-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=P19339-2; Sequence=VSP_005881;
 CC Name=CMI;
 CC IsoId=P19339-3; Sequence=VSP_005882, VSP_005884;
 CC Name=MS11;
 CC IsoId=P19339-4; Sequence=VSP_005883, VSP_005885;
 CC Name=MS16;
 CC IsoId=P19339-5; Sequence=VSP_005886;
 CC -!- TISSUE SPECIFICITY: Expressed in somatic tissues, but not in
 CC pole cells, which are the precursors of the germline.
 CC -!- DEVELOPMENTAL STAGE: Isoform 1 is embryo-specific. Isoform C
 CC male-specific. Isoforms MS3, MS11 and MS16 are female specific.
 CC Isoform 1 is expressed for a brief period during the syncyti-
 CC blastoderm stage. Isoform MS11 is expressed in 4-7 hours emb;
 CC interaction with RNA and for regulating the splicing activity;
 CC -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M23635; AAA28885.1; -;
 CC EMBL; M23636; AAA28884.1; -;
 CC EMBL; M59447; AAA28922.1; -;
 CC EMBL; M59448; AAA28921.1; -;
 CC EMBL; AE003439; AAG22410.1; -;
 CC EMBL; AE003439; AAG22411.1; -;
 CC EMBL; BT003583; AAO39587.1; -;
 CC EMBL; S88324; AAB21845.1; -;
 CC EMBL; D84425; BAA20294.1; -;
 CC PIR; A31639; A31639.
 CC PIR; A39725; B31639.
 CC PDB; 1SXU, 30-SEP-94.
 Query Match 1.5%; Score 8; DB 1; Length 354;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 212 PPPQPPA 219
 Db 313 PPPQPPA 320
 |||||
 |||||
 RESULT 126
 IF35 HUMAN
 ID IF35_HUMAN STANDARD; PRT; 357 AA.
 AC O00303;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsil-
 DE (eIF3 p47 subunit) (eIF3F).
 GN EIF3S5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98001678; PubMed=9341143;
 RA Asano K., Vornlocher H.-P., Richter-Cook N.J., Merrick W.C.,
 RA Hinnebusch A.G., Hershey J.W.B.;
 RT "Structure of cDNAs encoding human eukaryotic initiation factor 3
 RT subunits. Possible roles in RNA binding and macromolecular assembl

15-MAR-2004 (Rel. 43, Last annotation update)
Wnt-9b protein precursor (Wnt-15) (Wnt-14b).
WNT9B OR WNT15 OR WNT14B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21646332; PubMed=11786923;
RX Krikosian H., Katoh M.;
RA "Molecular cloning and characterization of mouse Wnt14b, clusters;
RT with mouse Wnt3 in mouse chromosome 11.";
RL Int. J. Mol. Med. 9:135-139(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/c;
RX MEDLINE=22461584; PubMed=12573259;
RA Qian J., Jiang Z., Li M., Heaphy P., Liu Y.H., Shackelford G.M.;
RT "Mouse Wnt9b transforming activity, tissue-specific expression,
RT evolution.";
RL Genomics 81:34-46(2003).
[3]
RN SEQUENCE OF 211-310 FROM N.A.
RX MEDLINE=98110581; PubMed=9441749;
RA Bergstein I., Eisenberg L.M., Bhalarao J., Jenkins N.A.,
RA Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
RT "Isolation of two novel WNT genes, WNT14 and WNT15, one of which
RT (WNT15) is closely linked to WNT3 on human chromosome 17q21.";
RL Genomics 46:450-458(1997).
CC -!- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters (By similarity).
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with
CC extracellular matrix.
CC -!- SIMILARITY: Belongs to the Wnt family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB073819; BAB83866.1; -;
CC EMBL; AF469004; AAL82385.1; -;
CC EMBL; AF031169; AAC39950.1; -;
CC MGD; MGI:1197020; Wnt9b.
CC InterPro; IPR005817; Wnt.
CC Pfam; PF00110; wnt; 2.
CC PRINTS; PR01349; WntPROTEIN.
CC SMART; SM00097; WNT1; 1.
CC PROSITE; PS00246; WNT1; 1.
CC Wnt signaling pathway; Developmental protein; Glycoprotein; Signa
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 359 WNT-9B PROTEIN.
CC CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
CC CONFLICT 310 310 D -> G (IN REF. 3).
CC SEQUENCE 359 AA; 38981 MW; C98D7B5F566B70F5 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; C

QY 119 PAAAAAAA 126
Db 18 PAAAAAAA 25

STANDARD; PRT; 359 AA.
0;
Rel. 36, Created)
Rel. 42, Last sequence update)

11:33:41 2004

us-09-976-740-43.olig.rsp

STANDARD; PRT; 372 AA.

4;
Rel. 23, Created)
Rel. 23, Last sequence update)
Rel. 40, Last annotation update)
wth/differentiation factor 1 precursor (GDF-1).
(Human).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
neria; Primates; Catarrhini; Hominidae; Homo.
36;

N.A.
545; PubMed=2034669;

growth/differentiation factor 1 in the nervous system;
of a bicistronic structure.";
ad. Sci. U.S.A. 88:4250-4254 (1991).

N.A.
McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Stensen M., Kyle A., Ramirez M., Stillwagen S.,
Nolan M., Truong S., Olsen A.O., Carrano A.V.,
1-1998) to the EMBL/GenBank/DBJ databases.
May mediate cell differentiation events during embryonic

homodimer; disulfide-linked (By similarity).
AR LOCATION: Secreted.
XIFICITY: Expressed in the brain.
; Belongs to the TGF-beta family.

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ul to license@isb-sib.ch).

AAAS8501.1;
; AAB94786.1;
39364.
1BMP.
14; GDF1.

; C:extracellular; ISS.
; F:cytokine activity; ISS.
; F:growth factor activity; ISS.
; P:cell differentiation; ISS.
02400; GF_cysknot.
02405; Inhibin_alpha.
01839; TGFb.
TGF-beta; 1.
8; GFCYSKNOT.
9; INHIBINA.
57; TGFb; 1.
; TGFb; 1.
50; TGF_BETA; 1.

factor; Cytokine; Glycoprotein.
factor; POTENTIAL.
1 29
0 253
4 372
EMRYONIC GROWTH/DIFFERENTIATION FACTOR
1.
7 337 BY SIMILARITY.
6 369 BY SIMILARITY.
0 371 BY SIMILARITY.
6 336 INTERCHAIN (BY SIMILARITY).
5 206 N-LINKED (GLCNAC. .) (POTENTIAL).
2 158 POLY-ALA.
9 118 V -> A (IN REF. 2).

SQ SEQUENCE 372 AA; 39502 MW; 10A484A406304232 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G

Qy 120 AAAAAAAP 127
Db 152 AAAAAAAP 159

RESULT 129

HXA2 HUMAN STANDARD; PRT; 376 AA.
AC O43364;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Hox-A2.
GN HOXA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jones K., Hinds K., Hawkins M., Duckels G.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is par
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC PROBOSCIPEDIA SUBFAMILY.

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EMBL; AC004079; -; NOT_ANNOTATED_CDS.
HSSP; P14653; 1B72.
TRANSFAC; T03317;
Genew; HGNC:5103; HOXA2.

MIM; 604685;
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambdarepressr.
Pfam; PF00046; homeobox; 1
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation; Polymorphism.
FT SITE 94 99 ANTP-TYPE HEXAPEPTIDE.
FT DNA BIND 143 202 HOMEBOX.
FT VARIANT 196 196 M -> L (in dbSNP:941002).
/FTID=VAR_011880.

SQ SEQUENCE 376 AA; 41001 MW; 78EB388FE1EEAD72 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Ga

Qy 151 AAAAAATA 158

|||||
AAATA 119

STANDARD; PRT; 377 AA.

(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
tein Chx10 (Chx-10 homeodomain containing homolog).
s (Chicken).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

031;

M N.A.
8593; PubMed=10640715;
, Cepko C.L.;
of Chx10 and Chx10-1 in the developing chicken retina.";
0:293-297(2000).
: Plays a significant role in the specification and
nesis of the sensory retina. May also participate in the
ent of the cells of the inner nuclear layer, particularly
cells (By similarity).
LAR LOCATION: Nuclear (By similarity).
PECIFICITY: Retina and spinal cord.
ENTAL STAGE: Expressed throughout the invaginating optic
at stage 12, and uniformly throughout the neural retina
age 14 to stage 18. Expressed in the spinal cord from stage
age 20.
TY: Belongs to the paired homeobox family.
TY: Contains 1 CVC domain.
TY: Contains 1 homeobox domain.
TY: Contains 1 OAR domain.

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71; AAF40313.1; -
1FJL.
1342; -
003654; Homeo OAR.
001356; Homeobox.
007104; Paired_homeo.
; Homeobox; 1.
; OAR; 1.
010; Homeobox; 1.
9; HOX; 1.
027; HOMEBOX_1; 1.
071; HOMEBOX_2; 1.
803; OAR; 1.
regulation; Vision; Developmental protein;
in; Homeobox; DNA-binding.
67 226 HOMEBOX.
128 280 CVC.
123 336 OAR.
11 110 PRO-RICH.
36 158 SER/THR-RICH.
52 365 GLU/ASP-RICH (ACIDIC).
77 AA; 40645 MW; 1FCD9EF4664A3C21 CRC64;

1.5%; Score 8; DB 1; Length 377;
arity 100.0%; Pred. No. 61;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 AAAAAPP 129
Db 22 AAAAAPP 29

RESULT 131

SOX1_HUMAN
ID -SOX1_HUMAN STANDARD; PRT; 387 AA.
AC 000570;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SOX-1 protein.
GN SOX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98051911; PubMed=9337405;
RA Malas S., Duthie S.M., Mohri F., Lovell-Badge R., Episkopou V.;
RT "Cloning and mapping of the human SOX1: a highly conserved gene
expressed in the developing brain.";
RL Mamm. Genome 8:866-868(1997).
CC -! SUBCELLULAR LOCATION: Nuclear (Probable).
CC -! TISSUE SPECIFICITY: Mainly in the developing central nervous
system.
CC -! SIMILARITY: Contains 1 HMG box domain.
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EMBL; Y13436; CAA73847.1; -
HSP; Q05086; LHRV.
Genew; HGNC:11189; SOX1.
MIM; 602148; -
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; P:transcription factor activity; NAS.
GO; GO:0006325; P:establishment and/or maintenance of chromatin;
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NA
InterPro; IPR000910; HMG_box; 1.
Pfam; PF00505; HMG_box; 1.
SMART; SM00398; HMG; 1.
PROSITE; PS01118; HMG_BOX_2; 1.
DNA-binding; Nuclear protein.
FT DOMAIN 27 43 POLY-GLY.
FT DNA_BIND 51 119 HMG_BOX.
FT DOMAIN 145 150 POLY-GLY.
FT DOMAIN 197 204 POLY-ALA.
FT DOMAIN 280 287 POLY-ALA.
FT DOMAIN 292 302 POLY-ALA.
FT DOMAIN 353 360 POLY-ALA.
SQ SEQUENCE 387 AA; 38855 MW; 8D43A38002CE3494 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; C

QY 119 PAAAAAA 126
Db 352 PAAAAAA 359

RESULT 132

MBNL_HUMAN
ID MBNL_HUMAN STANDARD; PRT; 388 AA.

rel. 41, Created)
 rel. 41, Last sequence update)
 rel. 42, Last annotation update)
 ke protein (triplet-expansion RNA-binding protein).
 OR EXP OR KIAA0428.
 (Human).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Primates; Catarrhini; Hominidae; Homo.
 16;
 N.A. (ISOFORM 1).
 rbieri A.;
 1-1997) to the EMBL/GenBank/DBJ databases.
 N.A. (ISOFORM 2).
 155; PubMed=9455477;
 . Nagase T., Nakajima D., Seki N., Ohira M.,
 Tanaka A., Kotani H., Nomura N., Ohara O.;
 : the coding sequences of unidentified human genes. VIII.
 : ones from brain which code for large proteins in
 7-313(1997).
 N.A. (ISOFORM 3), ALTERNATIVE SPLICING, AND
 ON.
 it4; PubMed=10970838;
 Irbinati C.R., Teng-Umuay P., Stenberg M.G., Byrne B.J.,
 Swanson M.S.;
 of human muscleblind proteins to (CUG) (n) expansions
 h myotonic dystrophy.";
 19-4448(2000).
 Binds to CUG triplet repeat expansion dsRNA.
 AR LOCATION: Nuclear.
 E PRODUCTS:
 ernative splicing; Named isoforms=3;
 ;
 ; NR56-1; Sequence=Displayed;
 ;
 ; NR56-2; Sequence=VSP_006430;
 ;
 ; NR56-3; Sequence=VSP_006429, VSP_006430;
 uscular dystrophy may be caused by aberrant recruitment
 ; the DMPK transcript (CUG) (n) expansion.
 ; Contains 4 C3H1-type zinc fingers.
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 CAA74155.1; -;
 ; BAA74858.1; -;
 ; AAF76138.1; -;
 ; 23; MEN11.
 ; C:cytoplasm; IDA.
 ; C:nucleus; IDA.
 ; F:double-stranded RNA binding; IDA.
 ; P:embryonic development (sensu Mammalia); ISS.
 ; P:limb morphogenesis; ISS.
 ; P:muscle development; ISS.
 ; P:myoblast differentiation; ISS.
 ; P:neurogenesis; ISS.
 100571; Znf.CCCH.
 ; Znf.CCCH; 4.
 ; Znf.C3H1; 4.
 ; Repeat; Nuclear protein; RNA-binding;
 icking.

FT ZN_FING 14 40 C3H1-TYPE 1.
 FT ZN_FING 47 72 C3H1-TYPE 2.
 FT ZN_FING 179 206 C3H1-TYPE 3.
 FT ZN_FING 216 240 C3H1-TYPE 4.
 FT VARSPLIC 116 183 Missing (in isoform EXP35).
 FT /FTId=VSP_006429.
 FT VARSPLIC 270 287 Missing (in isoform EXP35 and isoform
 FT EXP40).
 FT /FTId=VSP_006430.
 SQ SEQUENCE 388 AA; 41817 MW; 118D256A81A86695 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 119 PAAAAAAA 126
 Db 166 PAAAAAAA 173
 RESULT 133
 SOX1_MOUSE
 ID_SOX1_MOUSE STANDARD; PRT; 391 AA.
 AC P53783;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SOX-1 protein.
 GN SOX1 OR SOX-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=96189340; PubMed=8255802;
 RA Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M.,
 RA Norris D., Rastan S., Stevanovic M., Goodfellow P.N.,
 RA Lovell-Badge R.;
 RT "A comparison of the properties of Sox-3 with Sry and two related
 RT genes, Sox-1 and Sox-2.";
 RL Development 122:509-520(1996).
 CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -|- TISSUE SPECIFICITY: Mainly in the developing central nervous
 CC system. Expressed in developing urogenital ridge.
 CC -|- SIMILARITY: Contains 1 HMG box domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X94126; CAA63846.1; -;
 CC DR HSSP; Q05066; 1HRY.
 CC DR MGD; MGI:98357; Sox1.
 CC DR InterPro; IPR000910; HMG_12_box.
 CC DR Pfam; PF00505; HMG_box; 1.
 CC DR SMART; SM00398; HMG; 1.
 CC DR PROSITE; PS0118; HMG_BOX_2; 1.
 CC KW DNA-binding; Nuclear protein.
 CC FT DOMAIN 30 43 POLY-GLY.
 CC FT DNA_BIND 51 119 HMG_BOX.
 CC FT DOMAIN 145 150 POLY-GLY.
 CC FT DOMAIN 197 204 POLY-ALA.
 CC FT DOMAIN 280 288 POLY-ALA.
 CC FT DOMAIN 296 306 POLY-ALA.
 CC FT DOMAIN 357 364 POLY-ALA.
 CC SQ SEQUENCE 391 AA; 39237 MW; 9FB1ED667F947C05 CRC64;

1.5%; Score 8; DB 1; Length 391;

larity 100.0%; Pred. No. 63; 0; Mismatches 0; Indels 0; Gaps 0;

AAAAA 126

|||||

AAAAA 363

STANDARD; PRT; 392 AA.

(Rel. 28, Created)

(Rel. 40, Last sequence update)

(Rel. 41, Last annotation update)

ein engrailed-1 (Hu-En-1).

(Human).

stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

theria; Primates; Catarrhini; Hominidae; Homo.

506;

4 N.A.

3339; PubMed=1363401;

ks M.C., Noble-Topham S., Nallainathan D.,

Joyner A.L.;

sequence comparison of the mouse, human, and chicken

ies reveal potential functional domains and regulatory

3:345-358(1992).

288.

ks M.C., Noble-Topham S., Nallainathan D., Provart N.J.,

R-2000) to the EMBL/GenBank/DBJ databases.

AR LOCATION: Nuclear.

Y: Belongs to the engrailed homeobox family.

Y: Contains 1 homeobox domain.

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ail to license@isb-sib.ch).

AAA53502.2; -

AAA53502.2; JOINED.

B48423.

3HDD.

1015; -

1342; EN1.

5; P-embryogenesis and morphogenesis; TAS.

1; P-skeletal development; TAS.

000747; Engrailed.

001356; Homeobox.

000047; HTH lambrapressr.

1; homeobox; 1.

126; ENGRAILED.

124; HOMEBOX.

131; HTHREPRESSR.

1010; Homeobox; 1.

19; HOX; 1.

027; HOMEBOX 1; 1.

071; HOMEBOX 2; 1.

033; ENGRAILED; 1.

1-binding; Developmental protein; Nuclear protein.

99 218 POLY-ALA.

124 231 POLY-GLY.

103 362 HOMEBOX.

SQ SEQUENCE 392 AA; 40101 MW; DESE63E7BFC7B51 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 63;

Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126

|||||

Db 198 PAAAAAAA 205

RESULT 135

HGHI_YEAST

ID HGHI_YEAST STANDARD; PRT; 394 AA.

AC P48362;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE HGHI protein.

GN HGHI OR YGR187C OR G7538.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE OF 111-394 FROM N.A.

RA Sun Z., Liang J., Hampsey M.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RC SEQUENCE FROM N.A.

RC STRAIN=S288c;

RX MEDLINE=97279231; PubMed=9133739;

RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M

RA Nombela C.;

RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right

of Saccharomyces cerevisiae chromosome VII.";

RL Yeast 13:357-363(1997).

CC -!- SIMILARITY: TO S.POMBE SPAC26F1.12C.

CC

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CC

DR EMBL; U27358; AAA77038.1; -

DR EMBL; 272972; CAA97213.1; -

DR EMBL; X99074; CAA67531.1; -

DR PIR; S64505; S64505.

DR Germline; 141499; -

DR SGD; S0003419; HGHI.

DR InterPro; IPR008938; ARM.

DR InterPro; IPR007205; DUF383.

DR InterPro; IPR007206; DUF384.

DR Pfam; PF04063; DUF383; 1.

DR Pfam; PF04064; DUF384; 1.

FT DOMAIN 371 389

SQ SEQUENCE 394 AA; 44951 MW; 24D4EFAED5D7A48 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 64;

Matches 8; Conservative 0; Mismatches 0; Indels 0; C

QY 329 EEEEDDE 336

|||||

Db 379 EEEEDDE 386

RESULT 136

KIM4_HUMAN

ID KIM4_HUMAN STANDARD; PRT; 394 AA.

rel. 39, Created)
 rel. 39, Last sequence update)
 rel. 40, Last annotation update)
 I cuticular HA4 (Hair keratin, type I HA4).
 I OR HHA4.
 (Human).
 :azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 :eria; Primates; Catarrhini; Hominidae; Homo.
);
 N.A. PubMed=9756910;
 582; PubMed=9756910;
 Winter H., Wolf C., Heck M., Schweizer J.;
 tion of a 190-kilobase pair domain of human type I hair
 .".
 . 273:26683-26691(1998).
 30US: THERE ARE TWO TYPES OF HAIR/MICROFIBRILLAR KERATIN,
 I AND II (NEUTRAL TO BASIC).
 f: Belongs to the intermediate filament family.

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 ail to license@isb-sib.ch).

 CAA76386.1; -.
 i52; KRTHAA.
 .
 i; P:epidermal differentiation; TAS.
 301664; IF.
 002957; Keratin_I.
 ; filament; I.
 i8; TYPE1KERATIN.
 226; IF; 1.
 Filament; Coiled coil; Keratin.
 1 56
 57 ROD.
 54 394
 57 91
 32 102
 32 203
 34 219
 20 363
 35 305
 STUTTER.
 i AA; 44689 MW; A651BF32918A98BF CRC64;
 1.5%; Score 8; DB 1; Length 394;
 arity 100.0%; Pred.No. 64;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
 CLIQ 78
 ||||
 CLIQ 89
 STANDARD; PRT; 395 AA.
 Rel. 32, Created)
 Rel. 32, Last sequence update)
 Rel. 41, Last annotation update)
 ryotic translation initiation factor 5 (eIF-5).
 myces pombe (Fission yeast).
 :gi; Ascomycota; Schizosaccharomycetes;
 :mycetaceae; Schizosaccharomycetaceae;
 :myces.
 36;

RN SEQUENCE FROM N.A.
 RP STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitea
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
 RA Weltjens I., Vanneste E., Rieger M., Schaefer M., Mueller-Auer
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhod
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Spakovski G.V., Usery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 Nature 415:871-880(2002).
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: Catalyzes the hydrolysis of GTP bound to the 40S
 CC ribosomal initiation complex (40S.mRNA.Met-tRNA[eIF-2.GTP]
 CC the subsequent joining of a 60S ribosomal subunit resulting i
 CC release of eIF-2 and the guanine nucleotide. The subsequent
 CC joining of a 60S ribosomal subunit results in the formation o
 CC functional 80S initiation complex (80S.mRNA.Met-tRNA[eIF] (By
 CC similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.

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 CC EMBL; Z50142; CAA90492.1; -.
 DR PIR; T38553; S59149.
 DR GenDB SPombe; SPAC2F7.05c; -.
 DR InterPro; IPR002735; eIF5_eIF2B.
 DR InterPro; IPR003307; eIF5C.
 DR Pfam; PF01873; eIF5_eIF2B; 1.
 DR Pfam; PF02020; W2; 1.
 DR ProDom; PD004078; eIF5_eIF2B; 1.
 DR SMART; SM00653; eIF2B_5; 1.
 DR SMART; SM00515; eIF5C; 1.
 DR KW Hypothetical protein; Initiation factor; Protein biosynthesis;
 KW GTP-binding.
 FT NP BIND 28 35 GTP (POTENTIAL).
 FT DOMAIN 379 395 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT SEQUENCE 395 AA; 44944 MW; 18F49CB3CC8C2D11 CRC64;
 SQ
 Query Match 1.5%; Score 8; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred.No. 64;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; G
 QY 329 EEEEDDDE 336
 Db 388 EEEEDDDE 395

STANDARD; PRT; 396 AA.
(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 38, Last annotation update)
Retinal S-antigen (Rod photoreceptor arrestin).
is (African clawed frog).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
crachia; Anura; Mesobatrachia; Pipidae;
Xenopus.
355;
4 N.A.
a;
a S., Knox B.E.;
EC-1995) to the EMBL/GenBank/DBJ databases.
: Arrestin is one of the major proteins of the rod
rod outer segments; it binds to photoactivated-
ylated rhodopsin, thereby apparently preventing the
in-mediated activation of phosphodiesterase.
NEOUS: Arrestin binds calcium.
TY: Belongs to the arrestin family.
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: AAB88584.1; -;
: 1CF1.
3000698; Arrestin.
3007110; Ig-like.
; arrestin; 1.
; arrestin; 1.
; arrestin; 1.
309; ARRESTIN.
3099; Arrestin; 1.
3295; ARRESTINS; 1.
duction; Vision; Calcium-binding.
36 AA; 44623 MW; 3408AG5280CE7C14 CRC64;
1.5%; Score 8; DB 1; Length 396;
larity 100.0%; Pred. No. 64;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3EEDD 334
|||||
3EEDD 394
STANDARD; PRT; 396 AA.
(Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 42, Last annotation update)
1 factor SOX-11.
3 (Chicken).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
331;
4 N.A.
; 7693; PubMed-7748786;
Rex M., Cartwright E.J., Pearl G., Healy C.,
Scotting P.J., Sharpe P.T.;
"Embryonic expression of the chicken Sox2, Sox3 and Sox11 genes
suggests an interactive role in neuronal development.";
Mech. Dev. 49:23-36(1995).
-!- FUNCTION: May function as switches in neuronal development.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Low level expression is seen in
undifferentiated proliferating cells of neural epithelium. A
greater expression is seen in the maturing neurons after the
leave the neural epithelium. It is also found in the gut
epithelium and adrenal medulla.
-!- SIMILARITY: Contains 1 HMG box domain.

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or send an email to license@isb-sib.ch).

CC EMBL; U12534; AAB09664.1; -;
DR PIR; I50707; I50707.
DR HSSP; P48436; LSX9.
DR InterPro; IPR000910; HMG 12 box.
DR Pfam; PF00505; HMG box; 1.
DR SMART; SM00398; HMG; 1.
DR PROSITE; PS0118; HMG BOX 2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DNA BIND 49 117 HMG BOX.
FT DOMAIN 162 165 POLY-ALA.
FT DOMAIN 204 212 POLY-GLU.
FT DOMAIN 288 294 POLY-PRO.
FT DOMAIN 332 335 POLY-ARG.
SQ SEQUENCE 396 AA; 43503 MW; 8E4B0A457F8BA833 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 212 PPPQPPA 219
Db 288 PPPQPPA 295
RESULT 140
HXAA MOUSE STANDARD; PRT; 399 AA.
AC P31310;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A10 (Hox-1.8).
GN HOXA10 OR HOXA-10 OR HOX-1.8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1; TISSUE-Kidney;
RX MEDLINE=95166244; PubMed=7862151;
RA Benson G.V., Nguyen T.-H.E., Maas R.L.;
RT "The expression pattern of the murine Hoxa-10 gene and the sequel
recognition of its homeodomain reveal specific properties of
Abdominal B-like genes";
RL Mol. Cell. Biol. 15:1591-1601(1995).
RN [2]
RP SEQUENCE OF 325-384 FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";

ad. Sci. U.S.A. 88:10706-10710(1991).

{6-370 FROM N.A.

{7: TISSUE=Spleen;

{57: PubMed=1720547;

Leckman J.F., Ruddle F.H.;

homeobox genes in development and evolution.";

ad. Sci. U.S.A. 88:10711-10715(1991).

SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

MENTAL-REGULATORY SYSTEM THAT PROVIDES CELLS WITH

POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.

AR LOCATION: Nuclear.

FE PRODUCTS:

alternative splicing; Named isoforms=2;

{1310-1; Sequence=Displayed;

{1310-2; Sequence=VSP_002386, VSP_002387;

SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT

ATED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.

) IN DEVELOPING GUT AND UROGENITAL TRACT. IN ADULT

OTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM 1 IS EXPRESSED

AL MUSCLE.

ITAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9 TO

) THEN DECLINES TO DAY 15.

): Belongs to the Abd-B homeobox family.

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AAA67125.1; -;

AAA63312.1; -;

.49754.

9ANT.

715; -;

.. Hoxa10.

01356; Homeobox.

homeobox; 1.

14; HOMEBOX.

110; Homeobox; 1.

); HOX; 1.

127; HOMEBOX 1; 1.

171; HOMEBOX 2; 1.

binding; Developmental protein; Nuclear protein;

regulation; Alternative splicing.

16 38 GLY-RICH.

77 90 POLY-GLY.

3 144 GLN/PRO-RICH.

5 222 POLY-GLY.

71 274 POLY-GLY.

15 384 HOMEBOX.

1 305 Missing (in isoform 2).

/FTID=VSP_002386.

16 308 DSL -> MCQ (in isoform 2).

/FTID=VSP_002387.

) AA; 41415 MW; 7529624FC6057042 CRC64;

1.5%; Score 8; DB 1; Length 399;

arity 100.0%; Pred. No. 64;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

QPOP 233

||||

QPOP 124

HME1 MOUSE

ID HME1 MOUSE STANDARD; PRT; 401 AA.

AC P09065;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein engrailed-1 (Mo-En-1).

GN EN1 OR EN-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93185339; PubMed=1363401;

RA Logan C., Hanks M.C., Noble-Topham S., Nallainathan D.,

RA Provart N.J., Joyner A.L.;

RT "Cloning and sequence comparison of the mouse, human, and chicken

RT engrailed genes reveal potential functional domains and regulator

RT regions.";

RL Dev. Genet. 13:345-358(1992).

RN [2]

RP SEQUENCE OF 278-401 FROM N.A.

RX MEDLINE=88112776; PubMed=2892757;

RA Joyner A.L., Martin G.R.;

RT "En-1 and En-2, two mouse genes with sequence homology to the

RT Drosophila engrailed gene: expression during embryogenesis.";

RL Genes Dev. 1:29-38(1987).

RN [3]

RP SEQUENCE OF 298-401 FROM N.A.

RX MEDLINE=86079501; PubMed=2416459;

RA Joyner A.L., Kornberg T., Coleman K.G., Cox D.R., Martin G.R.;

RT "Expression during embryogenesis of a mouse gene with sequence

RT homology to the Drosophila engrailed gene.";

RL Cell 43:29-37(1985).

RN [4]

RP SEQUENCE OF 321-380 FROM N.A.

RX MEDLINE=91099509; PubMed=1980115;

RA Holland P.W.H., Williams N.A.;

RT "Conservation of engrailed-like homeobox sequences during vertebr

RT evolution.";

RL FEBS Lett. 277:250-252(1990).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: Belongs to the engrailed homeobox family.

CC -!- SIMILARITY: Contains 1 homeobox domain.

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EMBL; L12703; AAA03660.2; -;

DR EMBL; Y00201; CAA68361.1; -;

DR PIR; A48423; A48423.

DR HSP; P02836; 3HDD.

DR TRANSFAC; T02016; -;

DR MGD; MGI:95389; Enl.

DR InterPro; IPR000747; Engrailed.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR000047; HTH lambrepressr.

DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00026; ENGRAILED.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PS50071; HOMEBOX_2; 1.

DR PROSITE; PS00033; ENGRAILED; 1.

KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.

52 87 PRO-RICH.
73 87 POLY-PRO.
207 228 POLY-ALA.
312 371 HOMEBOX.
11 AA; 40950 MW; 1F90210950152FAE CRC64;
1.5%; Score 8; DB 1; Length 401;
arity 100.0%; Pred. No. 65;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 213
STANDARD; PRT; 405 AA.
35: Q9R221;
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
centiation factor 11 precursor (GDF-11) (Bone
protein 11).
(Mouse).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0990;
4 N.A.
7155; PubMed=10075854;
Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
expressed in developing mouse limb, spinal cord, and tail
ant mesoderm inducer in Xenopus embryos.";
82:222-232(1999).
4 N.A.
3097; PubMed=10391213;
J., Lawler A.M., Lee S.-J.,
of anterior/posterior patterning of the axial skeleton by
centiation factor 11.";
22:260-264(1999).
75-405 FROM N.A.
3787; PubMed=10072786;
Toyono T., Akanine A., Joyner A.,
of growth/differentiation factor 11, a new member of the
superfamily during mouse embryogenesis.";
0:185-189(1999).
: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
TICAL ROLBS IN PATTERNING BOTH MESODERMAL AND NEURAL
AND IN ESTABLISHING THE SKELETAL PATTERN.
Homodimer; disulfide-linked (by similarity).
LAR LOCATION: Secreted (probable).
PECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
Y DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
NS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
ULP AND BRAIN
ENTAL STAGE: First strongly expressed in restricted
at 8.5 dpc where it is highest in the tail bud. At 10.5
ressed in the branchial arches, limb bud, tail bud and
r dorsal neural tube. Later, expressed in terminally-
tiated odontoblasts, the nasal epithelium, retina and
regions of the brain.
Ty: Belongs to the TGF-beta family.
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CC -----
CC EMBL; AF100906; AAC72853.1;
CC EMBL; AF100904; AAC72853.1; JOINED.
CC EMBL; AF100905; AAC72853.1; JOINED.
CC EMBL; AF028337; AAF21633.1;
CC EMBL; AF028335; AAF21633.1; JOINED.
CC EMBL; AF028336; AAF21633.1; JOINED.
CC EMBL; AF028334; AAF21633.1; JOINED.
CC HSP; P18075; BMP.
CC MGD; MG1:1338027; Gdf11.
CC GO; GO:0005615; C:extracellular space; IDA.
CC GO; GO:0001656; P:metanephros development; IDA.
CC InterPro; IPR001839; TGFb.
CC InterPro; IPR001111; TGFb N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00888; TGF-beta; 1.
CC ProDom; PD000357; TGFb; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF BETA 1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 20
CC PROPEP 21 236
CC CHAIN 297 405
CC DOMAIN 29 39
CC DOMAIN 208 213
CC DISULFID 311 370
CC DISULFID 339 402
CC DISULFID 343 404
CC DISULFID 369 369
CC CARBOHYD 92 92
CC CONFLICT 75 75
CC CONFLICT 171 171
CC SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 119 PAAAAAA 126
Db 28 PAAAAAA 35
RESULT 143
ID GDFB_HUMAN STANDARD; PRT; 407 AA.
AC Q95390; Q9UID1; Q9UID2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 11 precursor (GDF-11) (Bone
DE morphogenetic protein 11).
GN GDF11 OR BMP11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99177155; PubMed=10075854;
RA Gamen L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.
RA Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, an
RT bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=99318097; PubMed=10391213;
RX

Lawler A.M., Lee S.-J.;
anterior/posterior patterning of the axial skeleton by
entiation factor 11.";
2:260-264(1999).
SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
ICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
ND IN ESTABLISHING THE SKELETAL PATTERN.
Homodimer; disulfide-linked (By similarity).
AR LOCATION: Secreted (Probable).
Y: Belongs to the TGF-beta family.
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ail to license@isb-sib.ch).
7; AAC72852.1; -;
3; AAF21630.1; -;
4; AAF21631.1; -;
BMP.
216; GDF11.
5; F: cytokine activity; NAS.
3; P: mesoderm development; TAS.
3; P: neurogenesis; TAS.
1; P: skeletal development; TAS.
001839; TGFb.
00111; TGFb.N.
; TGF-beta; 1.
; TGFb propeptide; 1.
357; TGFb; 1.
4; TGFb; 1.
250; TGF BETA 1; 1.
; Cytokine; Glycoprotein; Signal.
1 24
25 298 BY SIMILARITY.
39 407 GROWTH/DIFFERENTIATION FACTOR 11.
29 41 POLY-ALA.
10 215 POLY-GLY.
13 372 BY SIMILARITY.
41 404 BY SIMILARITY.
45 406 BY SIMILARITY.
71 371 INTERCHAIN (BY SIMILARITY).
94 94 N-LINKED (GLCNAC...) (POTENTIAL).
7 AA; 45090 MW; E8FF48E3635BA8 CRC64;
1.5%; Score 8; DB 1; Length 407;
arity 100.0%; Pred.No. 65;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 35
STANDARD; PRT; 407 AA.
rel. 28, Created)
rel. 28, Last sequence update)
rel. 42, Last annotation update)
zinc finger protein ZK686.4 in chromosome III.
elegans.
azoa; Nematoidea; Chromadorea; Rhabditida; Rhabditoidae;
peloderinae; Caenorhabditis.
39;

SEQUENCE FROM N.A.
STRAIN=BX1stol N2;
MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Pavello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showksee
Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.
Sulston J., Thiermy-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
elegans".
RT Nature 368:32-38(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 C2H2-type zinc finger.
CC
CC This SWISS-PROT entry is copyright. It is produced through a coll
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or send an email to license@isb-sib.ch).
CC
CC
CC EMBL: L17337; AAA28220.1; -;
DR PIR: S44909; S44909.
DR WormPep; ZK686.4; CE00458.
DR InterPro; IPR007087; Znf C2H2.
DR InterPro; IPR003604; Znf U1.
DR SMART; SM00355; Znf C2H2_1.
DR SMART; SM00451; Znf U1; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW Hypothetical protein; Zinc-finger; DNA-binding; Metal-binding;
FT Nuclear protein.
FT ZN FING 280 304 C2H2-TYPE.
SQ SEQUENCE 407 AA; 47058 MW; 3DD7BE44966FC771 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 407;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; G
QY 330 EEDDDDED 337
Db 378 EEDDDDED 385
RESULT 145
BBH3 MOUSE
ID_BBH3 MOUSE STANDARD; PRT; 410 AA.
AC Q99PV5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Class B basic helix-loop-helix protein 3 (bHLHB3) (Differentially
DE expressed in chondrocytes protein 2) (mDEC2).
GN BHLHB3 OR DEC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092582; PubMed=11162494;
RA Fujimoto K., Shen M., Noshiro M., Matsubara K., Shingu S., Honda
Yoshida E., Suaridita K., Matsuda Y., Kato Y.;
RT "Molecular cloning and characterization of DEC2, a new member of
RT helix-loop-helix proteins".
RL Biochem. Biophys. Res. Commun. 280:164-171(2001).
CC -!- FUNCTION: May be a transcriptional repressor that represses b

activated transcription.
 Homodimerize.
 AR LOCATION: Nuclear (By similarity).
 PEPTIDITY: Expressed in skeletal muscle, brain and lung.
 Y: Contains 1 basic helix-loop-helix (bHLH) domain.
 Y: Contains 1 orange domain.

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90; BAB21503.1; -;
 JC7584.
 9704; Bhlhb3.
 9001092; HLH basic.
 9003650; Orange.
 9; HLH; 1.
 93; HLH; 1.
 91; ORANGE; 1.
 9888; HLH; 1.
 91 regulation; Repressor; DNA-binding; Nuclear protein.
 45 57
 BASIC DOMAIN.
 58 100
 HELIX-LOOP-HELIX MOTIF
 129 175
 ORANGE.
 321 373
 ALA/GLY-RICH
 10 AA; 43946 MW; 40A87281B08E233D CRC64;

1.5%; Score 8; DB 1; Length 410;
 arity 100.0%; Pred. No. 66;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAA 126
 |||||
 AAAAA 341

STANDARD; PRT; 410 AA.
 (Rel. 41, Created)
 (Rel. 41, Last sequence update)
 (Rel. 42, Last annotation update)
 2 helix-loop-helix protein 3 (bHLHB3) (Enhancer-of-split
 lated protein 1) (SHARP-1).
 ARP1.
 jicus (Rat).
 stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 cheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 0116;
 N.A.
 e-Dawley; TISSUE=Cerebellum;
 3761; PubMed=9532582;
 Doert J., Gass P., Schwab M.H., Nave K.-A.;
 nalian enhancer-of-split- and hairy-related proteins
 eutral stimulation.";
 euroscl. 10:460-475(1997).
 May be a transcriptional
 d activated transcription.
 Homodimerize.
 LAR LOCATION: Nuclear (By similarity).
 PEPTIDITY: Highly expressed in subregions of the brain,
 ly expressed in skeletal muscle, heart. Weakly expressed
 TY: Contains 1 basic helix-loop-helix (bHLH) domain.
 TY: Contains 1 orange domain.
 This is a conceptual translation; a frameshift was
 ed in position 249 to extend the similarity with mouse

ortholog.
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EMBL; AF009329; AAB63586.1; ALT_FRAME.
 InterPro; IPR001092; HLH basic.
 InterPro; IPR003650; Orange.
 Pfam; PF00010; HLH; 1.
 SMART; SM00353; HLH; 1.
 SMART; SM00511; ORANGE; 1.
 DR PROSITE; PS50888; HLH; 1.
 DR Transcription regulation; Repressor; DNA-binding; Nuclear protei-
 KW DNA_BIND 45 57
 BASIC DOMAIN
 FT DOMAIN 58 100
 HELIX-LOOP-HELIX MOTIF.
 FT DOMAIN 129 175
 ORANGE.
 FT DOMAIN 321 344
 ALA/GLY-RICH.
 SQ SEQUENCE 410 AA; 43917 MW; 829705CA3A013127 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 410;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;

QY 119 PAAAAAAA 126
 |||||
 Db 334 PAAAAAAA 341

RESULT 147
 ID HMH2 DROME STANDARD; PRT; 410 AA.
 AC F10035;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Homeobox protein H2.0.
 GN H2.0.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88329003; PubMed=2901348;
 RA Barad M., Jack T., Chadwick R., McGinnis W.;
 RT "A novel, tissue-specific, Drosophila homeobox gene.";
 RL EMBO J. 7:2151-2161(1988).
 CC -!- FUNCTION: May have an important role in the morphogenesis of
 CC single tissue type.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- TISSUE SPECIFICITY: Exhibits a tissue specific pattern of
 CC expression. It accumulates in cells of the visceral musculat
 CC and its anlagen.
 CC -!- SIMILARITY: Belongs to the H2.0 homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.

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EMBL; Y00843; CAA68766.1; -;
 PIR; S00994; WJFFH2.
 HSP; P06601; 1FJL.

0001170; H2.0.
001356; Homeobox.
000047; HTH lambdarepressor.
; homeobox; 1.
24; HOMEBOX.
31; HTHREPRESSOR.
010; Homeobox; 1.
9; HOX; 1.
027; HOMEBOX 1; 1.
071; HOMEBOX 2; 1.
-binding; Developmental protein; Nuclear protein.
80 204 HTS/GLN-RICH (OPA-REPEAT).
87 346 HOMEBOX.
0 AA; 44950 MW; D81E71395A12D5BD CRC64;
arity 1.5%; Score 8; DB 1; Length 410;
conservative 0; Mismatches 0; Indels 0; Gaps 0;
AAAA 126
|||||
AAAA 259
STANDARD; PRT; 412 AA.
Rel. 35; Created)
Rel. 35; Last sequence update)
Rel. 42; Last annotation update)
binding nuclear protein (EC 5.2.1.8) (Peptidyl-prolyl
merase) (PPIase) (Rotamase).
ugiperda (Fall armyworm).
tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
ophrygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
phypyrinae; Spodoptera.
08;
N.A.
110; PubMed=7527037;
Fernandes-Alnemri T., Pomeroy K., Robertson N.M.,
bois G.C., Litwack G.;
vel Sf9 insect cell nuclear immunophilin that forms a
complex.";
. 269:30828-30834(1994).
PPIases accelerate the folding of proteins. It catalyzes
rans isomerization of proline imidic peptide bonds in
ides. Binds double-stranded DNA in vitro.
ACTIVITY: Peptidylproline (omega=180) = peptidylproline
. SULFATION: Inhibited by both FK506 and rapamycin.
AR LOCATION: Nuclear.
phorylated by a nuclear kinase in the presence of Mg(2+)
f: Belongs to the FKBP-type PPIase family.
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AAA58962.1; -.
455320.
1FKJ.
001179; FKBP_PPIase.
; FKBP; 1.
153; FKBP_PPIASE 1; FALSE_NEG.
154; FKBP_PPIASE 2; 1.
DR PROSITE; PS50059; FKBP_PPIASE 3; 1.
KW Isomerase; Rotamase; Nuclear Protein; DNA-binding; Phosphorylati
FT DOMAIN 91 112 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 120 145 LYS-RICH (BASIC).
FT DOMAIN 152 216 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 219 302 LYS-RICH (BASIC).
FT DOMAIN 324 412 PPIASE, FKBP-TYPE.
SQ SEQUENCE 412 AA; 45810 MW; F2A69159AEF4FE22 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
QY 331 EEDDEDE 338
DB 194 EEDDEDE 201
RESULT 149
CRTC MOUSE
ID_CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211,
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A. AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=9005955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calreguli
RT HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9301303; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encod
RT ERP60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;

907; PubMed=7523108;
Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
and sequencing of familial and novel murine proteins
active two-dimensional gel electrophoresis.";
his 15:735-745(1994).

: This protein binds calcium. There are both high and
low calcium-binding sites.

Monomer (By similarity).

AR LOCATION: Endoplasmic reticulum lumen.

RY: Belongs to the calreticulin family.

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/ CAA33053.1; -

53; AAA37569.1; -

53; AAA03453.1; -

S06763.

: P14211; MOUSE.

52; Calr.

09; F:calcium ion binding; IDA.

R009033; Calret_calmex_P.

R001580; Calreticulin.

R008985; ConA like lec_gl.

R000886; ER_target_S.

2; calreticulin; 1.

002356; Calreticulin; 1.

526; CALRETICULIN.

1866; Calreticulin; 1.

0014; ER TARGET; 1.

0803; CALRETICULIN; 1.

0804; CALRETICULIN; 1.

805; CALRETICULIN REPEAT; 3.

reticulum; Calcium-binding; Repeat; Signal.

1 17

18 416 CALRETICULIN.

18 197 N-DOMAIN.

198 308 P-DOMAIN.

309 416 C-DOMAIN.

191 255 4 X APPROXIMATE REPEATS.

191 202 1-1.

210 221 1-2.

227 238 1-3.

244 255 1-4.

259 297 3 X APPROXIMATE REPEATS.

259 269 2-1.

273 283 2-2.

287 297 2-3.

351 407 ASP/GLU/LYS-RICH.

137 163 BY SIMILARITY.

413 416 PREVENT SECRETION FROM ER.

16 AA; 47994 MW; 24C03B00913408D8 CRC64;

larity 100.0%; Score 8; DB 1; Length 416;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EDDED 342

|||||

EDDED 399

STANDARD; PRT; 416 AA.

52;

(Rel. 10, Created)

(Rel. 16, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CAL
GN Calcium-binding protein 3) (CABP3).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Hanville D., Srikant C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product a
the Onchocerca volvulus antigen Ral-1";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported
the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum.";
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function i
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatids of rat
testis.";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin
autoimmune antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: This protein binds calcium. There are both high an
affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
hydroxybutyrate dehydrogenase.

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BA11345.1; -.
CAA37446.1; -.
CAA31987.1; ALT_SEQ.
CAA55890.1; -.
JH0819.
-FEB-02.
-OCT-02.
-OCT-02.
009033; Calret calnex P.
001580; Calreticulin.
008985; ConA like lec_gl.
000886; ER target_S.
; calreticulin; 1.
02356; Calreticulin; 1.
26; CALRETICULIN.
366; Calreticulin; 1.
014; ER TARGET; 1.
303; CALRETICULIN 1; 1.
304; CALRETICULIN 2; 1.
305; CALRETICULIN REPEAT; 3.
; aticulum; Calcium-binding; Repeat; Signal; 3D-structure.
1 17
-8 416 CALRETICULIN.
-8 197 N-DOMAIN.
-8 308 P-DOMAIN.
-9 416 C-DOMAIN.
-1 255 4 X APPROXIMATE REPEATS.
-1 202 1-1.
-0 221 1-2.
-7 238 1-3.
-4 255 1-4.
-9 297 3 X APPROXIMATE REPEATS.
-9 269 2-1.
-3 283 2-2.
-7 297 2-3.
-1 407 ASP/GLU/LYS-RICH.
7 163 BY SIMILARITY.
3 416 PREVENT SECTATION FROM ER.
AA; 47995 MW; 2E6713CED31A2970 CRC64;
1.5%; Score 8; DB 1; Length 416;
rity 100.0%; Pred.No.67;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
BED 342
|||
BED 399

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